METABOLOMICS AND ETHNOPHARMACOLOGY IN THE DEVELOPMENT OF HERBAL AND TRADITIONAL MEDICINE

EDITED BY: Sayeed Ahmad, Chandra Kant Katiyar, Pulok Kumar Mukherjee and

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METABOLOMICS AND ETHNOPHARMACOLOGY IN THE DEVELOPMENT OF HERBAL AND TRADITIONAL MEDICINE

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Editorial: Metabolomics and Ethnopharmacology in the Development of Herbal and Traditional Medicine

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Editorial on the Research Topic

Metabolomics and Ethnopharmacology in the Development of Herbal and Traditional Medicine

Herbal and traditional medicines are again gaining popularity around the world for the management of a variety of health problems. As the use of herbal/traditional medicines and other botanical products grows and more new products are introduced to the market, new and efficient methods to assess safety and efficacy become a major concern for researchers in drug development. It is important to understand the composition, safety, effectiveness, drug-drug or drug-food interactions, and also the possible side effects of traditionally used herbal medicines. The safety and efficacy data for herbal and traditional medicines are presently insufficient to meet the requirements for their worldwide use.

Traditional medicines are derived from local and empirical knowledge often transmitted orally and have been developed over generations. The traditional healers of Indian AYUSH (Ayurveda, Yoga, Naturopathy, Unani, Siddha, Sowa-Rigpa, and Homeopathy), traditional Chinese medicine (TCM), and other traditional systems of medicine mainly emphasize on holistic approaches with a focus on therapeutic practice and outcomes.

Metabolomics and the metabolomic profiling of herbal medicines and medicinal plants have provided new avenues of research in drug development. Metabolomic approaches allow the simultaneous identification of thousands of metabolites present in medicinal plants or herbal medicines. Furthermore, these support the mechanistic understanding of the concept of multicomponent multitarget effects and polypharmacology as well as the holistic approaches of treatments as per the AYUSH and other traditional systems of medicine. Synergistic effects are often claimed in experimental and clinical studies using multicomponent herbal preparations. Incorporating omics technologies into the assessment of the mode of action of herbal and traditional medicine will help in rationalizing the biological effects by unfolding the possible mechanism of synergistic actions. Such tools will allow us to explore the possibilities of standardization of multi-component extracts and formulations, for dereplication, and prediction of toxicity and safety of herbal preparations. Such a system biology approach should include network pharmacology assessments as well.

Metabolomics is one of the techniques used to identify targeted and untargeted metabolites for scientific validation and the development of herbal and traditional medicine, especially by using

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high-throughput screening methods. The probability of repetition or working on numerous samples with similar active metabolites is one of the challenges of natural product-based drug development. To overcome these challenges, various "dereplication" methods have been developed. A metabolomic technique combined with a suitable biostatistical method has the ability to facilitate the fast analysis of composite data generated by high-throughput screening.

The scope of this special issue on ethnopharmacology and metabolomics is to focus on the quality, safety, and efficacy of traditional, specially AYUSH, and herbal medicines with more emphasis on metabolomic studies using hyphenated techniques. This issue contains four review articles and 29 research articles by different research groups around the globe on related topics.

Fu et al. studied the active constituents and mechanism of action of the Fuzheng Huayu formula (FZHY), which is a traditional Chinese medicine used for liver fibrosis. The main active components of FZHY are salvianolic acid B, schisantherin A, and amygdalin, which significantly improve the condition of CCl4- and BDL-induced fibrotic liver in rats and mice. In addition to this, the formulation inhibits the activation of hepatic stellate cells by inactivating notch signaling. The authors conclude that the results provide promising scientific evidence for further investigations with the ultimate goal to bring the formula into clinical research as a potential candidate for liver fibrosis.

Dendrobium officinale Kimura & Migo (Orchidaceae) polysaccharide is used in Chinese medicine for liver protection and hypoglycemic action. Qu et al. studied the *in vitro* and *in vivo* effects of *D. officinale* polysaccharides in insulin resistance and abnormal lipid metabolism. The results of the study proved that this traditional medicine may serve as a potential therapeutic agent for obesity-related insulin resistance and lipid metabolism.

Kulyal and group studied the variability in secondary metabolites across five cultivars of *Curcuma longa* L. and two cultivars of *C. aromatica* Salisb. The analysis was carried out on rhizomes and essential oils using gas chromatography–mass spectrometry (GC–MS) and liquid chromatography–mass spectrometry (LC–MS) methods. Among many compounds detected by the authors, 28 compounds were common in all seven cultivars and 39 new metabolites were detected from all seven species.

The work of Yan et al. includes the effect of Huanglong granule (HL Granule) in acute asthma and the possible underlying mechanism of action on mice. Changes in lipid composition were identified using UHPLC-Q-exactive Orbitrap MS with a focus on pulmonary lipid homeostasis. In positive and negative ion modes, a total of 304 and 167 lipids, respectively, were identified in lung tissues, with 162 and 109 lipids significantly elevated in the model group. The authors observed that the HL Granules reversed 104 and 73 lipids, respectively, with a statistical difference (false discovery rate <0.05). It was concluded that lipid homeostasis plays an important role in asthma, and HL Granule might be further investigated and developed as an adjuvant therapy for acute asthma.

The effect of *Lysimachia candida* Lindl. on fatty liver disease in rats was investigated by Kamboj et al. The majority of the

metabolites found in both control and treatment groups were related to lipid metabolism. Treatment with *L. candida* extract improved the control of lipid metabolism and reversed the metabolic syndrome phenotype in rats.

Zhao et al. investigated the mechanism of a traditional Chinese medicine, Erchen decoction. The composition and function of gut microbiota in obesity and its relation with lipid metabolism disorders were investigated. The underlying mechanism of obesity due to changes in the composition of gut microbiota was also studied by the authors. The Erchen decoction reduced body weight, improved insulin resistance and lipid metabolism, and reduced the concentration of free fatty acids released from white adipose tissue due to excessive lipolysis in rats. This study supports the hypothesis that the basis for treatment of obesity lies in changes in gut microbiota.

According to Liu et al., the traditional Chinese medicine Ramulus mori (Sangzhi) alkaloid (SZ-A) tablets improved the overall metabolic profile in mice, including glucose metabolism with enhanced insulin response, and also improved lipid metabolism, which was collectively linked to the modulation of gut microbiota.

Sharma et al. worked on three different dosage forms of Guduchi stem, *i.e.*, *Tinospora cardifolia* (Willd.) Miers, by adopting the Ayurvedic pharmaceutical process of Bhavana (levigation). The findings of this study indicated the effectiveness of Svarasa Bhavita Guduchi Churna and Kwatha Bhavita Guduchi Churna in the treatment of diabetes mellitus. This study provides scientific support to Ayurvedic claims that the Bhavana process has pharmaceutico-therapeutic significance in Ayurvedic drug development.

Zahiruddin et al. used response surface methodology to optimize the ratio of aqueous extracts of *Phyllanthus emblica* L., *Piper nigrum* L., *Withania somnifera* (L.) Dunal, and *T. cordifolia* (Willd.) Miers for the development of a combination formulation. The developed polyherbal formulation showed significant immunomodulatory activity on cyclophosphamide-induced immunosuppressed mice. The metabolomic study showed more than 180 metabolites, identified through LC–MS in the optimized combination. Polyherbal combination treatment significantly (p < 0.01) enhanced the subsets of immune cells such as NK cells, B cells, CD4 cells, and CD8 cells.

Berberis aristata DC. and Nigella sativa L. are plants traditionally used for several diseases. Mazhar et al. describe a method of standardization of B. aristata and N. sativa and investigated their anticancer activity in a 7,12-dimethylbenz [a]anthracene (DMBA)-induced mouse model. Molecular docking was carried out for the marker compounds of both plants with metabolomic studies of essential oils using GC-MS. The study showed that the extracts of N. sativa and B. aristata, as well as their marker compounds, showed an antitumor activity and had no harmful effects on female mice. Furthermore, they protected against DMBA-induced tumor in a mouse model.

Sigesbeckia orientalis L. (syn.: Siegesbeckia orientalis L.) (SO) is a remedy in TCM used to reduce the symptoms of joint disorders. It is a toxic herb, but it is hypothesized that by processing, according to TCM theory, its toxicity can be lowered. Jiang

and co-authors demonstrated using metabolomics that the raw SO causes pulmonary toxicity and that by processing with rice wine its toxicity is reduced. This supports the classical SO processing theory with scientific evidence.

Anadenanthera colubrina (Vell.) Brenan, a plant with antifungal and anti-inflammatory properties, was studied by Maia et al. for its antifungal activity against Candida albicans, C. glabrata, C. tropicalis, and C. dubliniensis using the broth microdilution method. Antifungal activity was assessed in terms of antibiofilm effects, proteolytic enzyme activities, viability assays, gene expression, and cytokine expressions. The extract showed a significant antifungal activity against different Candida strains with low toxic effects to the host cells.

Salunkhe et al. formulated two formulations of spray-dried alcoholic extracts from three different herbs, namely, *Trigonella foenum-graecum* L, *Momordica charantia* L, and *Cinnamomum verum* J. Presl. The oral bioavailability and pharmacokinetic profile of the formulations were evaluated in terms of their markers diosgenin, charantin, and hydroxychalcone in male Wistar rats. Maximum oral bioavailability was found for charantin, followed by diosgenin and then hydroxychalcone. A significant increase in bioavailability of all the markers was observed after the addition of piperine.

Supercritical fluid extraction is one of the extraction methods with the advantages of short extraction time and high purity of extracts. Mishra et al. described the metabolite profile of supercritical CO₂ extracts of the Indian variety of *Ophiocordyceps sinensis*, earlier known as *Cordyceps sinensis*, using high-performance thin-layer chromatography and GC-MS, followed by chemometric analysis. The extract was found effective against *Escherichia coli* and *Salmonella typhi* by the generation of reactive oxygen species and can be utilized in mycotherapeutics for multiple bioeffects.

Wang et al. explored the dose-effect/toxicity relationships between the high and low doses of the lower polar fraction of *Bupleuri Radix* (root of *Bupleurum chinense* DC) and its mechanism using liver metabolomics in chronic unpredictable mild stress (CUMS) rats. The median toxicity dose and effective safe dose of *Bupleuri Radix* which caused liver injury at a high dose and psychiatric diseases at a low dose were calculated.

Tene et al. investigated the cardioprotective effect of *Dillenia pentagyna* Roxb. (DP) against doxorubicin (Dox)-induced cardiotoxicity *in vitro* as well as *in vivo*. The finding suggested that the phenol-rich extract/fractions of DP helped in alleviating Dox-induced cardiotoxicity. The LC-quadrupole time-of-flight electrospray ionization MS analysis of bioactive extract/fractions indicated that polyphenols like gallic acid, syringic acid, and sinapic acid could be responsible for the potent cardioprotective effect due to their antioxidant properties.

Erukainure et al. investigated the cardioprotective mechanisms of a traditional medicinal plant of South Africa, *Turbina oblongata* (E. Mey. ex Choisy) A. Meeuse. The results indicated that such plant has the potential to mitigate lipotoxicity and control dysregulated cardio-metabolic activities due to its antioxidant potential and suppressive effects on angiotensin-converting enzyme, lipase, and acetyl cholinesterase enzymes.

Mahuang decoction (MHD) is a well-known traditional medicine; Chinese its protective effect lipopolysaccharide and D-galactosamine (LPS/D-GalN)induced acute liver failure (ALF) in a mouse model was reported by Liao and his co-workers. The MHD showed a protective effect by regulating the tricarboxylic acid cycle and acid metabolism. Ultra-performance amino chromatography (UPLC)-MS was undertaken for metabolomic studies, and it revealed that, in serum samples, 36 metabolites were identified as contributing to LPS/D-GalN-induced ALF, whereas 27 among them were ameliorated on the administration of MHD.

Erukainure et al. worked on the tetrahydrocannabinol-rich extract of *Cannabis sativa* L. in the context of neurodegenerative disorders. The extract was found to improve glucose intake and to suppress oxidative stress and cholinergic dysfunction as well as to modulate purinergic and gluconeogenic activity in the brain tissues of rats. The *in silico* analysis revealed that the constituents of the extract can pass through the blood–brain barrier, whereas the GC–MS analysis confirmed the presence of tetrahydrocannabinol in the plant extract.

Safoof-e-Pathar phori (SPP) is a poly-herbomineral formulation, which has been used traditionally for urolithiasis as per the Unani Pharmacopoeia of India. Ahmad et al. investigated the traditional claim pre-clinically. The study involved the oral administration of SPP at low and high doses. They significantly (p < 0.001) reduced urinary calcium, serum creatinine, blood urea, and lipid peroxidation in urolithiatic Wistar rats. The long-term oral toxicity study showed that SPP was safe in Wistar rats for up to 3 months. The study provides scientific evidence in support of traditional claims for SPP as an anti-urolithiatic formulation.

Luo et al. used high-throughput metabolomic analysis to identify the biomarkers and pathways that would reveal the therapeutic action and mechanism of andrographolide against lung cancer using UPLC–time-of-flight MS. The findings suggest that 11 metabolism pathways are regulated by andrographolides in cancer. The network pharmacology revealed the involvement of 570 proteins. Amino acid metabolism and arachidonic acid metabolism pathways are the potential target pathways for andrographolide in this model of lung cancer.

Kumar et al. investigated the neuroprotective effect of piperine on streptozotocin-induced hyperglycemia and also observed the gene expression in diabetic rats. Piperine leads not only to a significant improvement in memory but also to a significant reduction in the expression of specific Alzheimer's disease-related genes, like BACE1, PSEN1, APAF1, CASPASE3, and CATALASE.

Radix Bupleuri (RB) and Radix paeoniae Alba (RPA) are components of a well-known herb combination used clinically to treat depression. Chen et al. developed a novel and efficient technique for analyzing the impact of the combination of RB and RPA in *in vivo* behaviors by combining multi-component pharmacokinetics with metabolomics. The finding of the study suggested that the combination can increase the bioavailability of 6 components in RPA and 5 in RB and also boost neuroprotective and anti-inflammatory effects.

Tiwari et al. used chromatographically standardized extracts of *Clerodendrum serratum* (L.) Moon (Verbenaceae) for assessing its anti-inflammatory and anti-arthritic activities. Scientific evidence for the ethnomedicinal use of the plant in arthritis is thereby provided.

Nandanwadkar et al. used the inductive coupled plasmaoptical emission spectroscopy technique to carry out multielemental assessments of phyto-pigments. They also used a chromatographic technique to evaluate their biotherapeutic potential. The screening for heavy metals and micro- and macro-minerals was undertaken using routine quality control and the safety profile of food additives and contaminants.

Lin et al. focused on two traditional Chinese medicine [Acanthopanax senticosus (Rupr. and Maxim.) Harms and Gastrodia elata Blume] for the treatment of stroke and cerebrovascular diseases. Using transcriptomic and metabolomic studies together, the authors hypothesized that both drugs can be used for the treatment of cerebrovascular diseases. Six metabolites and six genes were found to be significantly altered. The therapeutic effect of the extracts in cerebrovascular diseases was found to be related to the regulation of the phenylalanine and pyrimidine metabolic pathways.

Pseudevernia furfuracea (L.) is an epiphytic lichen used in Indian spice mixtures, curries, and food preparations as a preservative. Goel et al. attempted to find the optimal extraction method for polyphenol- and flavonoid-enriched extracts of P. furfuracea. Scanning electron microscopy and high-performance liquid chromatography were used to analyze and compare the effect of pre-processing conditions on the Ultra-high-performance extraction method. liquid chromatography-diode array detector MS was used to study the metabolomic profile of the lichen extracts. After mixing and grinding the raw material by using Soxhlet, it was found that 70% methanol extract was the most effective for extracting a combination of polyphenolic and flavonoidal-rich metabolites. The work also suggested *P. furfuracea* as a potent antioxidant.

Sing et al. suggested a system for grading Andrographis paniculata (Burm. F) raw ground samples using near-infrared reflectance (NIR) spectroscopy and support vector machine (SVM) classifier based on the content of the marker, andrographolide. The estimation accuracy based on extracts was marginally higher than that based on powder leaf samples. However, it had no effect on the samples' grading pattern. The finding of the study suggested that combining the NIR-based estimate of powdered leaf samples with an SVM classifier can be a low-cost solution for grading the samples rapidly.

Mou et al. summarized the structural types, pharmacological activities, and mechanisms of *Dendrobium* alkaloids as well as the suggested biogenetic pathways of dendrobine, which is an important sesquiterpene alkaloid.

Tawfeek et al. provided a comprehensive overview of the phytochemistry, traditional use, and pharmacology of plant

extracts and constituents from the genus *Salix* (willows). They also demonstrated its ability to reduce inflammatory pathways and hypothesized that they could be useful in cancer prevention and therapy as well as other chronic diseases.

Bhatt et al. explored the Indian system of medicines for possible male and female contraceptives. The review concluded that the Indian system of medicine offers highly promising opportunities with potential analytical, biological, technological, and clinical advances collectively integrated with therapeutic rationale based on Ayurvedic principles.

Nille et al. provided information on a traditional plant, Avartaki [Senna auriculata (L.) Roxb.], and its wide usefulness in the Ayurveda and Siddha systems of medicine for the treatment of numerous diseases. The ethnomedicinal, phytochemical, pharmacological, and toxicological features of the plant were discussed in this review article, with more focus on therapeutic significance in diabetes.

Overall, this special issue provides an insight into the role of metabolomics and ethnopharmacology in the development of herbal and traditional medicine. It provides the readers with a plethora of generally up-to-date information to support their understanding of these rapidly evolving areas of metabolomics. There is still an enormous scope to work on the metabolomics and network pharmacology of traditional medicine for a better understanding of the molecular mechanism of pharmacological actions by identifying metabolites through dereplication and to provide data for scientific validation of traditional claims.

AUTHOR CONTRIBUTIONS

SA, CK, PM, and GU prepared the manuscript.

Conflict of Interest: Author CK was employed by company Emami Ltd.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Tetrahydrocannabinol-Rich Extracts From Cannabis Sativa L. Improve Glucose Consumption and Modulate Metabolic Complications Linked to Neurodegenerative Diseases in Isolated Rat Brains

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Reduced brain glucose consumption arising from impaired glucose uptake and utilization has been linked to the pathogenesis and complications of neurodegenerative diseases. The ability of Cannabis sativa L. tetrahydrocannabinol (THC)-rich extracts to stimulate brain glucose uptake and utilization as well as its modulatory effect on gluconeogenesis, antioxidative, purinergic and cholinergic activities were investigated in isolated rats' brains. C. sativa leaves were sequentially extracted to yield the hexane and dichloromethane extracts. The extracts were incubated at 37°C with freshly harvested brains in the presence of glucose for 2 h. The control consisted of incubation without the extracts, while brains without the extracts and glucose served as the normal control. Metformin was used as the standard drug. C. sativa extracts caused a significant (p < 0.05) increase in brain glucose uptake, with concomitant elevation of glutathione level, dismutase. ecto-nucleoside superoxide catalase. and triphosphate diphosphohydrolase activities compared to the controls. Incubation with C. sativa extracts also led to depletion in malondialdehyde and nitric oxide levels, acetylcholinesterase, butyrylcholinesterase, glucose 6-phosphatase and fructose-1,6biphosphatase activities. GC-MS analysis of the extracts revealed the presence of THC. In silico analysis predicted THC to be permeable across the blood-brain-barrier. THC was also predicted to have an oral LD₅₀ and toxicity class values of 482 mg/kg and 4 respectively. These results indicate that C. sativa improves glucose consumption with concomitant suppression of oxidative stress and cholinergic dysfunction, and modulation of purinergic and gluconeogenic activities in brain tissues

Keywords: brain glucose consumption, *Cannabis sativa*, neurodegenerative diseases, tetrahydrocannabinol 3, carbohydrate metabolism

INTRODUCTION

The brain's dependence on glucose for energy generation is well documented. Brain glucose homeostasis has also been reported to be important for neuronal generation and maintenance, regulation of neurotransmitter, cognitive function and synaptic plasticity (Neumann et al., 2008). Glucose transporters aid in transporting glucose across the blood brain barrier (BBB) from the blood stream to the brain. Altered glucose homeostasis in the central nervous system (CNS) has been reported in most neurodegenerative diseases such as Alzheimer's and Parkinson diseases (An et al., 2018). This has been attributed to abnormalities in insulin signaling pathways in the brain as well as alteration of the glucose transporters at the BBB (Gejl et al., 2017; An et al., 2018). These abnormalities and alterations often cause deceased brain glucose consumption which can lead to a hypometabolic brain state characterized by glucose dysmetabolism (Zilberter and Zilberter, 2017). Thus, making the brain susceptible to degenerative diseases. This is evident in studies which correlated the risk of Alzheimer's disease with reduced brain glucose metabolism (Duran-Aniotz and Hetz, 2016).

Increased oxidative stress has been linked with decreased brain glucose uptake (Erukainure et al., 2019c). Increased glucose uptake has been shown to improve proteostasis which causes an upregulation of the unfolded protein response that protects against endoplasmic reticulum stress (Scheper and Hoozemans, 2015; Duran-Aniotz and Hetz, 2016). Oxidative stress has been implicated in the etiology and pathogenesis of neurodegenerative diseases (Erukainure et al., 2019b; Salau et al., 2020b). This is evident in the use of antioxidants in treating and managing most neurodegenerative diseases such as Alzheimer's and Parkinson's diseases (Gilgun-Sherki et al., 2001; Kim et al., 2015). Antioxidants have been reported for their ability to scavenge free radicals as well as improve the activities of the endogenous antioxidant enzymes (Salau et al., 2020). Oxidative stress has also been implicated in the disturbances of cholinergic and purinergic enzymes activities of the CNS (Erukainure et al., 2019a; Salau et al., 2020). These enzymes have been reported for their respective neurotransmission and bioenergetic roles which are critical for normal functioning of the brain (Ademiluyi et al., 2016; Pepeu and Giovannini, 2017).

Cannabis sativa L. is among the medicinal plants used in the treatment and management of neurological diseases. It is an annual herbaceous plant that belongs to the Cannabis genus and Cannabaceae family. It is globally distributed, with Africa accounting for 25% of its global production (UNODC, 2012). Its common names include weed, Indian hemp and marijuana. C. sativa is utilized for food, therapeutic, recreational and religious purposes (Bonini et al., 2018). Phytocannabinoids make up the major phytochemical constituents of C. sativa, with tetrahydrocannabinol (THC), cannabinol, and cannabidiol among the most common (Andre et al., 2016). The therapeutic role of C. sativa against neurodegenerative diseases and other psychopathic ailments have been reported (Lafuente et al., 2011; Campos et al., 2017; Lim et al., 2017). The aqueous and ethanol extracts of the leaves have been reported to confer

protective effects on α-motor neurons via antioxidative and antiapoptotic activities (Moosavi et al., 2013). Cannabidiol has been reported for its ability to activate metabotropic receptors for serotonin and/or adenosine as well as nuclear receptors of the PPAR family (Fernández-Ruiz et al., 2013). The leaves improved tremor, bradykinesia and rigidity in Parkinsonian patients (Lotan et al., 2014). The neuroprotective effects of *C. sativa* have been demonstrated on basal ganglia disorders (Sagredo et al., 2007). Other reported medicinal properties of *C. sativa* include antidiabetes (Ren et al., 2016), anticancer (Guzman, 2003), pain suppression (Whiting et al., 2015), anti-epilepsy (Fusar-Poli et al., 2009), and sleep management (Ramar et al., 2018).

Despite the reported neuroprotective effect of *C. sativa* and its phytoconstituents, there are still dearth in its ability to promote brain glucose uptake and/or utilization. Thus, this present study was aimed at investigating the ability of the leaves to stimulate glucose uptake and utilization, as well as its modulatory effect on antioxidative, purinergic and cholinergic activities, and gluconeogenesis in isolated brains. The cytotoxic effect of the leaves was also investigated in glioblastoma multiforme (U87 MG) cells.

MATERIALS AND METHODS

Plant Permit Approval

This research has been undertaken under the permit approval (Permit No. POS 248/2019/2020) from the South African Health Products Regulatory Authority to conduct, collect, posses, transport and store cannabis plant, plant parts and products for research purposes. The study was also conducted to collect cannabis plants in Lesotho under the permit (Permit #: 01/LS/2019/10/02-01).

Plant Material

Cannabis sativa leaves were obtained from Mohale's Hoek District, Lesotho (GPS coordinates: -30.333776"S and 27.651201"E). They were authenticated by the Geo Potts Herbarium at the University of the Free State, Bloemfontein 9300, South Africa and assigned the voucher number, BLFU MGM 0018. The leaves were pulverized to dry powder, after air drying to a constant weight.

The powdered samples were thereafter sequentially extracted with solvents of increasing polarity vis-à-vis hexane and dichloromethane (DCM) for 48 h with mild agitation of 100 rpm at room temperature. The solvents were respectively decanted and concentrated *in vacuo* using an R–215 rotary evaporator (Buchi, Switzerland). The extracts were collected in glass vials and stored in the dark at ambient room temperature for further *ex vivo* studies.

Animals

A day to the experiment, sixteen male albino rats (Sprague Dawley strain) weighing 180 – 200 g were obtained from the Biomedical Research Unit, University of KwaZulu-Natal, Durban, South Africa and housed in plastic cages. They were fasted for 8 h before humanely sacrificed by euthanizing with

Isofor. Their brains were harvested and rinsed in normal saline to remove blood stains. Each brain was divided into its hemispheres and used immediately for *ex vivo* study.

Glucose Uptake in Isolated Rat Brain

Each hemisphere of the freshly harvested rat brains was incubated in 8 ml of Krebs buffer containing 11.1 mM glucose and the different concentrations of *C. sativa* extracts (hexane and DCM) for 2 h under a 5% CO₂, 95% oxygen and 37°C conditions as described in previously published methods (Erukainure et al., 2019c; Salau et al., 2020a). The untreated control consisted of incubation without the extracts, while brains incubated without the extracts and glucose served as the normal control. Metformin was used as the standard drug. Each treatment group consisted of 3 brain hemispheres.

After incubation, the brain tissues were collected and homogenized in 50 mM phosphate buffer (pH 7.5) with 1% triton X-100, and thereafter centrifuged at 15,000 rpm at 4° C for 10 min (Erukainure et al., 2019c). The supernatants were collected and stored at -20° C until further analysis.

The study was carried out under the approved guidelines of the animal ethics committee of the University of KwaZulu-Natal, Durban, South Africa (protocol approval number: AREC/020/017D).

Determination of Glucose Utilization

Aliquots from the incubating buffer was collected prior and after the incubation for determination of glucose utilization. This was carried out by measuring the glucose concentrations using an automated chemistry analyzer (Labmax Plenno, Labtest Inc., Lagoa Santa, Brazil). Glucose utilization was thereafter calculated with the formula:

Glucose uptake =
$$\frac{GC1 - GC2}{\text{Weight of brain tissue (g)}}$$

Where GC1 and GC2 are glucose concentrations (mg/dL) before and after incubation, respectively.

Determination of Antioxidative Activity Reduced glutathione level

The Ellman's method (Ellman, 1959) was used in determining the GSH level of the brain tissue. Briefly, the resulting supernatant was deproteinized with an equal volume of 10% Trichloroacetic acid (TCA) and centrifuged for 5 min at 3,500 rpm. 200 μl aliquot was collected from the deproteinized sample into a 96 well plate. 50 μl of Ellman reagent was thereafter added and the reaction mixture was allowed to stand for 5 min. Absorbance was read at 415 nm. The GSH concentration was extrapolated from a standard curve.

Superoxide dismutase Activity

The superoxide dismutase (SOD) activity of the brain tissues was determined using a method based on the principle that 6-hydroxydopamine (6-HD) is oxidized by H_2O_2 from SOD catalyzed dismutation of O_2^- , which produces a colored product (Gee and Davison, 1989). Briefly, 15 μ l of the tissue

supernatants were dissolved in $170 \,\mu$ l of $0.1 \,m$ M diethylenetriaminepentaacetic acid (DETAPAC) in a 96 well plate. Thereafter, $15 \,\mu$ l of $1.6 \,m$ M 6-HD was added. Absorbance was measured at 492 nm for 5 min at 1 min interval.

Catalase Activity

The catalase activity of the brain tissue was determined using a previously established protocol (Aebi, 1984). Briefly, 10 μ L of the tissue supernatants was mixed with 340 μ L of 50 mM sodium phosphate buffer (pH 7.0). Thereafter, 150 μ L of 2 M H₂O₂ was added to the reaction mixture. Absorbance was read at 240 nm at 1 min interval for 3 mins.

Lipid Peroxidation Level

The lipid peroxidation level of the brain tissues was determined by measuring the thiobarbituric acid reactive substances (TBARS) in the tissues and expressed as malondialdehyde (MDA) equivalent (Chowdhury and Soulsby, 2002). Briefly, a reaction mixture consisting of 100 μl of the supernatants, 100 μl of 8.1% SDS solution, 375 μl of 20% acetic acid, 1 ml of 0.25% thiobarbituric acid (TBA), and 425 μL of distilled water was heated at 95°C for 1 h in a water bath. A 200 μl aliquot was thereafter collected from the reaction mixture into a 96 well plate, and absorbance read at 532 nm.

Nitric Oxide Level

The brain tissues were assayed for nitric oxide level using the Griess method as previously described (Tsikas, 2005; Erukainure et al., 2019c). Briefly, $100~\mu l$ of the tissue samples and/or distilled water (blank) were incubated with an equal volume of Griess reagent for 30 min at $25^{\circ}C$ in the dark. Absorbance was read at 548~nm.

Cholinergic Enzymes Activities

The brain tissues were assayed for cholinergic activities by analyzing the activities of acetylcholinesterase (Ellman et al., 1961) and butyrylcholinesterase (Adefegha et al., 2017) respectively in the tissue supernatants. Briefly, 20 μl of the tissue supernatants was incubated with 10 μl of 3.3 mM Ellman's reagent (pH 7.0) and 50 μl of 0.1 M phosphate buffer (pH 8) for 20 min at 25°C. For acetylcholinesterase activity, the reaction was stopped by adding 10 μl of 0.05 M acetylcholine iodide to the reaction mixture. While 10 μl of 0.05 M butyrylcholine iodide was used to stop the reaction for butyrylcholinesterase activity. Absorbances were read at 412 nm at 3 min intervals.

Purinergic Enzymes Activities

Th brain tissues were assayed for purinergic activities by analyzing for the activity of ecto-nucleoside triphosphate diphosphohydrolase (E-NTPDase) (Akomolafe et al., 2017) in the tissue supernatants. Briefly, 20 μ l of the tissue supernatants was incubated with 200 μ l of the reaction buffer (1.5 mM CaCl₂, 5 mM KCl, 0.1 mM EDTA, 10 mM glucose, 225 mM sucrose and 45 mM Tris-HCl) at 37°C for 10 min 20 μ l of 50 mM ATP was added to the reaction mixture and further incubated at 37°C for 20 min in a shaker. The reaction was stopped with 200 μ l of 10%

TCA and incubated on ice for 10 min. Absorbance was read 600 nm.

Determination of Gluconeogenic Enzymes Activities

The gluconeogenic enzymes activities of the brain tissues were determined by analyzing the supernatants for glucose 6 phosphatase (Mahato et al., 2011; Erukainure et al., 2017), and fructose-1,6-bisphosphatase (Gancedo and Gancedo, 1971; Balogun and Ashafa, 2017) activities with slight modifications.

To determine glucose 6 phosphatase activity, $200\,\mu l$ of the tissue supernatants was incubated with $100\,\mu l$ of $0.25\,M$ glucose, $200\,\mu l$ of $5\,mM$ KCl, $1300\,\mu l$ of $0.1\,M$ Tris-HCl buffer, and $40\,\mu l$ of $50\,mM$ ATP at $37^{\circ}C$ in a shaker for $30\,min$. The reaction was stopped with 1 ml of distilled water and 1.25% ammonium molybdate. 1 ml of freshly prepared 9% ascorbic acid was then added to the reaction mixture and allowed to stand for $30\,min$. Absorbance was read at $660\,nm$. ATPase activity was calculated as the amount of inorganic phosphate (Pi) released/min/mg protein.

For fructose-1,6-biphosphatase activity, 100 μ l of the tissue supernatant was incubated with 1,200 μ l of Tris–HCl buffer (0.1 M, pH 7.0), 100 μ l of fructose (0.05 M), 250 μ l 0.1 M MgCl₂, 100 μ l 0.1 M KCl, and 250 μ l 1 mM EDTA at 37°C for 15 min. The reaction was stopped with 1 ml of 10% TCA and incubated on ice for 10 min. Absorbance was read at 680 nm and the activity calculated as the amount of inorganic phosphate (Pi) released/min/mg protein.

3-(4,5-Dimethylthiazol-2-yl)-2,5-Diphenyltetrazolium Bromide Assay

Cell Lines and Cell Culturing

The human U87 MG glioblastoma cancer (ATCC® HTB-14™) cell line was obtained from the American Type Culture Collection (ATCC, Virginia, United States). Dulbecco's Minimum Essential Media (DMEM), Eagle's Minimum Essential Media (EMEM), Fetal bovine serum (FBS) and Phosphate Buffer Saline (PBS) were purchased from Life technologies (Pty) Ltd. (Fairlands, Johannesburg, RSA). The 3-(4,5-Dimethylthiazol-2-vl)-2,5-Diphenyltetrazolium Bromide (MTT), Dimethyl Sulfoxide (DMSO), Trypsin, and all other chemicals and reagents were of analytical grade and acquired from Merck (Pty) Ltd. (Modderfontein, Johannesburg, RSA). The U87 cell line was maintained in DMEM:EMEM (1:1), supplemented with 10% heat-inactivated FBS and grown at 37°C in a humidified incubator set at 5% CO2. Cells were sub-cultured with 0.25% (w/v) trypsin 0.53 mM ethylenediaminetetraacetic acid (EDTA) for a maximum of 15 min every 2 and 3 days after they had formed an 80% confluent monolayer.

Cell Proliferation Assay

To analyze the effect of the samples on the cell viability, the MTT method was utilized. Cells were seeded in 100 μ l medium in 96-well microtiter plates at a concentration of 1 \times 10⁵. Stock

solutions of 4 mg/ml of the samples were prepared in 20% ethanol. The positive control, doxorubicin was dissolved in 50% DMSO to obtain a stock concentration of 10 mg/mL. Serial dilutions were made to achieve target concentrations of the samples and doxorubicin in a of range 30, 60, 120, 240 µg/ml and 12.5-100 µg/ml, respectively. Subsequently, cells were exposed to the samples, doxorubicin and the controls, which included vehicle-treated cells exposed to 1.2% ethanol or 0.5% DMSO and cells propagated in growth medium. After the 48 h treatment period, the cells were subjected to the MTT reagent (0.5 mg/mL). The colorimetric reaction was measured by means of a plate reader (Multiskan Go, Thermofischer Scientific) at 570 nm wavelength. Color control blanks were included and utilized to normalize the results and the vehicle control treated cells were regarded as 100% cell viability. The samples were evaluated in atleast three independent experimental repeats and each sample was evaluated in triplicate for each experimental repeat. The results given are representative of the average percentage inhibition of all the experimental repeats.

GC-MS analysis of *Cannabis sativa* Extracts Apparatus

An Agilent technologies 6890N GC-MS machine coupled with a 5973-network mass selective detector was used for the analysis. An Agilent technologies 7683 Series injector and screw neck glass vials (separations) were used for sample injection.

GC-MS Conditions

The extracts were analyzed using a HP-5ms capillary column phase. The injection volume was set to 2 μl at $80^{\circ}C$. the flow rate of the helium gas was 1 ml/min at a constant flow. The oven program was set at $80^{\circ}C$ for 2 min and increased to $300^{\circ}C$ at $20^{\circ}C/$ min for 3 min. A mass selective detector was used for the detection of the volatile compounds present in the standards and tests samples. The NIST mass spectral library database software was used to analyze the data. The mass spectrometer data system has a reporting software module that combines the data results with the NIST library and ADMIS software search for target compounds into a single report.

In Silico Prediction of Blood Brain Barrier Permeability and Oral Lethal Dose Toxicity

The ability of the GC-MS identified compound to cross the BBB was predicted *in silico* using the SwissADME online server (http://www.swissadme.ch/index.php) (Daina et al., 2017). Its oral lethal dose toxicity (LD₅₀) and toxicity class were predicted using the PROTOX II online server (http://tox.charite.de/protox_II/) (Banerjee et al., 2018). These were done by obtaining the Canonical SMILES of the GC-MS identified compound from PubChem (https://pubchem.ncbi.nlm.nih.gov/), and computed into the respective servers for the predictions.

Statistical Analysis

Data were subjected to one-way ANOVA and presented as mean \pm SD. Significant differences between means at p < 0.05 were obtained using the Tukey's HSD-multiple range post-hoc

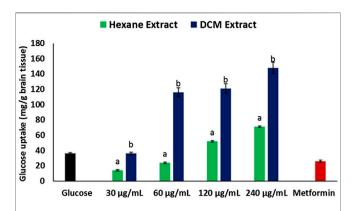


FIGURE 1 | Effect of *Cannabis sativa* on glucose uptake in brain tissues. *abValues with different letter above the bars for a given extract are significantly ($\rho < 0.05$) different from each other.

test. Statistical analyses were done using IBM Statistical Package for the Social Sciences (SPSS) for Windows, version 23.0 (IBM Corp., Armonk, NY, United States).

RESULTS

Incubation of brain tissues with glucose in the presence of hexane and DCM extracts of C. sativa leaves led to significant (p < 0.05)

increase in glucose utilization, with the DCM extract having a higher activity as depicted in **Figure 1**. The activity was dosedependent, with the highest concentration having the highest activity. Incubation with metformin had no significant effect on brain glucose utilization.

Incubation of brain tissues with glucose led to significant (p < 0.05) depletion in the levels of GSH, SOD and catalase activities, while significantly elevating MDA level as shown in **Figures 2A–D**. Incubation with the extracts significantly (p < 0.05) reversed these levels and activities dose-dependently to near normal.

As shown in **Figure 3**, incubation with glucose led to significant (p < 0.05) elevation of NO level in brain tissues. This level was significantly (p < 0.05) depleted on incubation with *C. sativa* extracts.

There was a significant (p < 0.05) elevation in acetylcholinesterase and butyrylcholinesterase activities in brain tissues incubated with glucose as depicted in **Figures**. **4A,B**. The acetylcholinesterase activity was significantly (p < 0.05) reversed dose-dependently on incubation with DCM extract (**Figure 4A**). However, the hexane extract significantly (p < 0.05) elevated acetylcholinesterase activity dose-dependently (**Figure 4A**). Both extracts significantly (p < 0.05) depleted butyrylcholinesterase activity in a dose-dependent manner (**Figure 4B**).

As shown in **Figure 5**, there was a significant (p < 0.05) depletion in E-NTPDase activity in brain tissues incubation with

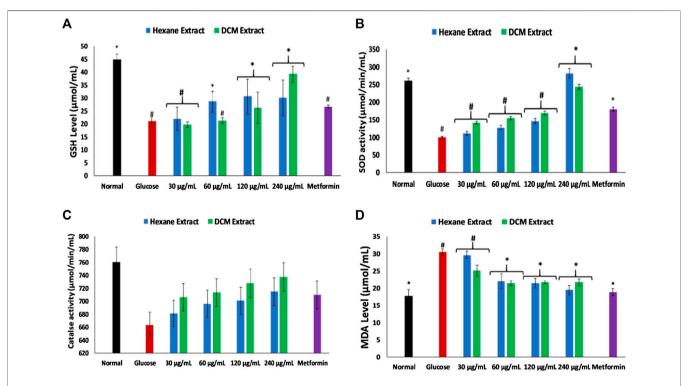


FIGURE 2 | Effect of *Cannabis sativa* on **(A)** glutathione (GSH) level, **(B)** superoxide dismutase (SOD) activity, **(C)** catalase activity, and **(D)** malondialdehyde (MDA) level in brain glucose uptake. Value = mean \pm SD; n = 3. *Statistically significant (ρ < 0.05) compared to glucose-treated tissue; #statistically significant (ρ < 0.05) compared to normal tissue. Normal, No glucose/*C. sativa*.

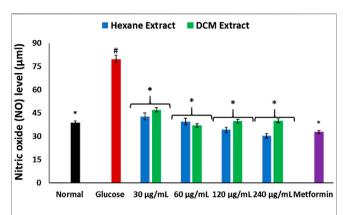
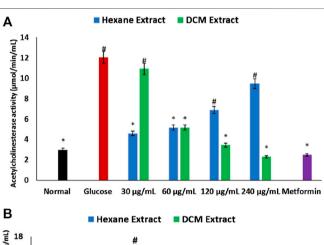


FIGURE 3 | Effect of *Cannabis sativa* on NO level in brain glucose uptake. Values = mean \pm SD; n = 3. *Statistically significant (ρ < 0.05) compared to glucose-treated tissue; #statistically significant (ρ < 0.05) compared to normal tissue. Normal, No glucose/*C. sativa*.



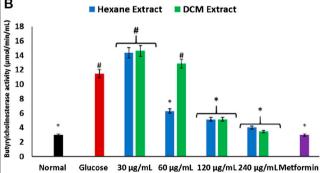


FIGURE 4 | Effect of *Cannabis sativa* on **(A)** acetylcholinesterase and **(B)** butyrylcholinesterase activities in brain glucose uptake. Values = mean \pm SD; n = 3. *Statistically significant (ρ < 0.05) compared to glucose-treated tissue; #statistically significant (ρ < 0.05) compared to normal tissue. Normal, No glucose/*C. sativa*.

glucose only. Incubation with *C. sativa* extracts led to significant (p < 0.05) reversion of the activity to levels indistinguishable from the normal tissues.

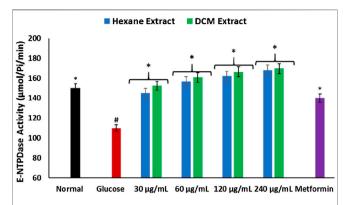


FIGURE 5 | Effect of *Cannabis sativa* on ecto-nucleoside triphosphate diphosphohydrolase activity in brain glucose uptake. Values = mean \pm SD; n = 3. *Statistically significant (ρ < 0.05) compared to glucose-treated tissue; #statistically significant (ρ < 0.05) compared to normal tissue. Normal, No glucose/*C. sativa*.

As depicted in **Figures. 6A,B**, there was a significant (p < 0.05) elevation in the activities of glucose 6-phosphatase and fructose-1,6-biphostase in brain tissues incubated with glucose only. These activities were significantly (p < 0.05) reversed in tissues incubated with C. sativa extracts to levels indistinguishable from the normal tissues.

MTT assay revealed *C. sativa* extracts had little or no cytotoxic effect on U87 MG cells, while doxorubicin significantly (p < 0.05) inhibited the proliferation of the cells as depicted in **Figure** 7.

GC-MS analysis of the extracts revealed the presence of THC in both extracts as shown in **Figure 8**; **Supplementary Figure S1**.

In silico BBB permeability prediction revealed THC to be permeable across the BBB as shown in **Table 1**. THC was further predicted *in silico* to be in the toxic class of 4, with a $\rm LD_{50}$ value of 482 mg/kg.

DISCUSSION

Impaired brain glucose uptake leading to diminished neuronal glucose consumption has been linked to the pathogenesis and progression of neurodegenerative diseases such as Alzheimer's and Parkinson's diseases (Zilberter and Zilberter, 2017; An et al., 2018). In the present study, the increased glucose uptake in brain tissues incubated with C. sativa extracts (Figure 1) indicates an increased glucose utilization which insinuates an increased neuronal glucose consumption. This activity portrays a facilitative uptake potential of C. sativa leaves which corresponds with previous studies on the use of medicinal plant leaves in facilitating brain glucose uptake (Erukainure et al., 2019c). This activity can be attributed to the GC-MS identified compound in the extracts, THC (Figs. 8 and S1) which can bind and activate the cannabinoid receptors of the endocannabinoid anandamide transporters at the BBB (Maccarrone et al., 2006). Thus, facilitating transportation across the BBB.

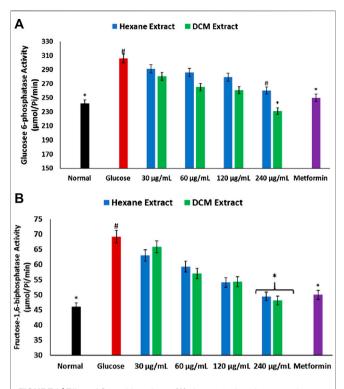
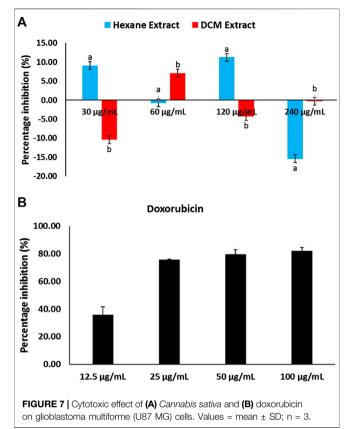


FIGURE 6 | Effect of *Cannabis sativa* on **(A)** glucose 6-phosphatase and **(B)** fructose-1,6-biphosphatase activities in brain glucose uptake. Values = mean \pm SD; n = 3. *Statistically significant (ρ < 0.05) compared to glucose-treated tissue; #statistically significant (ρ < 0.05) compared to normal tissue. Normal, No glucose/*C. sativa*.

Oxidative stress and proinflammation have been implicated in the pathogenesis of neurological diseases, and have been reported among the major mechanisms in the etiology of the diseases (Wajner et al., 2004; Mahadik et al., 2006). The depleted GSH level, SOD and catalase activities on incubation of brain tissues with glucose (Figures. 2A-C) insinuates an oxidative state. This is further revealed by the exacerbated MDA level (Figure 2D) which indicates an occurrence of lipid peroxidation. This is in agreement with previous studies on exacerbated oxidative activities in brain tissues incubated with glucose (Erukainure et al., 2019c). The brain has been reported for its high susceptibility to oxidative stress owing to its polyunsaturated fatty acids contents, redox-active metal load, low endogenous antioxidant system, and auto-oxidizable neurotransmitters dependence (Butterfield et al., 2001; Huang et al., 2004; Patel, 2016; Erukainure et al., 2019c). The increased brain NO level (Figure 3) with concomitant low SOD activity on incubation with glucose may insinuate a proinflammatory effect. In the presence of depleted SOD activity, peroxynitrite (ONOO-) is generated from the reaction of NO and superoxide (O2-) (Erukainure et al., 2020; Salau et al., 2020). Peroxynitrite has been reported for its potent proinflammatory roles in several diseases including neuropathy as it has been implicated in the pathogenesis of Alzheimer's and Parkinson's diseases, and multiple sclerosis (Smith et al., 1997; Pacher et al., 2007). Antioxidants have been reported for their therapeutic roles in the treatment and



management of neurodegenerative diseases (Gilgun-Sherki et al., 2001; Kim et al., 2015). The elevated GSH level, SOD and catalase activities, with concomitant depleted levels of MDA and NO on incubation with *C. sativa* extracts indicate an antioxidative and anti-proinflammatory effect. THC has been reported for its potent antioxidant and anti-proinflammatory activities in the treatment and management of neurological diseases (Hampson et al., 1998; Costa, 2007; Borges et al., 2013). Thus, may be responsible for the antioxidative effect of the extracts.

Cholinergic dysfunction has been recognized as one of the major defects of neurodegenerative diseases such as Alzheimer's, Parkinson's diseases and multiple sclerosis (Greig et al., 2002). It is characterized by increased activities of acetylcholinesterase and butyrylcholinesterase which catalyze the hydrolysis of the neurotransmitter acetylcholine (Reid et al., 2013). Thus, implying that the elevated activities of these enzymes on incubation of brain tissues with glucose (Figures 4A,B) indicates a cholinergic dysfunction and may insinuate a neurodegenerative symptom. Several therapies have targeted the inhibition of these enzymes in the treatment and management of neurodegenerative diseases (Erukainure et al., 2019a; Salau et al., 2020b). Thus, the inhibitory effect of the extracts on these enzymes portrays a neuroprotective activity of C. sativa. This corroborates previous reports on the inhibitory effect of C. sativa and its major phytochemical constituents on acetylcholinesterase butyrylcholinesterase and (Eubanks et al., 2006; Abdel-Salam et al., 2018). However, the increasing acetylcholinesterase activity with

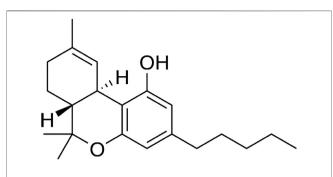


FIGURE 8 | Tetrahydrocannabinol identified from the hexane and DCM extracts of C. sativa.

TABLE 1 In silico prediction of BBB permeability and toxicity of tetrahydrocannabinol.

482 mg/kg 4 Yes

BBB, blood brain barrier: LD50, ethal dose,

concentration of the hexane extract (**Figure 4A**) may insinuate the inhibitory effect of the extract on the enzyme diminishes with increasing concentrations.

The depleted E-NTPDase activity in brain tissues incubated with glucose (**Figure 5**) indicates a depleted adenosine level which portrays a decreased purinergic activity. Impaired purinergic activity has been implicated in the pathogenesis of neurodegenerative diseases (Akomolafe et al., 2017; Salau et al., 2020). It is characterized by decreased production of adenosines which are involved in energy transfer reactions and facilitative transportation (Akomolafe et al., 2017). The increased E-NTPDase activity in brain tissues incubated with *C. sativa* extracts insinuates the ability of *C. sativa* to improve neuronal purinergic activity.

Diminished brain glucose consumption is often characterized by increased glycogenolysis and impaired glycolytic flux to compensate for the low glucose level (Hoyer, 1996; Atlante et al., 2017). This has been implicated in the pathogenesis of Alzheimer and other neurodegenerative diseases (Atlante et al., 2017). In the present study, the depleted brain glucose consumption (Figure 1) corroborates with the exacerbated glucose 6-phosphatase and fructose-1,6-biphosphatase activities in brain tissues incubated in glucose (Figures. 6A,B). Both enzymes are involved in gluconeogenesis, with glucose 6phosphatase and fructose-1,6-biphosphatase catalyzing the hydrolysis of glucose 6-phosphate to glucose in the glycogenolytic pathway and fructose-1,6-biphosphate to fructose 6-phosphate in the gluconeogenic pathway respectively. The continuous activation of these enzymes will lead to glucose accumulation which can serve as metabolite precursors for the hexosamine, polyol, protein kinase C, and AGE pathways which have been linked to the pathogenesis of neurodegenerative diseases (Li et al., 2012; Xu et al., 2016).

Glucose has also been reported as an intermediate for the generation of free radicals, as it is oxidized in its enediol form into reactive ketoaldehydes and superoxide anion radicals (Maritim et al., 2003). Thus, the dose-dependent inhibited activity of these enzymes in brain tissues incubated with *C. sativa* extracts further indicates the neuroprotective effect of *C. sativa*.

Glioblastoma multiforme (GBM) is a malignant primary brain tumor common in young kids (Erukainure et al., 2018). Studies have reported therapeutic failures in patients owing to difficulty in treatment (Puli et al., 2006). Although medicinal plants have reported to arrest the proliferation of GBM (Erukainure et al., 2018), *C. sativa* extracts showed no cytotoxic effect on the cells (**Figure 7**). Thus, insinuating that the plant may not be beneficial in the treatment of GBM.

The predicted ability of THC to permeate the BBB (**Table 1**) further connotes the neuroprotective effect of C. sativa and corroborates previous reports on the ability of cannabinoids to modulate the cannabinoid receptors of anandamide transport across the BBB (Maccarrone et al., 2006). The predicted oral LD₅₀ and toxicity class values of THC (**Table 1**) indicates that the compound is relatively safe when orally consumed.

CONCLUSION

As portrayed by these results, *C. sativa* improves glucose consumption with concomitant suppression of oxidative stress and cholinergic dysfunction, and modulation of purinergic and gluconeogenic activities in brain tissues. Further studies are recommended to decipher the molecular mechanisms that may be involved in these neuroprotective activities in *in vivo* studies.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding author.

ETHICS STATEMENT

The animal study was reviewed and approved by The animal ethics committee of the University of KwaZulu-Natal, Durban, South Africa (protocol approval number: AREC/020/017D).

AUTHOR CONTRIBUTIONS

MM and OE conceptualized and designed the research project; OE, VS and MI carried out the experiments; MM and OE wrote the original manuscript; all authors revised and approved the final manuscript draft; MM supervised the project.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2020.592981/full#supplementary-material

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Phytochemistry, Pharmacology and Medicinal Uses of Plants of the Genus Salix: An Updated Review

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The Willows (genus *Salix*), with more than 330–500 species and 200 hybrids, are trees, shrubs or prostrate plants that are widely distributed in Africa, North America, Europe, and Asia. The genus is traditionally used in folk medicine and represents a valuable source of biologically active compounds among them salicin, a prodrug for salicylic acid. Altogether, 322 secondary metabolites were characterized in the genus including flavonoids 94) (flavonols, flavones, flavanones, isoflavones, flavan-3-ols (catechins and procyanidins), chalcones, dihydrochalcone, anthocyanins, dihydroflavonols), phenolic glycosides (76), organic acids (28), and non-phenolic glycosides (17), sterols and terpenes (17), simple phenolics 13) and lignans 7) in addition to volatiles and fatty acids (69). Furthermore, willows exert analgesic, anti-inflammatory, antioxidant, anticancer, cytotoxic, antidiabetic, antimicrobial, antiobesity, neuroprotective and hepatoprotective activities. The current review provides an updated summary of the importance of willows, their chemical composition and pharmacological activities.

Keywords: salix, phytochemistry, pharmacology, medicinal and traditional uses, inflammation

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INTRODUCTION

Salicaceae (the Willow and Poplar family) traditionally includes the genera *Populus* (poplar) and *Salix* (willow), which are common in Northern temperate regions, and are amentiferous (bearing catkins) (Isebrands and Richardson, 2014). Presently, the Salicaceae have been enlarged to contain most tropical members of Flacourtiaceae, which do not produce catkin (Thadeo et al., 2014). Thus, the family Salicaceae now comprises about 56 genera and 1,220 species (Christenhusz and Byng, 2016).

The members of Salicaceae are fast growing trees or shrubs (Isebrands and Richardson, 2014). They are used for many economic purposes as production of timber, paper, fences, shelter, snowshoes, arrow shafts, fish traps, whistles, nets, rope, as a biomass fuel (a source of renewable energy), for ornamental, architectural and horticulture uses. Also, they are used for environmental enhancement through soil erosion control (Kuzovkina and Vietto, 2014). Willow twigs are elastic and were used to interweave baskets, for caning, and to manufacture woven fences and other lattices (Isebrands and Richardson, 2014).

The genus *Salix* (the willow) includes 330–500 species and more than 200 hybrids (Isebrands and Richardson, 2014), which are most widely distributed in the Northern hemisphere with a limited

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		R ₃					
No.	R_1	$egin{array}{cccccccccccccccccccccccccccccccccccc$	0 R ₃	R_4	\mathbf{R}_{5}	R_6	
(1)	OH	H	OH	H	H	OH	
(2)	OH	Н	O-Glc.	Н	Н	OH	
(3) (4)	OH OH	H H	O- p-CoumaroylGlc. O-Glac.	H H	H H	OH OH	
(5)	OH	H	O-Gle.	Н	OCH ₂ CH ₃	OH	
(6)	OH	H	ОН	H	OCH_3	OH	
(7)	OH	H	O-Glc.	Н	OCH ₃	OH	
(8) (9)	OH H	H H	O-Glucuronide OH	H H	$ \begin{array}{c} \text{OCH}_3\\ \text{H} \end{array} $	OH OH	
(10)	OH	H	OH	H	OH	Н	
(11)	OH	Н	O-Glc.	OH	H	OCH_3	
(14)	OH	H	OH	H	OH	OCH ₃	
(15) (16)	OH OH	H Glc.	OH OH	H H	OH OH	OH OH	
(17)	O-Glc.	H	OH	Н	OH	OH	
(18)	OH	Н	ОН	H	ОН	O-Glc.	
(19)	OH	H	O-Glc.	H	OH	OH	
(25)	Н	Н	OCH_3	Н	Н	Н	
OR		ÓН			C	ЭН	
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No.		R		но Он (12)		
(20)	tro	ans-Cinnamoyl			,		
(21)		Feruloy1					
(22) (23)		Ac p-Coumaroyl					
(24)	I	Glc.					
()							

number of species occur in the Southern hemisphere (Zhen-Fu, 1987). *Salix* species are widely distributed in Africa, North America, Europe, and Asia (Argus, 2007). *Salix* species are fast growing trees, shrubs or prostrate plants; they can withstand a wide range of different weathers more than *Populus* species, as they grow in temperate, subtropic and tropic regions (Isebrands and Richardson, 2014).

Taxonomy

General morphological characters of genus *Salix* were reported (Argus, 2006; Lauron-Moreau, et al., 2015). Willows are 6–10 m high trees or shrubs with spirally arranged, sometimes silvery, oblong leaves. The latter is commonly hairy on the underside and often turn black when drying. Leaves are simple, petiolate showing different shapes of lamina (oblong, linear, ovate, obovate or round), stipulate with linear to rounded stipules

and with entire, serrate or dentate margin. Their arrangement is mostly alternate or rarely opposite (Lauron-Moreau, et al., 2015). The flowers are catkins, dioecious, with nectaries (glands) instead of perianth and they have bracts, which are pale or black, pubescent or glabrate, constant in male flowers and deciduous in female ones. The flowers blossom in spring, generally prior the leaves (Mabberley 2008). The male catkins have mostly two stamens, more prominent yellow, with few species having 3-12 stamens while the female catkins are greenish, have single pistil with single ovary, style, two-lobed stigma and 2 to 42 ovules per each ovary (Mabberley 2008). The nectar of flowering Willow is the first food source for bees in spring. The seeds are small, with limited longevity, fine hairy coat enabling their spread by wind and they germinate after few days of exposure to moistured surfaces (Mabberley 2008). Recently, the taxonomy of neotropical Salicaceae (formerly

Flacourtiaceae) is difficult, as they show very different morphology and exhibit numerous characteristics in common with several other families. The neotropical Salicaceae and Salicaceae displayed similar characters such as the presence of salicoid leaf teeth, collateral and arch-shaped vascular system at the midrib, abundance of crystals, brachyparacytic stomata, secondary growth of the petiole and sclerenchyma accompanying the bundles (Thadeo et al., 2014).

Phytochemistry

Different phytoconstituents or secondary metabolites of the genus *Salix* as flavonoids, glycosides (phenolic and non-phenolic glycosides), procyanidins, organic acids and their derivatives, simple phenolics, sterols and terpenes, lignans, volatiles and fatty acids were reported (**Supplementary Tables S1–S7**, included in Supplementary materials). *Salix* leaves mainly

contain flavonoids, phenolic acids, their derivatives, and phenolic glycosides, while stem bark mainly contains procyanidins.

Flavonoids

Salix contains a wide variety of flavonoids, which are distinctive for each species, as flavones, flavonols, flavanones, dihydroflavonols, isoflavones, chalcones, dihydrochalcones, flavan-3-ols and anthocyanins (Nasudari et al., 1972; Pobł ocka-Olech and Krauze-Shao et al., 1989; Du et al., 2004; Zeid, 2006; Jürgenliemk et al., 2007; Baranowska, 2008; Freischmidt et al., 2010; Li et al., 2013). Data are summarized in **Supplementary Table S1** and the structures are presented in **Figure 1**.

The highest numbers of different classes of flavonoids (A-E) were detected in leaves and rarely in roots. The flavones as apigenin and its glycosides (1, 2, 4, 5) are major constituents of *S. acutifolia* Willd. leaves (Shelyuto and Bondarenko, 1985), *S.*

matsudana Koidz. leaves (Han et al., 2003a) and S. babylonica L. leaves and roots (Khatoon et al., 1988; Singh et al., 2017). Whereas, chrysoeriol (6), its 7-O-D-glucoside 7) and 7-O-glucuronide 8) are major constituents of S. babylonica L. (Liu et al., 2008), S. matsudana Koidz. leaves (Han et al., 2003b) and S.

subserrata Willd. leaves (Tawfeek et al., 2019), respectively. Compounds (12, 14) were reported in *S. denticulate* leaves (Rawat et al., 2009; Semwal et al., 2011). *S. gilgiana* Seemen. leaves were characterized by the accumulation of acylated luteolin glucosides (19–23) (Mizuno et al., 1987). Compounds (25, 35) are

chemical markers for *S. matsudana* Koidz. leaves (Li et al., 2008). Kaempferol 32) and its 7,4'-dimethyl derivative 33) were found to be most prominent constituents in *S. bordensis* Turcz. (Zhao et al., 2014). Also, kaempferol-7-O-glucoside 34) is a major

compound in *S. babylonica* L. leaves and roots (Khatoon et al., 1988; Singh et al., 2017).

Angeloxyflavone 13) and isoflavones (63, 64) are chemical markers for *S. cheilophila* C. K. Schneid. twigs (Shen et al., 2008).

S. integra \times S. suchowensis young stem was characterized by the accumulation of sulfated flavanones and dihydroflavonol as compounds (49, 52, 58, 60). Compound 11) was reported in the erial parts of S. denticulate Andersson.

The highest number of chalcones, catechins, procyanidins and anthocyanins were detected in the bark of willows. The bark of *S. daphnoides* Vill., *S. elbursensis* Boiss., *S. acutifolia* Willd. and *S. rubra* Huds. were characterized by the accumulation of chalcones

(65–67) (Kompantsev, 1969; Kompantsev and Shinkarenko, 1975; Vinokurov, 1979; Zapesochnaya et al., 2002; Krauze-Baranowska et al., 2013). Catechin 69) and its derivatives (70, 71), epicatechin (72), procyanidin B1 77) and its derivative (78), procyanidin B3 (80) and its derivative (81), procyanidins B6 (84), B7 85) and trimeric procyanidins (87–89) were found to be major constituents of *S. sieboldiana* Blume bark (Hsu et al., 1985). Also, procyanidins (77, 79, 80, 82, 83, 85, 86, 89, 90, 92) are major

(123)	cis -p-Coumaroyl	(114) (115)	OH OH	O-Glc. O-GlucGlc.	OH OH	H H
		(113) (130)	Н	O-GlucGlc.	ОН	P-Hydroxy
						benzoyl Glc.
		(138)	H	ОН	ОН	Glc.
				R ₁ O	//0	
	OCH₃					
	Ö-Glc.		R_2		R_4	
				I R ₃		
	(111) O-Glc.	No.	R_1	R_2	R_3	R_4
	0-610.	(108)	Galloyl-C	Gle. H	ОН	Н
_						
	0					
	(131)	(109)	Galloy		ОН	Н
		(110)	pent. Glc.	Н	ОН	Н
		(112)	Glc.	Н	ОН	OCH_3
		(162)	Glc.	OCH_3	ОН	OCH_3
	0.0					
	OR ₅					
		٥ ِ				
		\sim	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	a		
	HO	OR ₃				
	R ₄ 0		/ \//	R_1		
			R_2			
No. (97)	$egin{array}{ll} R_1 & R_2 \\ H & Salicyloyl \end{array}$	R ₃ H		$ m R_4 \ H$		R_5 Ac
	OH Sancyloyl	Н		Benzoyl		Ac H
(101)	Н	Н		Benzoyl		Н
(107) (113)	H HCH H H	Н Н		Benzoyl H		H Ac
(113)	Н НСН	Ac		Н		HCH
(136)	Н Н	Н		Н	E	Benzoyl
(137) (141)	H p-Coumaroyl H H	H H		H H		H H
FIGURE 2 (Continued).	11	11		11		
FIGURE 2 (Continued).						

(1.43)	11	II	A -	11	TI
(142)	Н	H H	Ac H	H	Н
(143)	Н			Ac	Н
(144)	Н	Н	-(E)- <i>p</i> -Coumaroyl	Н	H H
(145)	Н	Н	-(Z)- <i>p</i> -Coumaroyl	Н	
(146)	Н	Н	Н	Н	-(E)- <i>p</i> -Coumaroyl
(147)	Н	Н	Н	Н	-(Z)-p-Coumaroyl
(148)	Н	Н	<i>p</i> -Coumaroyl	Н	Dihydrobenzoyl
(149)	Н	Н	Cinnamoyl	Н	H
(150)	Н	H	Dihydrocinnamoyl	Н	H
(151)	Н	Malate	Н	Н	H
(152)	Н	چې ړه	Н	Н	Н
		S SOH			
(153)	Н	Salicyloyl (<i>o-</i> Hydroxybenzoyl)	Н	Н	Н
(154)	Н	HCH (1-hydroxy-6-oxo- 2-cyclohexen-l- carboxylate) =	Н	Н	Н
		HOO			
(155)	Н	HCH	Ac	Н	Н
(156)	Н	НСН	Н	Ac	Н
(157)	Н	НСН	Н	Н	Ac
(158)	H	НСН	Ac	H	Ac
(159)	Н	НСН	(E)-Cinnamoyl	Н	H
(161)	Н	ses O	Ac	Н	Н
(164)	Η	Н	Benzoyl	Н	Н
(165)	Η	Salicyloyl	Benzoyl	Н	Н
(166)	Н	НСН	Benzoyl	Н	Н
(167)	Н	Н	Н	Н	<i>p</i> -Coumaroyl
FIGURE 2 (Continued).					

constituents of *S. daphnoides* Vill. bark (Wiesneth, 2019). Anthocyanins (93–95) were detected in the bark of *S. purpurea* L., *S. daphnoides* Vill., *S. alba* L., *S. phylicifolia* L., *S. nigricans* Sm., *S. calodendron* Wimm. *and S. viminalis* L., *S. triandra* L. and *S. amygdalina* L. (Bridle et al., 1970; Bridle et al., 1973).

Phenolic Glycosides

Glycosides are major secondary metabolites in Salicaceae (Binns et al., 1968; Kompantsev and Shinkarenko, 1973; Kompantsev et al., 1974; Nichols-Orians et al., 1992; Fernandes et al., 2009). Phenolic glycosides represent up to 30% of dry plant mass.

They are classified into two main classes: Salicin derived glycosides (salicinoids) and other phenolic glycosides as glycosylated phenylpropanoids, phenylethanoids and benzenoids and glycosylated salicylic acid derivatives. Salicinoids, which are considered as taxonomic markers for genus *Salix*, are derivatives of salicin, produced by esterification of one or more hydroxyl groups of salicyl alcohol or glucose moieties, mainly 2' and/or 6' of glucose, with organic acids as acetic, benzoic and 1-hydroxy-6-oxocyclohex-2-en-1-carboxylic (HCH) acids. The phenolic glycosides isolated and/or identified from genus *Salix* are presented in **Supplementary Table S2** and **Figure 2**.

The highest number of phenolic glycosides were reported in *Salix* leaves, followed by twigs, stems and bark. Salicin (141), tremuloidin (164), tremulacin 166) were found to be the major constituents in *S. Acutifolia* Willd. juvenile stem and bark (Zapesochnaya et al., 2002; Wu et al., 2016), *S. chaenomeloides* Kimura leaves (Mizuno et al., 1991), *S. glandulosa* Seemen. twigs (Kim et al., 2015) and *S. tetrasperma* Roxb. leaves (El-Shazly et al., 2012).

Some phenolic glycosides were identified as taxonomic markers for different *Salix* species. Acmophyllin A 96) and acmophyllin B 97) identified as taxonomic marker for *S. acmophylla* Boiss. leaves (Shah et al., 2016). Chaenomeloidin (101), cochinchiside A (107), lasiandrin (133), leonuriside A (134), salicin-7-sulfate 152) identified

as taxonomic markers for *S. chaenomeloides* Kimura leaves (Mizuno et al., 1991), *S. glandulosa* Seemen. twigs (Kim et al., 2015), *S. lasiandra* leaves and twigs (Reichardt et al., 1992), *S. matsudana* Koidz. leaves (Li et al., 2008) and *S. koriyanagi* Kimura. Stems (Noleto-Dias et al., 2018), respectively. Sachaliside 1 139) and sachaliside 2 (140) were identified as taxonomic markers for *S. sachalinensis* F. Schmidt (Mizuno et al., 1990).

Some *Salix* species were characterized by accumulation of 1,2-cyclohexanediol glycosides. Compounds (116–128) were detected in *S. glandulosa* Seemen. twigs (Kim et al., 2014). Also, acutifoliside, a benzoic acid derivative 98) was a chemical marker for *S. acutifolia* Willd. juvenile stem (Wu et al., 2016).

$$(172) \qquad (173) \qquad No. \qquad (174) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (175) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (175) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (175) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (176) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (178) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (178) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (188) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (188) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (188) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (186) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (187) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (188) \qquad \alpha -1-Arap-1 = 6j\beta D-Gilc. \qquad (187) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (187) \qquad \beta D-Apjf(1) = 6j\beta D-Gilc. \qquad (188) \qquad \alpha -1-Arap-1 = 6j\beta D-Gilc. \qquad (188)$$

Non-Phenolic Glycosides

Non-phenolic glycosides (172, 173, 174, 175, 176, 182–188) were found to be the major constituents in *S. triandra* L. *x dasyclados* Wimmer Wood (Noleto-Dias et al., 2019). Also, compounds (170, 171) are the major constituents in *S. arbusculoides* Andersson twigs (Evans et al., 1995). Some *Salix* species were characterized by accumulation of 1,2-cyclohexanediol glycosides. Compounds (177, 180) were detected in *S. glandulosa* Seemen. twigs (Kim et al., 2014) and grandidentin 181) was reported in *S. purpurea* L. bark (Pearl and Darling, 1970) (Supplementary Table S3 and Figure 3).

Organic Acids

Salix species are rich sources for phenolic acids, either in free or esterified form, as benzyl, cinnamyl or phenyl ethyl esters. The aromatic acids are either benzoic or cinnamic acid derivatives: benzoic acid derivatives as *p*-hydroxybenzoic, *p*-anisic, gallic, salicylic, gentisic, vanillic, 2-amino-3-methoxy benzoic and protocatechuic acids, while hydroxycinnamic acid derivatives as *p*-coumaric, caffeic, isoferuolic, and feruolic acids, (Supplementary Table S4 and Figure 4).

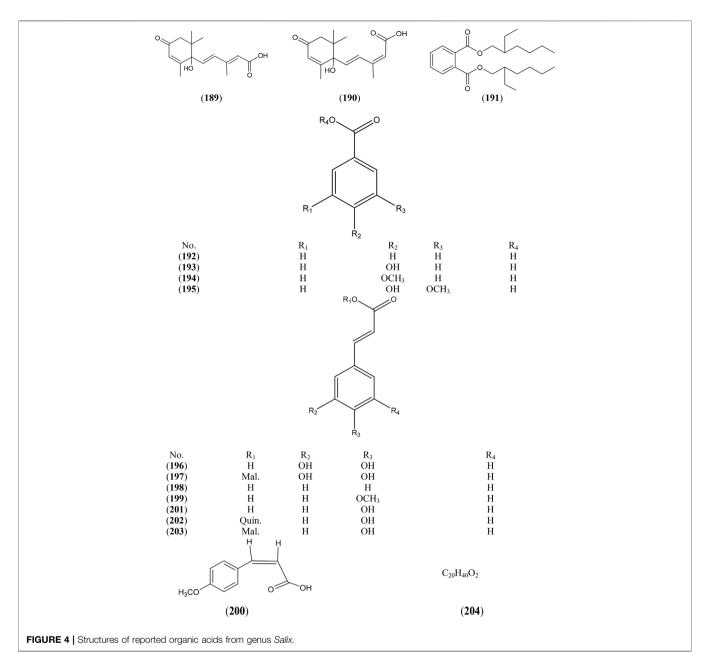
The higest number of organic acids were detected in *S. purpurea* L., *S. alba* L. bark (Agnolet et al., 2012) which contain compounds (192–194, 198–200, 214), *S. tetrasperma* Roxb. flowers and bark (Sobeh et al., 2019; Mostafa et al., 2020) which contain compounds (197, 202, 203, 204, 205–206, 208, 209, 215).

Simple Phenolics

Genus Salix comprises a vast variety of simple phenolic compounds (Phenolic acids and their derivatives) (Tuberoso et al., 2011). S. capensis Thunb. bark (Masika et al., 2005), S. acutifolia Willd. bark (Zapesochnaya et al., 2002), S. subserrata Willd. bark (Hussain et al., 2011), S. caprea L. inflorescence (Ahmed et al., 2017) were characterized by the accumulation of salicyl alcohol 228) which is the basic nucleus for salicinoids. Also, S. caprea L. wood was characterized by the accumulation of different simple phenolics as aucuparin (218), methoxyaucuparin (219), coniferyl alcohol (221), p-coumaryl alcohol (222), 4,2'-dihydroxy-3,5-dimethoxybiphenyl 223) and sinapylaldehyde 229) (Malterud and Dugstad, 1985; Pohjamo et al., 2003), as illustrated in Supplementary Table S5 and Figure 5.

Sterols and Terpenes

The highest number of sterols and triterpenes was detected in *S. cheilophila* C. K. Schneid. twigs (Shen et al., 2008), *S. tetrasperma* Roxb. bark, leaves and flowers (El-Shazly et al., 2012; Sobeh et al., 2019), *S. subserrata* Willd. leaves (Balbaa et al., 1979), *S. denticulate* erial parts (Rawat et al., 2009), *S. babylonica* L. roots (Singh et al., 2017), *S. subserrata* Willd. bark and leaves (Hussain et al., 2011). Whereas phytane and pimarane diterpene were found to be the major constituents in *S. cheilophila* C. K. Schneid. twigs (Shen et al., 2008), as illustrated in **Supplementary Table S6** and **Figure 6**.



Lignans

Sisymbrifolin a lignan derivative 247) had been isolated from the bark of *S. alba* L. (Du et al., 2007). Recently, pinoresinol (248), lariciresinol (249), secoisolariciresinol (250), 7-hydroxymatairesinol (251), medioresinol (252), and lariciresinol-sesquilignan 253) were detected in the biomass of five willow sp. cultivated in Quebec, Canada (Brereton et al., 2017) as illustrated in **Figure 7**.

Volatiles

Terpenes (hemi-, mono- and sesqui-terpenes) and non-terpene (aliphatic, aromatic acids, their esters, carbonyl compounds and hydrocarbons) volatiles were identified in the genus *Salix*. The highest percent of volatiles and fatty acids was reported in *S. caprea* L. inflorescence (Ahmed et al., 2017), and the leaves of *S. egyptiaca*

L. (Karimi et al., 2011), S. babylonica L. (Salem et al., 2011), and S. alba L. (Zarger et al., 2014) (Supplementary Table S7and Figure 8).

Traditional Uses

Salix plants have been used medicinally since antiquity and have been linked to the discovery of acetylsalicylic acid and aspirin. These plants had been traditionally used to treat painful musculoskeletal joint pain conditions, inflammation, and fever. Salicin is a major pharmacologically active metabolite in Salix and hydrolyzes in the gastrointestinal tract to confer salicyl alcohol and D-glucose. The latter is oxidized, upon absorption, into salicylic acid, the active drug which inhibits cyclooxygenases (COX I, II) (Mahdi, 2010).

S. egyptiaca L (Musk Willow) was important in the Middle East, especially in Iran, as it has been traditionally used to treat anemia and

vertigo, as a cardiotonic agent, and also in the preparation of local candies as a fragrance additive (Asgarpanah, 2012). *S. alba* L (white willow), had used in folk medicine to treat fever, chronic and acute inflammation, pain and infection (Zengion and Yarnell, 2011; Maistro et al., 2019). *S. tetrasperma* Roxb. had been used to treat diseases such as epilepsy, diabetes, fever, rheumatism, piles, swellings, stones in bladder, dysentery, wound, ear pain, cough and cold (Prashith Kekuda et al., 2017). *S. alba* L. bark is traditionally used for treatment of flu, rheumatism, fever and headache (Van Wyk and Wink, 2018).

Pharmacological Activity

Different *Salix* species and the isolated compounds as salicylic acid and salicin have been utilized in folk medicine to treat rheumatic diseases, back pain, toothache, headache, and menstrual cramps (Highfield and Kemper, 1999). They exert analgesic, anti-inflammatory, antioxidant, anticancer, cytotoxic,

antidiabetic, antimicrobial, anti-obesity, neuroprotective and hepatoprotective activities. The main targets of salicylic acid are cyclooxygenases (COX I, II) which are key enzymes of pathway to prostaglandins which control inflammation and pain. The available scientifically based reports on biological activities of genus *Salix* are summarized in **Tables 1–8**.

Antimicrobial Effects of Salix

Multidrug-resistant bacteria are widely spread, and natural resources have been used as a means of discovering novel antibacterial compounds as they offer limitless opportunities for the discovery of new agents, particularly against multidrug resistant bacteria.

The main methods used to evaluate the antimicrobial activity of *Salix* extracts are disc diffusion assays, agar well diffusion, broth microdilution methods and the assessment of antibiofilm function (Masika et al., 2005; Fayaz and Sivakumaar, 2014;

Popova and Kaleva, 2015; Mostafa et al., 2020). As detailed in **Table 1**, microbial growth inhibition zones and percentages along with minimum inhibitory concentrations (MICs) displayed the potential of *Salix* species as substantial antimicrobials and predict their efficacy as functional foods (Mostafa et al., 2020).

Antibacterial Activity

Many previous studies evaluated the antibacterial activity of Salix plants and active constituents of their extracts against different types of bacteria such as Pseudomonas eruginosa, Escherichia coli, Staphylococcus aureus and Bacillus subtilis, dental biofilm forming bacteria (Streptococcus mutans and Lactobacillus), and Salmonella enterica (Table 1). Catechol and 2-hydroxybenzyl alcohol derived from the bark of *S. capensis* Thunb. were previously tested for their antibacterial activity. Both compounds exhibited similar antibacterial activity against P. eruginosa (Masika et al., 2005). Moreover, Salix alba L. bark extract demonstrated antimicrobial activity against the dental biofilm forming bacteria with MIC of 125 µg/ml. Furthermore, it also exhibited a moderate potential against the Staphylococcus aureus but the least activity was observed against E. coli (Fayaz and Sivakumaar, 2014). Previous studies also showed that the twigs aqueous extract with leaves of S. babylonica L. exhibited potent antimicrobial properties against Gram-negative bacteria (E. coli, Salmonella enterica, MIC50 is $70.4 \pm 17.41 \,\mathrm{mg/ml}$) with a comparable activities to thiamphenicol (The broad spectrum antibiotic). Its effects cover Gram-positive bacteria such as S. aureus (Popova and Kaleva,

2015). A recent study performed in our laboratories tested the extracts of both stem bark and flowers of *S. tetrasperma* Roxb. for anti-quorum sensing activity against *Pseudomonas eruginosa*. Both extracts inhibited *P. eruginosa* bacterial growth at 40 mg/ml; however, the bacterial viability was not affected by 1/4 and 1/8 MIC concentrations. When the extracts were tested as anti-quorum sensing agents, they impaired virulence of *P. eruginosa* by declining its swimming and swarming motilities and reducing its hemolytic and proteolytic properties (Mostafa et al., 2020).

Antifungal Activity

Poisoned food technique, broth microdilution method, filter disc assay and growth curve study methods were used to determine the antifungal properties of *Salix* extracts (**Table 2**). The antifungal activity was evaluated against *Candida guilliermondii*, *C. glabrata*, *C. parapsilosis* and *Fusarium oxysporum*.

Anthelmintic Activity

The anthelmintic potential of *Salix* species to inhibit gastrointestinal and pulmonary parasites in animals was studied. The anthelmintic activity was evaluated against *Ostertagia*, *Moniezia*, *Dictyocaulus*, *Eimeria*, *Chabertia*, *Cooperia*, and *Hemonchus contortus* (**Table 2**). It was reported *Salix babylonica* L (at dose of 20 ml, weekly) was effective against the main parasite species detected in sheep (*Eimeriaspp.*, *Dictyocaulus* spp., and *Chabertia* spp.) more than the most

common parasites in goats in southern Mexico farms (*Dictyocaulus* spp. and *Chabertia* spp.) (Salem et al., 2017).

Anti -HIV Activity

Human immunodeficiency virus (HIV) infection that causes acquired immunodeficiency syndrome (AIDs) represents a major health problem worldwide. Chemical anti-retroviral agents are usually used to treat AIDs patients. However, they possess many adverse effects and resistance emerged for many of them. Recently, novel anti-retroviral agents isolated from medicinal plants, played an essential role to replace synthetic drugs. One study investigated the anti-retroviral effects of *S. egyptiaca* L. extract. Results of this study and bioinformatics

analyses suggested that the plant had anti-HIV properties and might be a substantial candidate for AIDS patients (**Table 2**) (Eftekhari et al., 2014).

Antioxidant Activity

Reactive oxygen species (ROS) are associated with several human diseases, such as inflammation, diabetes, ulcers, autoimmune and cardiovascular diseases, viral infections and cancer (Howlett, 2008; Rubió et al., 2013; Salem et al., 2020). Most of the activities of *Salix* species were attributed to the presence of several polyphenolic with robust antioxidant activities (**Table 3**). The antioxidant effects of *Salix* extracts and their flavonoids were mainly assessed by DPPH, ABTS, FRAP, total

antioxidant capacity (TAC) assays, Folin-Ciocalteu method, β-carotene bleaching, lipid peroxidation capacity, inhibition of linoleic acid oxidation, superoxide anion radical scavenging, and alkyl radical scavenging assays (Ceyhan, 2014; Gawlik-Dziki et al., 2014; Tavakoli et al., 2016; Zaiter et al., 2016; Nauman et al., 2018; Zabihi et al., 2018; Gligoric' et al., 2019). A recent study from our lab investigated the possible effect of *S. tetrasperma* Roxb. extract on neuropathic pain and its mechanism of action showed a potent *in vitro* and *in vivo* antioxidant effects (Sobeh et al., 2019). Furthermore, *S. atrocinerea* Brot., *S. fragilis* L. and *S. viminalis* L. showed antioxidant effects mediated by their polyphenolic contents (Ramos et al., 2019). Another study from our laboratory showed that *S. subserrata* Willd. leaf extracts contained

isorhamnetin-3-O- β -D-rutinoside, triandrin, gallocatechin, tremuloidin, aromadendrin, salicin, and chrysoeriol-7-O-glucuronid and exerted antioxidant effects against oxidative stress in *Caenorhabditis elegans* (Tawfeek et al., 2019).

Anti-Inflammatory Activity

Inflammation is a frequent condition because of exposure to different stimuli including microbial infection and wounding. It decreases the spread of infection, followed by resolution and the restoration of normal structural and functional of affected tissues (Nathan and Ding, 2010). However, non-resolving inflammation contributes significantly to the pathogenesis of many diseases such as atherosclerosis, obesity, cancer, and inflammatory bowel

disease. *Salix* extracts exert potent anti-inflammatory effects that are responsible for many biological effects. The hydroalcoholic extract of *S. tetrasperma* Roxb. in two dose levels (100 and 200 mg/kg) demonstrated anti-inflammatory effects in carrageenan induced rat paw edema model (Kishore et al., 2014). We showed previously that the flower extract of *S. tetrasperma* Roxb. has analgesic, antipyretic, and anti-inflammatory effects against carrageenan induced vascular permeability and carrageenan induced hind paw edema. It inhibited COX-1, COX-2 and LOX and suppressed elevated levels of TNF-a and NF-κB in chronic neuropathic pain model (Sobeh et al., 2019). Oral administration of *S. canariensis* extract

significantly decreased writhing, moderately reduced formalin-induced pain and showed a promising dose-dependent anti-inflammatory activities. These effects were attributed to the presence of pentacyclic triterpenes and polyphenolics (Gutiérrez et al., 2017). An early study showed that *S. caprea* L. is a potent cyclooxygenase inhibitor (Tunon et al., 1995). Another study showed that *S. subserrata* Willd. and *S. tetrasperma* Roxb. showed anti-inflammatory effects against carrageenan induced hind paw edema due to the presence of phenolic glycosides mainly salicin as well as the flavonoids luteolin, quercetin and rutin (Karawya et al., 2010). *S. matsudana* Koidz. leaves methanol extract also showed

significant inhibitory activities against cyclooxygenases (COX-1 and COX-2) due to the presence of matsudone, luteolin 7-O-glucoside and 4',7-dihydroxyflavone (Li et al., 2008).

Anticancer Activity

There are several risk factors that can increase the development of cancer that have a basis of low-grade inflammation and oxidative stress. Therefore, targeting inflammatory pathways and suppressing oxidative stress may contribute to inhibition of initiation, proliferation and even cancer metastasis and subside resistance to chemotherapy and radiation. *Salix* extracts, by possessing both anti-inflammatory and potent antioxidant potential, are promising natural

sources in fighting cancer. The antiproliferative activities of Salix extracts were determined by cell viability percentages and IC_{50} values using several $in\ vitro$ assays. The most commonly utilized cancer cell lines were human acute lymphoblastic leukemia (ALL cells), human acute myeloid leukemia cells (AML cells), PC3 cells (Prostate cancer cells), Hep G2 cells (Liver cancer cells), HCT116 (Colorectal cancer cells), MCF7 (Breast cancer cells), HT-29 and HCT 116 (human colon COX-2 positive and negative cells respectively), A549, SW2 cells, and human lung cancer cell line (H1299).

It was observed that a fraction of *Salix* extracted by non-polar solvents such as (petroleum ether, ether, and chloroform) has the minimum killing potential against AML cells while fraction

extracted by polar solvents such as 70% ethanol and water has major destructive effect on AML cells (El-Shemy et al., 2003). Thus, *Salix* cytotoxic activity could be attributed to the polyphenolics, tannins, and glycosides, that are commonly dissolved in water or ethanol solutions including salicin and saligenin. When salicin is tested against leukemic cells it caused destruction of myeloblasts by 70–75%. Eight compounds isolated from *S. hulteni* Flod (1-p-coumaroyl-β-D-glucoside, aromadendrin, catechin, 4-hydroxyacetophenone, picein, sachaliside 1, naringenin and dihydromyricetin) were tested

for their cytotoxic potential against brine shrimp and a human lung cancer cell line (H1299). Naringenin, aromadendrin, catechin, and 1-*p*-coumaroyl-β-D-glucoside showed mild cytotoxic activity, with dihydromyricetin showing the strongest cytotoxic effects. 4-Hydroxyacetophenone, picein, and sachaliside one did not show a significant cytotoxic activity indicating that flavonoid compounds are responsible for the cytotoxic effects of *S. hulteni* Flod. (Jeon et al., 2008). Brine shrimp lethality test is commonly used to test cytotoxic effects of natural products. The methanol extract of *S. nigra* exerted

TABLE 1 | Anti-bacterial activity of Salix species.

Bacteria	Extract/Compound	Used method	Effects	References
B. subtilis S. aureus E. coli P. eruginosa	S. capensis thunb. Bark catechol 2-hydroxybenzyl alcohol	Bioautographic assay on TLC plate, microplate dilution method broth culture	MIC = 62.5–250 μg/ml	Masika et al. (2005)
S. mutans S. aureus Lactobacillus sp	S. alba L. bark methanol extract	Disc diffusion method	MIC = 125 μg/ml 250 μg/ml for lactobacillus	Fayaz and Sivakumaa (2014)
E. coli Salmonella enterica	Aqueous extracts of S. babylonica L. leaves	Agar-gel diffusion method and twofold serial dilutions on mueller-hinton s agar	Inhibition zones with an average diameter of 13.38 ± 2.22 mm MIC50 = 70.4 ± 17.41 mg/ml	Popova and Kaleva (2015)
E.coli, S.aureus Listeria monocytogenes	Hydroalcoholic extract, fractions, and subfractions of S. babylonica L	Broth microdilution method	MIC = 0.78 mg/ml for <i>Listeria monocytogenes</i> , MIC = 0.39 mg/ml for <i>S. aureus</i>	González-Alamilla et a (2019)
P. eruginosa	Methanol extracts of S. tetrasperma roxb. Stem bark and flower	Broth microdilution method, skim milk agar method	Inhibition of swimming and swarming motilities, and proteolytic and hemolytic activities	Mostafa et al. (2020)

TABLE 2 | Antifungal, anthelmintic and anti-retroviral activity of Salix species.

Micro-organism	Extract/compounds	Used method	Effects	References
Fungi				
Fusarium oxysporum	Ethanol extract of S. babylonica L. root	Poisoned food technique	Good fungicidal activity at 20% concentration	Sati et al. (2013)
Candida guilliermondii, C. glabrata and C. parapsilosis	Methanol extract of S. alba L. leaves	Broth microdilution method, filter disc assay and growth curve study	MIC = 800 μg/ml, 800 μg/ml and 1,600 μg/ml respectively. Inhibition i.e. 12 mm for <i>C. glabrata</i> followed by 11 mm measured in <i>C. parapsilosis</i> . <i>C. guilliermondii</i> inhibition was 10 mm	Zarger et al. (2014)
Parasites				
Hemonchus contortus, Eimeria Cooperia, Chabertia, Dictyocaulus,	Leaves of S. babylonica L. extract	Oocyst and egg count technique in goat and sheep	20 ml oral doses decrease oocyst and egg count in both species	Salem et al. (2017)
Moniezia, and Ostertagia				
Bonostomum sp., Strongiloides papillosus, and Nematodiruss pathiger Nematodirus battus	Leaves extract of S. babylonica L	Salt floatation technique and McMaster method	The extract caused egg and worm count reductions in lamb feces by 47% vs. the control lambs	Hernandez et al (2014)
Virus				
HIV-1	S. egyptiaca L. Pl extract	XTT method. Inhibition of p24 Ag production level assay	The IC $_{50}$ in HeLa infected cells was 45 $\mu g/ml$ 100 $\mu g/ml$ extract inhibited the production of HIV-1 p24 Ag by more than 80%	Eftekhari et al. (2014)

concentration dependent cytotoxic effects against brine shrimp indicating promising cytotoxic effects (Ahmed et al., 2016). Willow bark extract (A pharmaceutically used extract BNO 1455) and its fractions (flavonoids, proanthocyanidins, salicyl alcohol derivatives) showed dose dependent cytotoxic effects against human colon and lung cancer irrespective of their COX-2 selectivity (Hostanska et al., 2007). S. caprea L. exerted a protective effect against phorbol ester induced skin tumor promotion when applied to the skin of mice prior to the application of phorbol ester. Anti-tumor activity of S. caprea L. may be attributed to potent antioxidants constituents of S.

caprea L. such as luteolin, dihydrokaempferol and quercetin (Sultana and Saleem, 2004).

Neuroprotective Effect

Only few studies investigated the effect of *Salix* species on central and peripheral nervous system. Virupaksha et al. (2016) investigated the effects of *S. tetrasperma* Roxb. leaf extract on locomotor activity and muscle relaxant activity. They demonstrated that the extract decreased locomotor activity indicating central nervous system (CNS) depressant activity and induced a decrease in fall off time due to loss of muscle grip implying skeletal relaxation (Virupaksha

TABLE 3 | Invitro antioxidant activity of Salix species.

Plant part	Extract/compound	Method	Effects	References
Stem and leaves	Four sulfated flavonoids (taxifolin-7-sulfate, dihydrokaempferol-7-sulfate, eridictyol-7-sulfate andnaringenin-7-sulfate) isolated from hybrid species of <i>Salixxalberti</i> L	DPPH	7-Sulfation of taxifolin and eriodictyol attenuated but does not remove antioxidant activity	Noleto-Dias et al. (2020)
Leaves	Methanol extracts of S. purpurea L., S. cinerea L., Salixxsmithiana willd., S. alba L., S. eriocephala michx., Salixxrubra huds	DPPH	The scavenging effect ranged between 33.6 (S. purpurea L.) and 45.7% (S. cinerea L.), 50.7 (S. purpurea L.) to 56.3% (Salix×rubra huds.)	Gąsecka et al. (2017)
Leaves	Ethyl acetate extract of S.tetrasperma roxb	DPPH assay	$IC_{50} = 65.89 \mu\text{g/ml}$	Januarti et al.
Leaves	Methanol extract of S. mucronata andersson	DPPH, ABTS and TAC assays	DPPH (EC $_{50}$ = 98.76 ± 0.46 (µg/ml), ABTS = 45.83 ± 0.32 mm, trolox eq./100 gm extract and TAC = 199.18 ± 2.19 mg equivalent of ascorbic acid/g extract). EtOAc fraction derived from MeOH (85%) extract demonstrated the highest antioxidant potential; DPPH EC $_{50}$ = 50.19 ± 0.24 (µg/ml), ABTS = 76.22 ± 1.61 (mm trolox eq./100 gm extract) and TAC = 249.86 ± 3.74 (mg equivalent of ascorbic acid/g extract)	(2019) El-Sayed et al. (2015)
Male inflorescence	Methanol extract of S. egyptiaca L	DPPH and the folin-Ciocalteu method	Butanol fraction showed the highest antioxidant potential with an IC ₅₀ value of 27.7 µg/ml	Sonboli et al. (2010)
Flowers	Ethanol extract of S. caprea L	DPPH, superoxide hydrogen peroxide and nitric oxide scavenging assay	At a concentration of 250 μg/ml, 85.04% of DPPH radicals and at μg/mL 45.97%, 17.97% and 56.53% of O ₂ ·-, H ₂ O ₂ and NO, respectively, were scavenged by the S. caprea L. flower extract	Alam et al. (2006)
Leaves, bark, catkins	Cyclohexane, butanol, ethanol and water extract of <i>S. egyptica</i> L	DPPH assay	Ethanol extract of the bark (highest activities, IC ₅₀ = 19 μg/ml)	Enayat and Banerjee (2009
Bark	Hot ethanol extract of S. alba L	DPPH and folin-ciocalteu method	Free radical scavenging activity values ranged between 12.50, 37.50 and 80.00% of 10, 50 and 100 μg/ml, respectively	Sulaiman et al. (2013)
Bark	S. alba L., S. daphnoides Vill., S. purpurea L., and S. daphnoides Vill. x purpurea L. hybrid willow clones	ABTS	S. daphnoides Vill. x purpurea L. extracts were the most active ones.	Gawlik-Dziki et al. (2014)
Leaves and young stems	Hydroethanolic extract of S. alba L.	DPPH	$IC_{50} = 19.1 \ \mu g/ml.$	Zabihi et al. (2018)
Leaves and male inflorescence catkin	S. matsudana Koidz. S. aegyptiaca L. S. babylonica L. S. excelsa S. G. Gmel. S. acmophylla Boiss.	DPPH, superoxide, nitric oxide and hydrogen peroxide radical scavenging activity	DPPH results ranged from 40.08% (S. excelsa) to 91.94% (S. aegyptiaca L.) and S. excelsa S. G. Gmel. displayed the potent superoxide (99.00%) and nitric oxide (71.73%) scavenging potential. Similar activities were found for hydrogen peroxide radical scavenging (50%) for S. matsudana Koidz., S. acmophylla Boiss. and S. babylonica L Male inflorescence catkin extracts, S. excelsa S. G. Gmel (70.63%), S. acmophylla Boiss. (60.25%) and S. matsudana Koidz. (62.37%) presented the most activities in DPPH, nitric oxide and hydrogen peroxide, respectively. The S. excelsa S. G. Gmel, S. aegyptiaca L. and S. babylonica L. showed 99% superoxide radical inhibition.	Tavakoli et al. (2016)
Bark	Gallic acid, quercetin, rutin, vanillin and acetylsalicylic acid obtained from <i>S. aegyptiaca</i> L.	DPPH	gallic acid > quercetin >rutin> vanillin > acetylsalicylic acid.	Nauman et al. (2018)
	aogyphaoa E.			

TABLE 3 | (Continued) Invitro antioxidant activity of Salix species.

Plant part	Extract/compound	Method	Effects	References
Bark	S. alba L.	DPPH	All granulometric classes revealed a high antioxidant activity. The best results were obtained for the 50–100 μm granulometric class.	Zaiter et al. (2016)
Flowers	Methanol extract of S.tetrasperma Roxb	TAC	30.97 ± 2.6 , 26.8 ± 2.1 U/L for the extract and ascorbic acid, respectively.	Sobeh et al. (2019)
Bark	S. atrocinerea Brot., S. fragilis L., and S. viminalis L. bark polar extracts	DPPH and ABTS.	Strong free radical scavenging activity (5.58–23.62 μ g mL-1 IC ₅₀ range.	Ramos et al. (2019)
Leaves and bark	n- Hexane, dichloromethane, ethyl acetate and n- butanol extracts of <i>S. subserrata</i> Willd.	DPPH and FRAP assays.	IC_{50} μ g/mL = 9.30 - 206.67 for DPPH assay and 2.90-26.89 mM FeSO ₄ /mg extract for FRAP assay.	Tawfeek et al. (2019)
bark and leaves	S. alba L., S. amplexicaulis Bory & Chaub., S. babylonica L., S. eleagnos Scop., S. fragilis L., S. purpurea L. and S. triandra. L.	DPPH and OH radical scavenging assay.	IC ₅₀ of DPPH ranged from 1.83–7.79 µg/mL in bark and 1.95–8.07 µg/mL in leaves extracts of different species of the genus Salix	Gligorić et al. (2019)

TABLE 4 | In vitro antiproliferative effects of Salix species.

Extract/compound	Cell line	Methods	Results	Mechanism of action	References
Aqueous extract from <i>S. safsaf</i> forsk	AML	Trypan blue exclusion test	Killed most of the blasts of acute myeloid leukemia (AML, 73.8%)	Cells are killed through denaturation of some enzymes and proteins that are induced by salicin and saligenin	El-Shemy et al. (2003)
Aqueous extract of leaves extract of <i>S. safsaf</i> forsk. Salicin and saligenin	ALL and AML	Trypan blue exclusion test	A remarkable destruction of lymphoblasts (75%) was observed after 24 h incubation of the mononuclear ALL cells with extract. Similar trends were observed for mononuclear AML cells. The mean viability of willow extract treated cells was 26.2%	Unknown receptors on the surface of leukemic cells may be binding with Salix extract compounds and leading to DNA destruction	El-Shemy et al. (2007)
Salicylalcohol derivatives, flavonoids, proanthocyanidins, and salicin isolated from willow bark extract BNO 1455	Human colon cyclooxygenase-2 (COX-2)- positive HT 29 and (COX-2)- negative HCT 116 or lung COX-2 proficient a 549 and low COX-2 expressing SW2 cells	WST-1 assay and propidium iodide uptake by flow cytometry, annexin V adhesion using flow cytometry for apoptosis	Gl ₅₀ 33.3–103.3 μg/ml for flavonoids and proanthocyanidins fractions and 50.0–243.0 μg/ml for salicyl alcohol derivatives and extract	ND	Hostanska et al. (2007)

et al., 2016). The CNS depressant activity of the extract was attributed to binding of flavonoids to gamma-aminobutyric acid (GABA) receptors in the CNS (Hossain et al., 2009). Another study from our laboratory investigated the possible protective effect of *S. tetrasperma* Roxb. on neuropathic pain model, chronic constriction injury of sciatic nerve model. In this work, we explored the effects of the extract on central and peripheral nervous system in this model. We showed that the extract improved hyperalgesia and allodynia, the major signs of neuropathic pain through inhibition of oxidative stress and inflammation in sciatic nerve and brain stem (Sobeh et al., 2019).

Hepatoprotective Effects

S. subserrata Willd. flower extract showed marked hepatoprotective effects mostly through lowering the elevated

liver enzymes and decreasing the protein levels of two inflammatory biomarkers (NF- κ B and TNF- α) in carbon tetrachloride (CCl₄)-induced liver damage model (Wahid et al., 2016). It also presented a remarkable ability to reduce lipid peroxidation and had antioxidant effects related to several active ingredients that include flavonoids such as quercetrin, luteolin-7-glucoside, rutin, and quercetin and phenolic compounds such as salignin and catechins.

Anti-Obesity and Anti-lipidemic Effects

As shown in **Table 8**, remarkable anti-obesity and anti-lipidemic effects have been attributed to *Salix* extracts. The reduction of parametrial adipose tissue weight and body weight gain, the reduction of liver total cholesterol contents and inhibition of the elevated blood triacylglycerol are among the most

TABLE 5 | In vivo anticancer effects of Salix species.

Extract/compound	Doses	Route of administration	Methods	Effects	Mode of action	References
Aqueous extract from the young developing leaves of willow (S.safsaf forsk.)	0.2 and 0.6 ml of extract (10% w/v)	Oral	EACC were injected into the intraperitoneal cavity of mice	The willow extract reduced the tumor growth and delayed the death was delayed	Promote apoptosis, cause DNA damage, and affect cell membranes and/or denature proteins	El-Shemy et al (2007)
Acetone soluble fraction of <i>S.caprea</i> L.flowers	0.5, 1.0 and 1.5 mg/kg	Topical application on the skin	7,12-Dimethyl benz [a] anthracene DMBA- initiated croton oil (phorbol ester)mice	Reductionin tumor incidence and number of tumors per mouse ranging from 20 to 50% and 50–63%	Intercept the free radicals and protect cellular macromolecules from oxidant damage. Effectiveness in inhibiting the ornithine decarboxylase activity and maintaining the activity of phase II enzymes after toxicant exposure	(Sultana and Saleem (2004)

Extract/Compound	Doses	Route	Model	Effect	References
Ethanol and aqueous extracts of S.	200 and	Oral	Mice	Decrease locomotor activity indicating CNS depressant activity	Virupaksha et al.
tetrasperma roxb. Leaves	400 mg/kg			in mice and has muscle relaxant activity	(2016)
Methanol extract of S. tetrasperma roxb.	200 and	Oral	CCI rat	Relieve hyperalgesia and allodynia responses	Sobeh et al. (2019)
FLowers	400 mg/kg		model		

TABLE 7 | In vivo hepatoprotective effects of Salix species and their major constituents.

Extract/Compound	Doses	Route	Model	Effect	References
Ethanol extract of S.	150 mg/kg	Oral	CCl ₄ -induced chronic	The elevated serum levels of intracellular liver enzymes and the	Wahid et al.
subserrata willd. Flowers			hepatotoxicity in rats	expression levels of TNF- α and NFkB proteins were reduced	(2016)
S. caprea L. flowers	50, 100,	Oral	Mice injected with ferric	Decreased hepatic lipid peroxidation, increased hepatic	Alam et al.
	150 mg/kg		nitrilotriacetate (FeNTA)	glutathione (GSH) content and the activities of antioxidant	(2006)
				enzymes (catalase (CAT), glutathione reductase (GR) and	
				glutathione peroxidase)	

TABLE 8 | In vivo anti-obesity and anti-lipidemic effects of Salix species and their major constituents.

Extract/compound	Doses	Route of administration	Model	Effects	References
Ethanol extracts prepared from S. babylonica L. leaves	2.5 or 10 g (extract)/kg food	Supplemented in diet	HFD mice	Decreased body weight and parametrial adipose tissue weight	Liu (2012)
Ethanol extracts prepared from <i>S. babylonica</i> L. leaves	10%	Supplemented in diet	Rats orally administered 1 ml of a lipid emulsion composed	The extracts inhibited the elevation of blood triacylglycerol	Liu (2012)
Polyphenol fractions of S. matsudana koidz. Leaves	5%	Supplemented in diet	HFD mice	Decreased body weight and reduced the hepatic total cholesterol content	Han et al. (2003a)

prominent, directly attributed to its ability to inhibition of intestinal absorption of dietary fat (Liu, 2012). These effects have been mostly attributed to polyphenol fractions (apigenin-7-O-D-glucoside, luteolin-O-D- glucoside and chrysoeriol-7-O-D-glucoside) which inhibited palmitic acid incorporation into small intestinal brush border membrane vesicles (Han et al., 2003). It was reported that

methanol extract of S. pseudo-lasiogyne H. Lév. twigs and salicortin derivatives reduced lipid accumulation in a concentration-dependent manner. They inhibited the differentiation of adipocytes in 3T3-L1 cells. The $2^\prime,6^\prime-O$ -acetylsalicortin exhibited the most potent inhibitory activity with IC50 = 11.6 μM . It remarkably downregulated the expressions of sterol regulatory element binding protein

1 (SREBP1c) and CCAAT/enhancer binding protein α (C/EBP α). Thus, salicortin derivatives possessed antiadipogenic effects via down-regulation of SREBP1c and C/EBP α dependent pathways (Lee et al., 2013).

CONCLUSION AND FUTURE PERSPECTIVES

The current review outlined the complete research progress in the phytochemistry, traditional use and pharmacology of genus *Salix* plant extracts and constituents. *Salix* extracts and some of its components exerted potent antioxidant, anti-inflammatory, antiproliferative, and antimicrobial properties confirming the traditional use of willow extracts in folk medicine. They also demonstrated substantial abilities in suppressing inflammatory pathways, both in cancer prevention and treatment, and in other chronic diseases. Thus, as a potential perspective, *Salix* extracts alone or their isolated active components should be examined more thoroughly, and its anti-HIV, hepatoprotective and neuroprotective therapeutic approach should also be discussed.

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AUTHOR CONTRIBUTION

NT retrieved the relevant literature and drafted the manuscript. AME and MW originated the work, led the discussions, provided helpful comments, and revised the manuscript. MF wrote the biological activity part. DH, MS and NF provided helpful comments and revised the manuscript. All authors read and approved the final version of the manuscript.

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SUPPLEMENTARY MATERIAL

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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GLOSSARY

ABTS 2,2'-azinobis-(3- ethylbenzothiazoline-6-sulfonic acid)

AIDs Acquired immunodeficiency syndrome

Apif Apiofuranosyl

Araf Arabinofuranosyl

Arap Arabinopyranosyl

CCl₄ Carbon tetrachloride

C/EBPα CCAAT/enhancer binding protein α

DPPH 2,2-Diphenyl, one- Picryl Hydrazyl

EACC Ehrlich ascites carcinoma cells

EtOAc Ethyl acetate

FRAP Ferric reducing antioxidant power

Glac Galactosyl

Glc Glucosyl

Gluc Glucuronoyl

Hex Hexosyl

HFD High-fat diet

HIV Human immunodeficiency virus

 IC_{50} Half maximal inhibitory concentration

MeOH Methanol

MIC Minimal inhibitory concentration

NF-κB Nuclear factor kappa-B

ORAC Oxygen radical absorbance capacity

Pent Pentosyl

Ph Phenyl

Rh Rhamanosyl

Rut Rutinosyl

SREBP1c Sterol regulatory element binding protein 1

TAC Total antioxidant capacity

TFC Total flavonoid content

TLC Thin layer chromatography

TNF-a: Tumor necrosis factor-alpha

TPC Total phenolic content

 $\boldsymbol{XTT}\ 2,3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-\ tetrazolium-5-sulfophenyl)$

carboxanilide

Xylp Xylopyranosyl.





Downregulation of Candidate Gene Expression and Neuroprotection by Piperine in Streptozotocin-Induced Hyperglycemia and Memory Impairment in Rats

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Kumar S, Chowdhury S, Razdan A, Kumari D, Purty RS, Ram H, Kumar P, Nayak P and Shukla SD (2021) Downregulation of Candidate Gene Expression and Neuroprotection by Piperine in Streptozotocin-Induced Hyperglycemia and Memory Impairment in Rats. Front. Pharmacol. 11:595471. doi: 10.3389/fphar.2020.595471 There is accumulating evidence showing that hyperglycemia conditions like diabetes possess a greater risk of impairment to the neuronal system because high glucose levels exacerbate oxidative stress, accumulation of amyloid-beta peptides, and mitochondrial dysfunction, and impair cognitive functions and cause neurodegeneration conditions like Alzheimer's diseases. Due to the extensive focus on pharmacological intervention to prevent neuronal cells' impairment induced by hyperglycemia, the underlying molecular mechanism that links between Diabetes and Alzheimer's is still lacking. Given this, the present study aimed to evaluate the protective effect of piperine on streptozotocin (STZ) induced hyperglycemia and candidate gene expression. In the present study, rats were divided into four groups: control (Vehicle only), diabetic control (STZ only), piperine treated (20 mg/kg day, i.p), and sitagliptin (Positive control) treated. The memory function was assessed by Morris water maze and probe test. After treatment, biochemical parameters such as HOMA index and lipid profile were estimated in the serum, whereas histopathology was evaluated in pancreatic and brain tissue samples. Gene expression studies were done by real-time PCR technique. Present data indicated that piperine caused significant memory improvement as compared to diabetic (STZ) control. The assessment of HOMA indices in serum samples showed that piperine and sitagliptin (positive control, PC) caused significant alterations of insulin resistance, β cell function, and insulin sensitivity. Assessment of brain and pancreas histopathology shows significant improvement in tissue architecture in piperine and sitagliptin treated groups compared to diabetic control. The gene expression profile in brain tissue shows significantly reduced BACE1, PSEN1, APAF1, CASPASE3, and CATALASE genes in the piperine and sitagliptin (PC) treated groups compared to Diabetic (STZ) control. The present study demonstrated that piperine not only improves memory in diabetic rats but also reduces the expression of specific ADrelated genes that can help design a novel strategy for therapeutic intervention at the molecular level.

Keywords: neuroprotection, gene expression, hyperglycemia, piperine, Alzheimer's

INTRODUCTION

There is growing evidence showing a link between Diabetes mellitus (DM) and Alzheimer's disease (AD). However, the mechanism is not known vet at the molecular level (Butterfield et al., 2014). The intricate link between these two diseases might be due to the dysregulation of blood sugar levels in the body that affects many cells, including brain cells in the central nervous system (CNS) (Malone, 2016). Blood glucose homeostasis is a well-coordinated physiological process controlled by hormone insulin and glucagon released by the pancreas (Roder et al., 2016). Alteration in blood sugar levels in conditions like hyperglycemia deteriorates brain cells and its functions, leading to the development of mild cognitive impairment, which is the early stage of AD (Duarte, 2015). A higher level of glucose not only increases amyloid-beta production in the brain but affects tau phosphorylation in the brain (Mullins et al., 2017). There is accumulating evidence showing that hyperglycemia conditions like diabetes possess a greater risk of impairment to the neuronal system (González-Reyes et al., 2016; Pruzin et al., 2018; Rojas-carranza et al., 2018) because high glucose levels exacerbate oxidative stress, accumulation of amyloid-beta peptides, and mitochondrial dysfunction, and impair cognitive functions, and cause neurodegeneration conditions like Alzheimer's diseases (Macauley et al., 2015; Gaspar et al., 2016; Kim et al., 2016; Rom et al., 2018; Silzer and Phillips, 2018). It is well established that administration of dexamethasone and streptozotocin (STZ) induced hyperglycemia in rodents (rats), resulting in increased levels of amyloid aggregation, tau phosphorylation, synapses loss, impairment of memory performance, and cognition deficit. STZ is commonly used to induce diabetes in rats. STZ uptake by pancreatic β cells is detrimental for β cells as STZ causes the generation of reactive oxygen species (ROS) (Vessal et al., 2003). It also results in cognitive impairment, glucose metabolism dysfunction, oxidative stress, and phosphorylation of tau protein resulting in neuronal cell death, a hallmark feature of AD (Salkovic-Petrisic et al., 2013; Moreira-Silva et al., 2018).

Oxidative stress is also responsible for many metabolic and neurologic disorders such as Alzheimer's disease, Parkinson's disease, cardiovascular disease, diabetes, and cancer (Kumar et al., 2015). In AD, oxidative stress is triggered by the accumulation of free radicals in the brain that leads to neuronal cell damage. Some of the genes that play a crucial role in amyloid processing, apoptosis, and oxidative stress are BACE1, PSEN1, APAF1, CASPASE3, and CATALASE. Hence, decreasing the expression levels of specific genes involved in apoptosis and oxidative stress pathways by particular therapeutic intervention will be an attractive strategy to counter neurodegeneration in a disease like AD. Several foods, nutrients, and phytocompounds such as resveratrol and curcumin have been investigated for preventive and intervention approaches that might help to prevent diabetes-related cognitive impairment (Mazzanti and Di Giacomo, 2016). Because of these, the present study demonstrated the neuroprotective effects of piperine on a high rich sucrose diet with Dexamethasone and STZ induced hyperglycemia and memory impairment in rats and relevant gene expression profile to address the molecular mechanism underlying the pathway.

MATERIAL AND METHODS

Materials

Roswell Park Memorial Institute (culture medium) (RPMI1640), Fetal bovine serum, penicillin (100 U/ml), and streptomycin (100 μ g/ml) were purchased from Himedia, India. The general chemicals were also purchased from Sigma or Merck, India. The rat pheochromocytoma (PC12) cells line used in the present study were obtained from the National Center for Cell Science, Pune, India

GC-MS Analysis for Authentication of Piperine

The commercially procured piperine sample was identified using GC-MS for its authentication and purity check. GC-MS analysis was achieved using GC-MS-QP2010 Plus, with 230°C and 270°C selected for ion source and an interface temperature, respectively. An Rtx 5 MS capillary column (Restek Company, Bellefonte, United States) with 30 m (length) \times 0.25 mm (diameter) \times 0.25 µm (film thickness) was used with a solvent cut time of 3.50 min, a threshold of 1,000 eV, and a mass range of 40-650 m/z settings input, as described previously (Chowdhury and Kumar, 2020). In brief, a 260°C injector temperature was programmed from 50°C for 2 min and further increased for up to 250°C with a rate of 4°C/min (3 min hold), followed by an increase of 280°C with a rate of 10°C/ min (7 min hold). The peak obtained was compared with the spectrum of the known compounds available in the National Institute of Standards and Technology, U.S. Department of Commerce, and Wiley (John Wiley & Sons Ltd.) libraries.

Animals and Treatments

Development of Type -2 Diabetic Animal Model and Experimental Design

The healthy colony bred albino rats were used to develop a type 2 diabetic animal model with a weight of 150 gm to 200 gm. The rats were fed with a high sucrose diet, and dexamethasone intraperitoneal injections were administered (1.0 mg/kg/day i.e., for 20 days). A single dose of STZ (40 mg/kg) was given on the 21st day to properly develop the diabetic status (Chao et al., 2018). After the development of imbalance in glucose homeostasis through the sucrose feeding with dexamethasone, the mild dose of STZ (40 mg/kg) aggravated the induction of type 2 diabetes and started the treatments of piperine and sitagliptin from the next day as following the modified method of Ghasemi et al. (2014). The diabetic status was confirmed by monitoring glucose levels and insulin production by calculating glucose homeostasis (HOMA). The animals were kept under controlled environmental conditions as per CPCSEA norms. All the experimental protocols were approved by IAEC (Institutional Animal Ethical Committee) registered under the CPCSEA, India (Reg. No.1646/GO/a/12/CPCSEA valid up to 27.03.23).

The experimental design [1s(b)] was categorized into two comparative sets of control groups and treatment groups (**Supplementary Material**). The control groups consisting of two groups i.e., vehicle control and diabetic control, whereas

treatment groups were divided into two groups i.e., piperine treatment groups and sitagliptin treated groups (Positive control). Each group consisted of seven animals (n=7). The contributing animal groups were categorized as follows.

Group A: Vehicle control (VC) Group B: Diabetic control (STZ) Group C: Piperine treatment (STZ/PIP) Group D: Sitagliptin group (STZ/SITA)

Both piperine (20 mg/kg/day) and Sitagliptin (25 mg/kg/day) were administered daily for 4 weeks during the course of the experiment. The dose of 20 mg/kg/day of piperine is considered the standard dose, also mentioned in the literature (Ren et al., 2018; Guo et al., 2020).

Morris Water Maze

To evaluate the neurocognitive damage in these animal groups, a spatial memory task was used. Morris water maze (MWM) was employed to compare the spatial task performances of diabetic rats with that of control animals. The procedure for the training and assessment of behavioral task was carried out as described elsewhere (Dasari et al., 2016).

Animals were allowed to swim in a circular tank filled with water and a hidden (1 cm below the water level) platform in an isolated area. On the first day, animals were dropped on the opposite quadrant (in relation to the hidden platform), and the time required for finding the platform was noted as escape latency. If any animal could not find the platform within 3 min of exposure, they were guided to the platform, and the escape latency was noted as 180 s. Once the animal has reached the platform, it was allowed to rest there for 1 min. On the first day, three training trials were given with a gap of 30 min between tests. However, escape latency (Day 0) was recorded from the first trial only. On the 2nd day, escape latencies (Day 1) of animals were recorded with a single trial releasing the animals from the opposite quadrant. On the third day, escape latencies (Day 2) were noted with releases from the opposite quadrant, left quadrant, and right quadrant with respect to the quadrant where the platform was hidden. The hidden platform was removed on the fourth day (probe test), and the times the animal spent in all the quadrants were noted during a swimming session of 3 min.

Serum Biochemistry of Insulin, Glucose and Glucose Homeostasis (HOMA)

The HOMA was calculated for insulin and glucose by following the standard formula of Matthews et al. (1985).

$$\begin{split} &HOMA-IR\\ &=\frac{Fasting\ Insulin\ (\textit{U/L})\times\ Fasting\ Glucose\ (mmol/L)}{22.5}\\ &Insulinsensitivity\ (IS)=\frac{1}{\left[\left(Insulin\ (\textit{U/L})\times Log\ (glucose\ (mmol/L))\right]}\\ &HOMA-\beta=\frac{20\ \times\ fasting\ Insulin\ (\textit{U/L})}{fasting\ Glucose\ (mmol/L)}-3.5 \end{split}$$

Lipid Profile

The lipid profile parameters, total cholesterol, triglyceride, HDL-cholesterol, VLDL-cholesterol, LDL-cholesterol, and atherogenic indices of plasma were calculated by following standard methods using the Fieldward formula (Dobiášová and Frohlich, 2001; Ram et al., 2020).

$$LDL - C (mg/dL) = TC (mg/dL) - HDL - C (mg/dL)$$

- $TG (mg/dL)/5$.

Histopathology of Pancreases and Brain

The animals were sacrificed after four weeks of experimentation (28 days) by cervical dislocation as per standard norms and further proceeded for histological preparations.

Pancreas Histology. The pancreatic histology was evaluated by following the paraffin sectioning following ascending and descending dehydration with hematoxylin-eosin (H&E) staining (Saravanan et al., 2017). The microphotography of stained slides of the pancreatic islets of the Langerhans performed by the Radical microscope (Model No. RXLr-5), India attached with supported software of ProgRes® SpeedXT core 5 by Jenopatric, Germany.

Histopathology of Brain Tissues. Paraffin sections were stained with Cresyl violet to study the neurodegenerative and cytoarchitectural changes. 10 µm thick coronal sections were cut using a rotary microtome. Sections passing through the hippocampus (bregma –1.8 mm to –5.8 mm) were stained with cresyl violet.

Morphological Variables

To measure the effects of various treatments on hippocampal neurons, neuronal cells were subjected to morphological parameters somatic perimeter (μ m), somatic area (μ m²), somatic aspect ratio, somatic compactness, somatic form factor, and somatic roundness. Both area and perimeter can be used to mark the size, and the rest can be assigned to the shape of a neuron. The following table depicts the methods and formulas for calculating the morphological variables (McGarry et al., 2010).

S. No	Morphological variable name	Abbreviation	Formula
1	Somatic perimeter (µm)	SP	The perimeter of the Soma
2	Somatic area (µm²)	SA	Area of Soma
3	Somatic aspect ratio	SAR	Max diameter of soma/min diameter of soma
4	Somatic compactness	SCom	$[(4/\pi)^*$ Area) ^{1/2}]/max diameter
5	Somatic form factor	SFF	$(4\pi^*Area)/(Perimeter^2)$
6	Somatic roundness	SRo	$(4*Area)/(\pi^* max diameter^2)$

Cell Counting

Brain areas were identified using the brain atlas, and slides were examined under an Olympus Ch20i microscope. Images were captured, and cell count was performed using ImageJ. Only neurons with clear somatic nuclei and nucleolus were counted. To obtain an unbiased estimate of cell numbers, Abercrombie's correction factor was applied to total cell count, which compensates for the over counting of sectioned profiles, using the equation:

$$P = A * \left[\frac{M}{M + L} \right]$$

P is the corrected value, A is the raw density measure, M is the thickness of the section (in micrometers), and L is the average diameter of cell bodies along the axis perpendicular to the section's plane (Abercrombie, 1946).

To Determine the Cytoprotective Activity of Piperine Against H_2O_2 Induced Oxidative Stress and $A\beta_{1-42}$ Induced Toxicity in PC12 Cells

RPMI-1640 media enriched with 10% heat-inactivated fetal bovine serum and 1% penicillin (100 U/ml), streptomycin (100 U/ml) was used to maintain PC12 cells in a carbon dioxide (CO2) incubator at 37°C in a T-25 flask. The protective effect of piperine against H₂O₂ induced oxidative stress in PC12 cells was determined by supplementing the cells with different piperine concentrations and performing an MTT assay described previously (Chowdhury and Kumar, 2020). In brief, cells were pre-treated with piperine at concentrations ranging from 1 µM to 0.25 µM for 2 h before exposure to a half-maximal (IC50) concentration of H2O2 (100 µM final concentration). In another experiment, piperine's protective effect was determined against $A\beta_{1-42}$ (40 μM final concentration) induced toxicity. In this experiment, $A\beta_{1-42}$ pre-formed fibrils were used to induce toxicity to PC12 cells. MTT assay was carried out, and absorption was read at 570 nm using a UV spectrophotometer (Molecular Device Spectramax M3, equipped with Softmax Pro V 5.4.1 software).

Gene Expression Studies

RNA Isolation

Total RNA was extracted from each mice group's cerebral cortex brain tissue using the standard Trizol method (Chomczynski 1993). The RNA quantity and purity were estimated by analyzing their A260/A280 ratio using the NanoDrop spectrophotometer (Thermo scientific). For further confirmation, the isolated RNA was analyzed by 1.2% agarose gel electrophoresis and visualized using the AlphaImager Gel documentation system (Alpha Innotech Corporation, CA, United States).

cDNA Preparation

Total RNA isolated from four different treatment groups i.e., untreated group (Vehicle control), Streptozotocin (STZ) treated group (Diabetes control), piperine plus STZ treated

group, and sitagliptin plus STZ treated group (Positive control), were used as a template for the cDNA synthesis. Around $4\,\mu g$ total RNA was used for first-strand cDNA synthesis by following the manufacturer's protocol.

Quantitative Real-time PCR was performed with the SYBR green PCR master mix kit with the following thermocycling conditions: Gene-specific primers for all the genes were designed manually using the exon-exon junction region amplify, and their specificity was examined through Primer Blast software of NCBI. OligoAnalyzer tool was used to calculate the Tm of the primers. The forward and reverse primers sequences for the following genes were as follows: forward 5'-CTCTTCCCAGGA CAACTCC-3' and reverse 5'-TGAGTGGCCTGACTTTTGAC-3' for Apaf1, forward 5'-GGAGCTTGGAACGCGAAGA-3' and reverse 5'-CATCGGTACCATTGCGAGC-3' for Caspase3. forward 5'-CAAGAGCTGCTGTCCAGGA-3' and reverse 5'-GTAAGGCACAGGCCGATCA-3' for Presenilin-1, 5'-ACC AACCTTCGTTTGCCCAA-3' and 5'-CACCAATCAGTCCTT CCGC-3' for BACE-1, 5'-CTTCTGGAGTCTTTGTCCAG-3' and 5'-CCTGGTCAGTCTTGTAATGG-3' for Catalase, forward 5'-AGATCAAGATCATTGCTCCTC-3' and reverse 5'-CGCAGC TCAGTAACAGTCC-3' for β -actin. β -actin was used as an internal control. The melting curve obtained was analyzed, and the relative expression of transcripts was quantified by $2^{-\dot{\Delta}\Delta ct}$ value method (Livak and Schmittgen 2001).

Molecular Docking

Docking studies were carried out using the SwissDock server (Grosdidier et al., 2011). The X-ray crystallographic structure of APAF1(PDB code: 1Z6T), BACE1(PDB code: 4D8C), PSEN1(PDB code: 6IDF), Catalase (PDB code: 1TGU) and Caspase 3(PDB code: 3DEK) were retrieved from Protein Data Bank. The missing hydrogen atoms and charges were added by DockPrep application within UCSF Chimera, followed by energy minimization using Gasteiger charges (Pettersen et al., 2004). The structure of piperine was downloaded from PubChem in sdf format and converted to. mol format. Docking of piperine with proteins was carried out using the default parameter of the SwissDock server.

Statistical Analysis

All the data represent the means \pm standard deviation of triplicate determinations. The student t-test was performed for statistical analysis using online software, GraphPad. The significance value of p < 0.05 was considered significant, and p < 0.01 was considered very significant, and p < 0.001 was extremely significant.

RESULTS

Characterization of Piperine

For piperine's characterization, the GC-MS of commercially procured piperine was compared with the fragmentation pattern of piperine structure present in the NSIT library (**Figure 1A**). The chromatogram shows the presence of three

very minor peaks of 3-cyclohexene-1-methanol, alpha, alpha,4-trimethyl-, acetate; piperidine, and pyrrolidine, 1-[5-(1,3-benzodioxol-5-yl)-1-oxo-2,4-pentadienyl]- (E,E) with area percentage of 0.97, 0.40, and 1.12, respectively. Though the sample showed a strong peak of piperine with an area of 97.51%.

Effect of Piperine on the Viability of PC12 Cell Against H₂O₂ Induced Oxidative Stress

The PC12 cells were pre-treated with piperine, followed by H_2O_2 induction to determine the protective effect of piperine against H_2O_2 induced oxidative stress. At $1 \mu M$ final concentration of piperine, 99.39 \pm 4.70% percentage of viability was observed as compared to the negative control (H_2O_2 only) (**Figure 2A**), showing that piperine significantly protected PC12 cells against H_2O_2 induced oxidative stress (p < 0.01).

Effect of Piperine on the Viability of PC12 Cells Against $A\beta_{1-42}$ Induced Toxicity

To study the protective effect, PC12 cells were pre-treated with varying concentrations of piperine (0.25–1 μ M). The pre-treatment of piperine prior to induction of A β_{1-42} fibrils (40 μ M), showed concentration-dependent attenuation of A β_{1-42} induced toxicity, with maximum cell viability of 78.28 \pm 13.90% as compared to the negative control at 1 μ M concentration of piperine (**Figure 2B**).

Effect on Glucose Homeostasis (HOMA) and Lipid Profile of Serum

Effect of Treatments in Glucose Homeostasis (HOMA)

The significant (p < 0.001) increased insulin resistance (IR), β -cell function (β %), and insulin sensitivity (S%) were seen in the diabetic group in comparison to the vehicle control group. Accordingly, the insulin and glucose levels were represented its levels in the diabetic group. Although the piperine and sitagliptin, treatments caused significant alterations in HOMA indices of IR, β %, and S%. Accordingly, reductions were observed in levels of insulin and glucose (**Figure 3**).

Effects of Treatments in Lipid Profile and Al

In the diabetic group, lipid profile (total cholesterol, LDL-cholesterol, VLDL-cholesterol, and triglyceride (Tg)), as well as the atherogenic index (AI = log(Tg/HDL)), were elevated significantly in comparison to the vehicle control group. The piperine and sitagliptin treatments made significant reductions in lipid profile and AI (**Figure 4**).

Effects of Piperine on Learning and Memory in STZ-Treated Rats

The cognitive-behavioral task was evaluated through MWM. The water escape task evaluates spatial learning and memory. On day 1, when the animals were exposed to a circular water tank

for the first time, diabetic group B took the maximum time to find the hidden platform. In contrast, the sitagliptin-treated group D took the lowest time, which was even better than the control group of rats A (**Figure 5A**). The piperine-treated group C demonstrated escape latency that was lesser (38%) than the Diabetic control B but higher (21%) than the group D. Interestingly, the swimming speeds of A, D, and C were in the comparable range (<5% differences), while that of group B was relatively less (~17%) compared to other groups. Similarly, group B showed the most unsatisfactory performance in terms of path length and cumulative path distance. Contrary to these observations, swim path efficiency was better in group B and group C.

Exposure to the same task after 24 h evaluated the memory function of the animals. The animals of group B took the longest time to escape with the longest path and slowest swimming speed (**Figure 5B**). Though group B animals' path efficiencies were very close to that old vehicle control animals, their slow swimming speed increased the nominal high path length (15%) into a considerably higher cumulative distance (100%). On the other hand, PR and SR animals showed very good escape latency, path length, cumulative distance, and swimming path efficiency. Their values were comparable for these parameters, even in the presence of significant differences in swimming speed. The swimming speed in SR was lesser than group C and was comparable to group B.

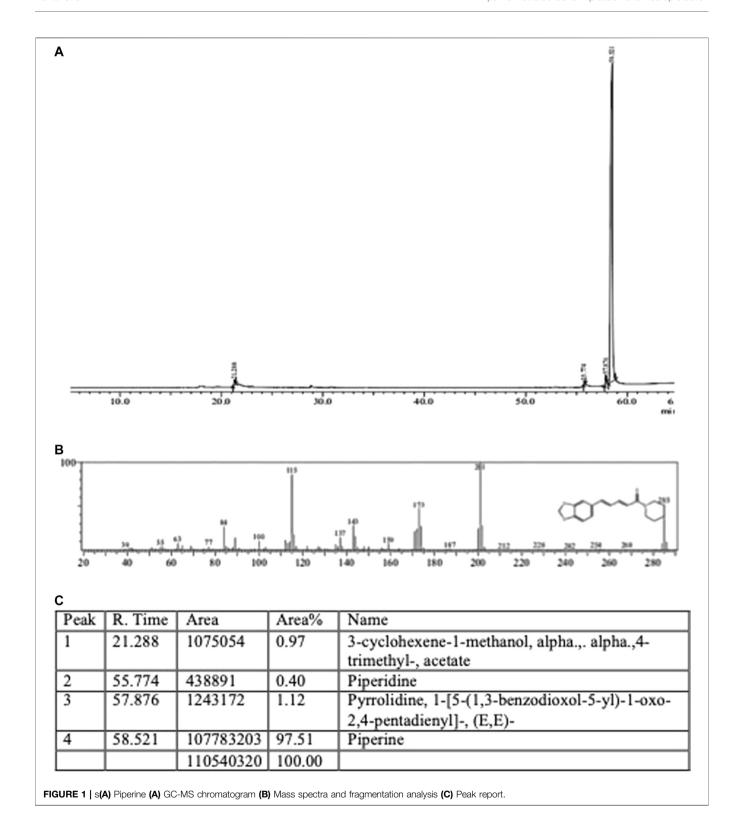
There were increases in escape latencies, path length, cumulative distance, and decreases in swim path efficiencies for groups A, D, and C on day 3 compared to that2 for the same task performances (**Figure 5C**). Nevertheless, cumulative distance, path length, and escape latency of group B were high with lower swim path efficiency, in comparison to group D and group C. The speed of swimming in B was in between that of D and C.

When the starting point for the task changed by +90° or -90°, DR animals performed very poorly in swim path efficiency. However, variations in performances of D and C were also noted. Even group A animals also deteriorated in their performances in some cases. A probe test on day 4 was carried out to evaluate the cognitive functions in the absence of the hidden platform. Of all the animal groups, the B group animals spent the minimum time in the target quadrant and maximum time in the opposite quadrant.

Histopathology

Effect of Piperine on Pancreatic Histoarchitecture of the Islet of Langerhans

The high sucrose diet and a mild dose of STZ caused significant alterations in histoarchitecture of the pancreas by promoted degenerative changes in the islet of the Langerhans as well as different degrees of necrosis in the nucleus in comparison to the vehicle control group (**Figures 6A,B**). The degenerative changes also were seen in vascular tissues and connective tissues. Whereas the treatments of piperine and sitagliptin promoted the restoration of histoarchitectures by increasing cellular mass and subsiding the necrosis of nucleus of islet cells with rearrangements of vascular tissues and connective tissues (**Figures 6C,D**).



Effect of Piperine on Brain Tissue Histopathology

Significant differences were observed in CA3 (Cornu Ammonis areas) and dentate gyrus (Dg) neurons

morphology between the experimental groups. Other regions of hippocampus CA1, CA2, and CA4 have not exhibited any marked changes. The present study shows

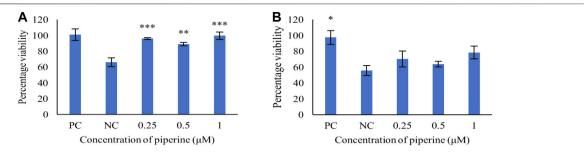


FIGURE 2 | Concentration-dependent protective effect of piperine against **(A)** H_2O_2 induced oxidative stress and **(B)** $A\beta_{1-42}$ fibrils induced cytotoxicity in PC12 cells. NC: Negative control ($A\beta_{1-42}$ only), PC: Positive control (No $A\beta_{1-42}$). Data are presented as mean \pm SD of three separate experiments performed in triplicate. *p < 0.05, **p < 0.01 with the negative control (NC).

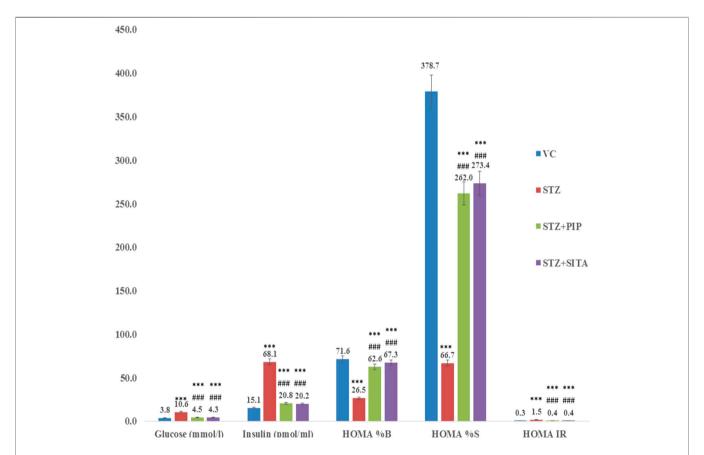


FIGURE 3 [Effect of the piperine on glucose homeostasis (HOMA) (A, B, C, and D were experimental group) (See the experimental design in material and methods section) (Data are means \pm S.E.M. (n = 7); *, $p \le 0.05$ and c, *** ≤ 0.001 as compared to the respective control values and g, ### ≤ 0.001 and d = nonsignificant as compared to the respective values of the diabetic control group). Blue-Vehicle Control (VC); Red-Diabetic control (STZ); Green-Piperine treatment (STZ + PIP); Purple-Sitagliptin treatment (STZ + SITA).

more significant effects on neuronal soma size as compared to neuronal shape factors.

Treatment with dexamethasone reduced the size probably because of the degenerative process. In contrast, treatment with piperine and sitagliptin exhibited recovery, and larger soma could be interpreted as protective effects (Figures 7i,ii). Larger soma may have better metabolic and cellular systems

required to have better synaptic connections and neuronal activities, which corresponds to enhanced learning ability and memory. SA of CA3 neurons in the Diabetics group was 266.40 \pm 10.72 μm^2 , whereas it was 306.73 \pm 13.96 μm^2 for the control group. Treatment with piperine and sitagliptin increased the SA and found to be 279.15 \pm 16.71 and 289.15 \pm 15.60 μm^2 , respectively. More significant changes were observed in Dg Neurons after dexamethasone

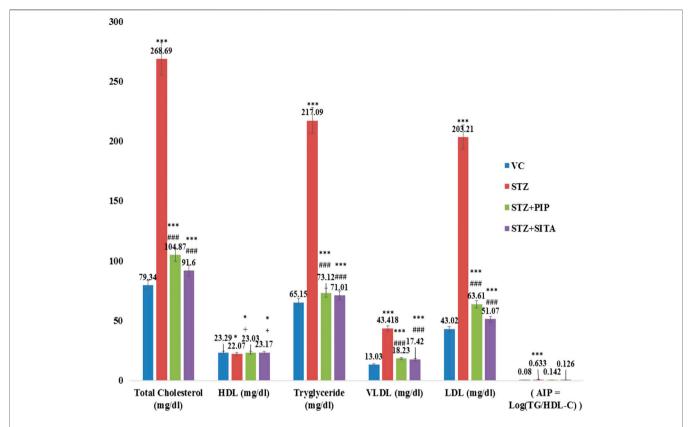


FIGURE 4 [Effect of the piperine on lipid profile and Al (Atherogenic Index) (Data are means ± S.E.M. (n = 7); *, p ≤ 0.05 and c, *** ≤ 0.001 as compared to the respective control values and g, ### ≤ 0.001 and d = non-significant as compared to the respective values of the diabetic control group). Blue-Vehicle Control (VC); Red-Diabetic control (STZ); Green-Piperine treatment (STZ + PIP); Purple-Sitagliptin treatment (STZ + SITA).

treatment SA was decreased by 18.36 percent, and piperine and sitagliptin treatment exhibited SA values matching with control animals (249.15 \pm 13.76 and 251.95 \pm 12.98), respectively.

A 23 percent decrease in SP was observed for CA3 neurons in dexamethasone-treated animals. This was found to approximately close to control animals in piperine and sitagliptin treated animals; a change of 10.57 and 3.39 percent was observed, respectively. Similar observations were evident for Dg also SP for control neurons was measured 61.63 \pm 3.67 μm and reduced to 51.26 \pm 1.16 μm in dexamethasone-treated animals, here no doubt to state that sitagliptin performed better (59.61 \pm 3.99 μm) as compared to piperine (56.46 \pm 1.35 μm) (**Figures 8i,ii**].

Morphometry

Cell count shows a decrease in number after dexamethasone treatment in CA3 and Dg area; this was further restored with the treatment of piperine and sitagliptin. A significant decrease was observed both in CA3 and Dg neurons after treatment with dexamethasone. A close analysis of data exhibited that both the areas were affected equally with a reduction of 29 and 28 percent, respectively. The total number of neuronal cells in the CA3 and Dg sub-region of the hippocampus of piperine and sitagliptin was approximately closer to control animals, and values for the CA3 sub-region were 22.43 \pm 0.40 and 23.03 \pm 0.55 (**Table 1**). For the Dg sub-region, the total number of cells in piperine and

sitagliptin treated animals was 38.76 ± 1.05 and 38.96 ± 1.19 , respectively (**Table 2**). The decrease in cell number indicates cell death, and protective effects are indicated by the restored number of cells compared to control animals.

The morphological shape of cell bodies was analyzed based on the somatic aspect ratio (SAR), somatic circularity index (SCI), and somatic roundness (SRo). SAR exhibits the symmetry of cellular shape. SAR value close to 1 is indicative of circular or spherical shape. CA3 neurons exhibited higher SAR values, and this was further increased in dexamethasone-treated animals (1.40 \pm 0.05), indicative of a disruption of pyramidal shape. Animals treated with piperine and sitagliptin exhibited SAR values close to control animals, reflecting the pyramidal shape's retention. As expected, Dg neurons exhibited SAR values close to 1.0, and no significant difference was observed between various experimental groups. We found no significant changes in the SCom, SFF, SRo, suggesting that the soma size changes were uniform rather than shrinkage or expansion along a particular axis.

Gene Expression Analysis in the Cerebral Cortex Brain Tissue of Rat

For gene expression analysis, total RNA was isolated from the cerebral cortex, and its quality was analyzed by assessing the RNA

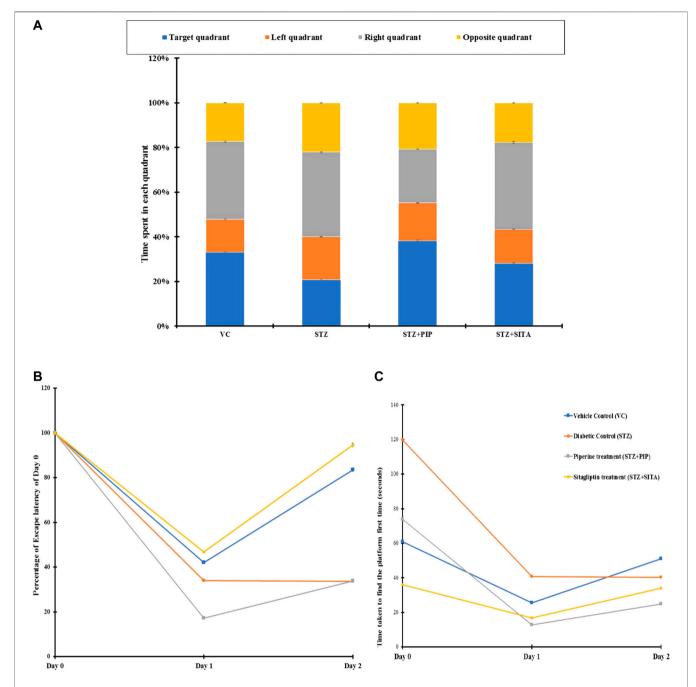


FIGURE 5 | (A) Percentage distribution of time spent by the animals in different quadrants in search of the hidden platform (probe test) in MWM. Figure 5B. Day wise changes in time required to find the hidden platform when the animals were released on the opposite quadrant of MWM. Vehicle control (VC); Diabetic control (STZ); Piperine treatment (STZ + PIP); Sitagliptin treatment (STZ + SITA). Figure 5C. Changes in escape latency after 24 h (Day 1) and 48 h (Day 2) in different groups of animals in comparison to their respective first-time exposure (Day 0) to MWM. Vehicle control (VC); Red-Diabetic control (STZ); Green-Piperine treatment (STZ + PIP); Purple-Sitagliptin treatment (STZ + SITA).

purity and integrity. The absorbance ratio A260/280 ratios were greater than 1.9 of all the RNA samples. The sharp bands for 28S and 18S ribosomal RNA were observed when separated in 1.2% agarose gel electrophoresis, indicating the good quality RNA. Using the manufacturer instructions, cDNA was prepared and

used as a template for gene expression analysis. Using the Real quantitative Time-PCR, the expression of selected genes, including *BACE1*, *PSEN1*, *APAF1*, *CASPASE3*, *and CATALASE*, in rat's cerebral cortex brain tissue was analyzed in four different treatment groups. In STZ treated group

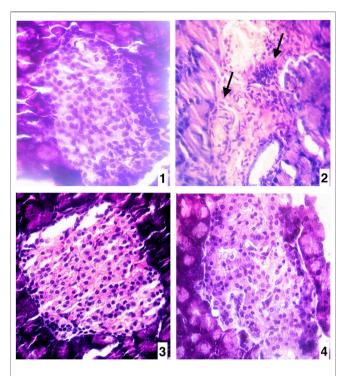


FIGURE 6 | (A) Pancreas of vehicle control (VC) (400X H&E) (B) Pancreas of diabetic control (STZ)(400X H&E) (C) Pancreas of the piperine treatment (STZ + PIP)(400X H&E) (D) Pancreas of sitagliptin treatment (STZ + SITA)(400X H&E).

(Diabetes control), the expression of BACE1, PSEN1, APAF1, CASPASE3, and CATALASE genes were upregulated in the cerebral cortex of the rat brain as compared to the untreated group (Vehicle control) (Table 3). The fold change increase in these genes' expression levels varied, and it ranged between 1.5 and 2.8-fold increases (Figure 9). However, their expression decreased drastically when treated with sitagliptin (Positive control). Reduction percentage in the expression of these genes ranged between 59 and 96% decreases in sitagliptin treated (Positive group) in comparison to the STZ treated group (Diabetes control). Upon treatment with piperine, the expressions of these genes were significantly decreased ($p \le 0.05$). When these genes' expression was compared between the piperine treated group and the Diabetes control group, statistically significant changes ($p \le 0.05$) were observed.

Molecular Docking Analysis

In the present study, the interaction between piperine and some proteins involved in amyloid processing, apoptosis, and oxidative stress such as BACE1, PSEN1, APAF1, CASPASE3, and CATALASE were studied to explore the binding mode, using SwissDock server. The binding affinity of the proteins with piperine was measured by FullFitness score and deltaG (kcal/mol). The FullFitness score was highest for APAF1 with –8.02 kcal/mol deltaG followed by CATALASE (–7.51 kcal/mol), PSEN1 (–7.35 kcal/mol), BACE1 (–7.20 kcal/mol), and the least score was found CASPASE3 (–6.55 kcal/mol) as shown

in Table 4 and Figure 10. Besides, hydrogen bond formation was seen in all four proteins except CATALASE when docked with piperine. The molecular docking study predicted a binding interaction between each protein and piperine ligand, validated by hydrogen bonding between the proteins and piperine. Molecular docking of piperine with APAF1 revealed H-boding with Val127 of α/β fold of protein (**Figure 10A**). Docking analysis of BACE1 revealed that Thr221 residue participates in forming H-bond with piperine. Thr221 was also found to interact with the ligand of the X-ray crystal structure of BACE1 (PDB code: 4D8C); therefore, this interaction plays an important role (Figure 10B). In CATALASE protein, no single H-bond interaction was found to be formed with the catalytic residues (Figure 10C). The binding interaction of PSEN1(PDB code: 6IDF) revealed that Gly384 residues are involved in H-bond formation with piperine (Figure 10D). CASPASE 3 was found to interact with amino residue Arg 164, to form H-bond interaction with piperine (Figure 10E).

DISCUSSION

AD and DM are two independent metabolic syndromes but recently reported increasing evidence shows a link between AD and DM (Akter et al., 2011). The complications associated with DM leads to a hyperglycemic condition. The increase in blood sugar level affects neuronal cells. The higher blood sugar levels lead to faster cognitive decline and neuronal cell death. The increased blood glucose levels also result in higher glycation endproducts (AGEs) that damage the neuronal cells by inducing oxidative stress, promoting inflammation, and causing direct neurotoxicity to brain cells. The other pathway involved in neuronal cell death is apoptosis (Singh et al., 2014). The administration of dexamethasone and STZ increases oxidative stress in the rat brain. This oxidative stress causes ROS accumulation in the brain that further damage cellular components such as proteins and neuronal cells' membranes (Uttara et al., 2009). STZ treatment produces free radical's oxidative stress, generation causing mitochondrial abnormalities which further trigger caspase mediated apoptotic cell death, neuroinflammation which are collectively detrimental to neuronal function which further implicate in the AD pathology (Rai et al., 2013). STZ produces brain insulin resistance or impaired insulin receptor in the brain which leads to $A\beta$ accumulation forming senile plaques and increased tauphosphorylation forming neurofibrillary tangles by increasing the activity of GSK-3\beta that results in neuronal and synaptic dysfunction, memory impairment which further leads to AD like pathology (Shingo et al., 2012; Stöhr et al., 2013). STZ exacerbates the pathological changes associated with AD such as amyloidogenic processing of APP, glucose metabolism, insulin signaling, synaptic function (Chen et al., 2014; Zhang et al., 2015).

This study evaluated the neuroprotective effects of piperine and expression of five candidate genes (BACE1, PSEN1, APAF1, CASPASE3, and CATALASE) in rat's cerebral cortex induced hyperglycemia with STZ rat model. Our results showed that all

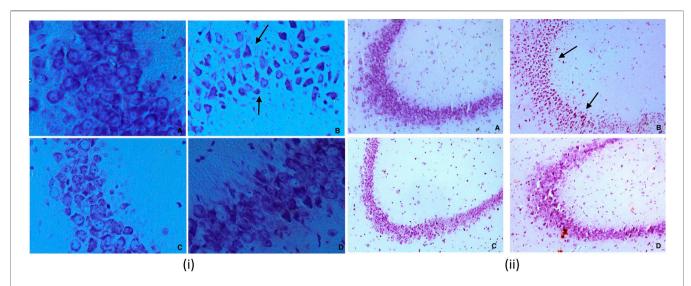


FIGURE 7 | (i) Nissl staining for CA3 sub region of hippocampus for various groups at 40X (A) Vehicle control (VC) (B) Diabetic control (STZ) (C) Piperine treatment (STZ + PIP) (D) Sitagliptin group (STZ + SITA). 7 (ii) Nissl staining for CA3 sub region of hippocampus for various groups at 10X (A) Vehicle control (VC) (B) Diabetic control (STZ) (C) Piperine treatment (STZ + PIP) (D) Sitagliptin group (STZ + SITA).

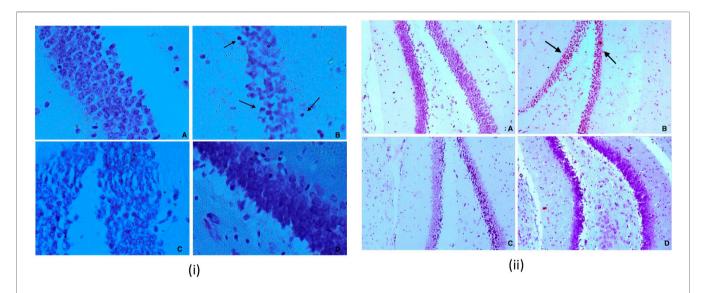


FIGURE 8 | (i) NissI staining for Dg sub region of hippocampus for various groups at 40X (A) Vehicle control (VC) (B) Diabetic control (STZ) (C) Piperine treatment (STZ + PIP) (D) Sitagliptin group (STZ + SITA). 8 (ii) NissI staining for Dg sub region of hippocampus for various groups at 10X (A) Vehicle control (VC) (B) Diabetic control (STZ) (C) Piperine treatment (STZ + PIP) (D) Sitagliptin group (STZ + SITA).

TABLE 1 | Measurements of the morphological size and shape of CA₃ neurons.

CA3	Control	Diabetic	Piperine	Sitagliptin
Area	306.73 ± 13.96	266.40 ± 10.72*	279.15 ± 16.71	289.15 ± 15.60
Perimeter	115.44 ± 7.90	95.13 ± 7.58	103.23 ± 9.73	111.52 ± 7.20
Cell count	24.99 ± 0.21	17.66 ± 0.26**	22.43 ± 0.40**	23.03 ± 0.55**
Somatic aspect ratio	1.27 ± 0.042	1.40 ± 0.05	1.32 ± 0.04	1.29 ± 0.05
Somatic compactness	1.02 ± 0.03	1.09 ± 0.04	1.01 ± 0.06	1.00 ± 0.04
Somatic form factor	0.47 ± 0.08	0.79 ± 0.3	1.60 ± 0.98	0.48 ± 0.09
Area	1.08 ± 0.07	1.25 ± 0.10	1.14 ± 0.17	1.06 ± 0.09

Significance level *p value < 0.05, **p value < 0.01.

TABLE 2 | Measurements of the morphological size and shape of Dg neurons.

Dg	Control	Diabetic	Piperine	Sitagliptin 251.95 ± 12.98	
Area	272.94 ± 12.06	222.75 ± 9.71**	249.15 ± 13.76		
Perimeter	61.63 ± 3.67	51.26 ± 1.16**	56.46 ± 1.35	59.61 ± 3.99	
Cell count	43.33 ± 0.80	31.00 ± 0.67**	38.76 ± 1.05**	38.96 ± 1.19**	
Somatic aspect ratio	1.03 ± 0.03	1.01 ± 0.05	1.01 ± 0.03	1.02 ± 0.02	
Somatic compactness	1.08 ± 0.02	1.20 ± 0.09	1.24 ± 0.05*	1.15 ± 0.03	
Somatic form factor	1.13 ± 0.14	1.11 ± 0.07	1.03 ± 0.07	2.78 ± 1.56	
Somatic roundness	1.20 ± 0.06	1.68 ± 0.30	$1.64 \pm 0.15^{**}$	1.36 ± 0.08	

Significance level *p value < 0.05, **p value < 0.01.

TABLE 3 | Gene expression profile.

Groups	Genes					
	Caspase 2	PSEN1	BACE1	Apaf 1	Catalase	
Control (NORMAL GP)		1	1	1	1	
Diabetic control (STZ)	1	1	1	1	1	
Positive control (SITA/STZ)	\downarrow	\downarrow	\downarrow	\downarrow	\downarrow	
Piperine (PIPERINE/STZ)	\downarrow	\downarrow	\downarrow	\downarrow	\downarrow	

five genes BACE1, PSEN1, APAF1, CASPASE3, and CATALASE were significantly down-regulated in the piperine treated group compared to the Diabetic rats (STZ induced) group. It has been reported that piperine has the ability to enhance the bioavailability of compounds by several different mechanisms such as modulation of cell signal transduction, DNA receptor binding, inhibition of drug efflux pump and increasing the absorption of drugs (Bajad et al., 2001). Moreover, study suggested that piperine strongly inhibits human P-glycoprotein and cytochrome P4503A4 (Bhardwaj et al., 2002). A previous study reported the protective role of Piperine in cerebral ischemia induced inflammation rat model by downregulating the expression of Cox-2, NOS-2 and NFKB (Vaibhav et al., 2012). The neuroprotective effect of Piperine in 6-OHDA induced Parkinson's rat model by its anti-apoptotic and antiinflammatory activity (Shrivastava et al., 2013). Piperine attenuated Trauma brain injury (TBI) by downregulating the expression of TNF-α, IL-1β and BDNF in TBI mice (Song et al., 2020). A more recent study showed that Piperine treatment enhances memory performance and improves myelin repair in LPC induced demyelination rat model. (Roshanbakhsh et al., 2020). The present study substantiates the claim that piperine can binds to the molecular targets as mentioned in the previous studies mentioned above and can have effect of CNS related neuroprotective effects.

AD is characterized by neuritic plaques, the main pathological hallmarks of AD, primarily consist of amyloid β (A β) peptides. A β peptides are generated by the nonamyloidogenic pathway when amyloid precursor protein (APP) was cleaved by an enzyme called β -site APP cleaving enzyme 1 (BACE1). BACE1 plays an important role in APP processing (Resende et al., 2008; Da Costa Dias et al., 2011). Expression of the β -secretase gene is implicated in late-onset

Alzheimer's Disease (LOAD) because of its function in initiating AB production of PSEN1 (Presenilin 1) component of y secretase enzyme. BACE1 gene expression is upregulated in oxidative stress, ischemia, and hypoxia (Guglielmotto et al., 2009). BACE1 cleavage is also affected by a mutation in gene PSEN1 and PSEN2, resulting in the overproduction of A β isoforms. A β induced toxicity ultimately leads to neuron cell death by activating caspases 3, 6, and 7 (Elmore, 2007). Piperine downregulated both BACE1 and PSEN1 gene expression as compared to STZ treated group. Another, pro-apoptotic genes such as APAF1 and CASPASE are involved in the apoptotic pathway. Gene expression study showed increased expression of pro-apoptotic genes such as CASPASE and APAF1 involved in neuronal cell death via an apoptotic pathway in the AD brain (Papaliagkas et al., 2007). APAF1 is the gene responsible for encoding a multiprotein complex that plays a crucial role in cell death's mitochondrial pathway. The role of APAF1 is not very clear in neurodegeneration, although evidence has shown a correlation between APAF1 and CASPASE. The activated Apaf1 is required for the downstream executioner caspase family of genes (Shakeri et al., 2017). Caspase-3 is a cysteine protease family of genes. Many caspases are involved in initiating the signaling and execution of the apoptosis pathway. Caspase-3 is an executioner caspase an important component of the apoptosis pathway (Shi, 2004). It has been found that the activation of caspase-3 is an early event in the pathogenesis of AD. Activation of caspase-3 results in morphological changes leading to neuronal cell death. In vitro and in-vivo studies suggested that Caspase-3 has a significant role in the neuronal cell death associated with a high level of expression and activation of caspase-3 seen in AD models (Gorman et al., 1998). Gene expression study showed increased expression of pro-apoptotic genes such as caspases and apaf1 are involved in neuronal cell death via an apoptotic pathway in the AD brain (Fortin et al., 2001; Papaliagkas et al., 2007). Both Apafl and caspase gene expression were significantly downregulated in the piperine treated group compared to the diabetic control group (STZ treated). The biological system has an antioxidant defense system consists of an enzyme such as catalase widely distributed in the human body (Chen et al., 2012). Catalase breaks down two hydrogen peroxide into oxygen and water using iron or manganese as a cofactor and thus protects cells (Nandi et al., 2019). The catalase gene expression was

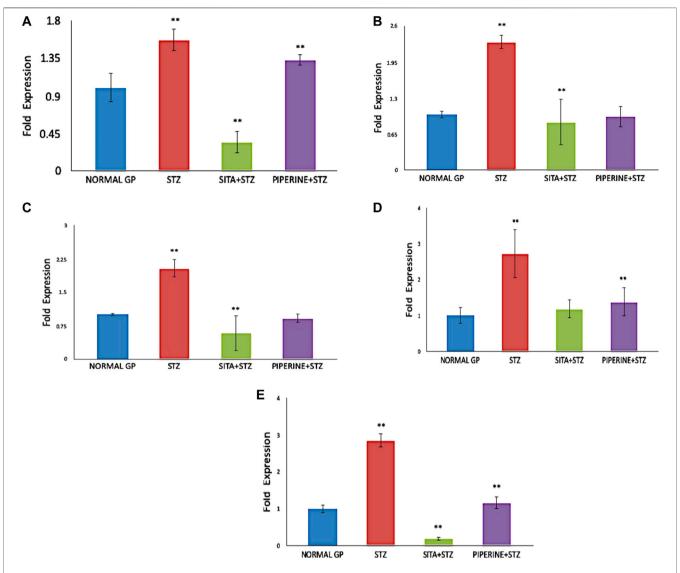


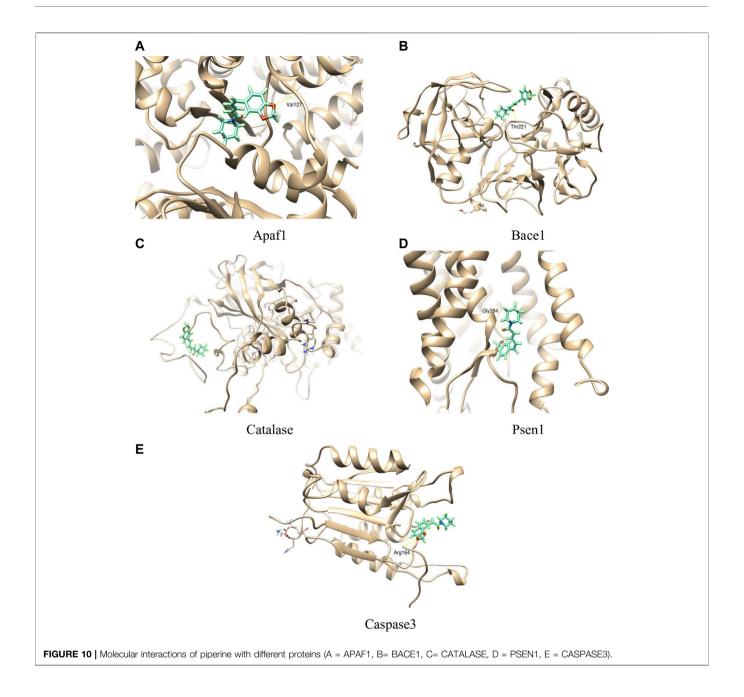
FIGURE 9 [Gene Expression analysis in the cerebral cortex brain tissue of rat (NORMAL GP = Control group; STZ = Streptozotocin treated group; SITA + STZ = Streptozotocin and sitagliptin treated group; PIPERINE + STZ = Streptozotocin and piperine treated group). In compared to the untreated control group, the expression of BACE1, PSEN1, APAF1, CASPASE3, and CATALASE genes were significantly upregulated ($p \le 0.05$) in STZ treated group (Diabetes control). However, when the STZ treated group (Diabetes control) was treated with either sitagliptin (Positive control) or piperine, the expression of all the five genes were significantly down-regulated ($p \le 0.05$). Data are presented as mean \pm SD. **p < 0.01 with the control (NORMAL GP).

TABLE 4 | Molecular docking result of piperine in terms of full fitness and estimated ΔG values predicted by SwissDock.

Protein	deltaG (Kcal/mol)	FullFitness	Interacting residues	Bond length (Å)	
Apaf1	-8.02	-3452.89	Val 127	2.275	
Catalase	-7.51	-2139.90	_	_	
Psen1	-7.35	-1129.81	Gly384	2.049	
Bace1	-7.20	-1529.14	Thr 221	2.216	
Casapase3	-6.55	-1380.32	Arg164	2.685	

significantly increased in the group treated with STZ alone (Diabetic control), whereas it was significantly down-regulated in the piperine treated group.

In vivo experiments in the diabetic rat model demonstrated improvement of memory functions in the piperine treatment group was observed in neurocognitive function assays. The



piperine group showed a relatively shorter time to find the hidden platform in the Morris Water Maze test. However, the escape latency for this group was not better than the diabetic group of animals. Similarly, the memory function of the piperine treated group of animals was also found to be improved compared to that of the diabetic group. This has been further confirmed by the probe test, where similar effects of piperine treatment were reflected.

The increased glucose and insulin levels with abnormal HOMA indices seen in a diabetic animal model may be following the decreased uptake of glucose and insulin resistance, which is further seen in degenerative cellular changes in pancreatic tissues.

Several studies reported that increased insulin resistance caused reductions in glucose uptake, which also resulted in apoptosis in several tissues, as seen in pancreatic tissues of the diabetic animal model (Borona, 2008; Khan et al., 2016). The treatments of piperine and sitagliptin caused significant alterations in HOMA indices of IR, β %, and S%, which indicate the interferences of piperine in the metabolism of glucose as well as insulin action. Accordingly, it is a well-established illustration that dietary or orally administered supplement stimulates insulin secretion by increasing GLP-1 activity through gut action (Girard, 2008; Mudaliar and Henry, 2012; Brandt et al., 2018). Supportively, the glucose transporter isoform GLUT4 might be a critical target to treat insulin resistance.

Meanwhile, GLUT4 is an insulin-dependent isoform that is accountable for furthermost insulin-encouraged glucose uptake (Abdel Aziz et al., 2020). Consequently, the treatments caused significant reductions in lipid profile and the atherogenic index, which may follow the subside of the gluconeogenesis and inhibition of lipid biosynthesis (Bano, 2013; Petersen and Shulman, 2018). Accordingly, the pancreatic tissues gained restorations in histoarchitecture, which indicates the interference of stimulation may produce by the piperine to increase islet cell mass, which is also seen in reduced insulin resistance and related HOMA indices. It is reported that postprandial dietary stimuli promote the secretion of GLP-1 and GIP by gut cells, which further stimulate insulin secretion and restoration or regeneration of islet β -cells (Wu et al., 2015; Prassannaraja et al., 2020).

There were significant differences in hippocampal CA3 and Dg neuronal morphology between the experimental groups (Tables 1, 2; Figures 7, 8). Here we have used a chronic dose of dexamethasone and a single mild streptozotocin dose to induce Hyperglycemia and Insulin resistance. Diabetics' control animals exhibited changes both in neuronal morphology and number. Histology revealed cell death both in CA3 and Dg sub-regions of the hippocampus. Dexamethasone treatment is comparable to adrenalectomy and leads to corticosteroid depletion and cell death in the hippocampus's Dg (Hassan et al., 1996; Hornsby et al., 1996), a phenomenon that is well documented after adrenalectomy (Sloviter et al., 1993). Streptozotocin can also induce cell death in the hippocampus, especially in CA3 neurons, by altering the brain antioxidant status and energy impairment (Salkovic-Petrisic et al., 2013). Neuronal damage in the hippocampus contributes to cognitive brain dysfunctions (Agrawal et al., 2009; Saxena et al., 2010).

Nazem et al. (2015) suggested that neuroinflammation leads to the accumulation of AB and tau and ultimately leading to Alzheimer's. Streptozotocin treated animals exhibit an insulinresistant brain state, which promotes the accumulation of tau and Aβ (Salkovic-Petrisic et al., 2013). Our *in vivo* results also confirm this streptozotocin up-regulated BACE1, PSEN1, APAF1, CASPASE3, and CATALASE genes in the animal model. Molecular interaction between piperine and protein of these genes was also studied using molecular docking. Antioxidants are considered to be good neuroprotectants and can ameliorate cognitive impairments. Quercetin, a flavonoid, is useful in the amelioration of STZ-induced cognitive impairment (Liu et al., 2012). Piperine also possesses antioxidant properties and can cross the blood-brain barrier (Srinivasan, 2007; Elnaggar et al., 2015). The beneficial effects of piperine on neurons' morphology and cognitive functions can be attributed to inherent antioxidant capabilities. The down-regulation of BACE1, PSEN1, APAF1, CASPASE3, and CATALASE genes in the animal model and binding of piperine with protein in the silico model, shows that the neuroprotective activity of piperine may be closely related.

In cells, $A\beta_{1-42}$ toxicity causes deterioration of chaperoning and proteasomal processing involved in clearance of deposited peptides (Mena et al., 2009). To overcome this failure, cytoprotective property elucidation of a molecule is necessary. This cytoprotective effect of piperine was demonstrated in PC12 cells, which is the standard in vitro model used to study neuroprotective compounds. Piperine showed significant protection of PC12 cells against both H_2O_2 and $A\beta_{1-42}$ induced toxicity under in vitro conditions. Understanding molecular interaction with protein targets and genes regulated by the piperine can provide information regarding its mechanisms of action. Additionally, drug targets do not always affect gene expression changes; they work via signaling cascades. Hence, drugs act on their drug targets and modulate the signaling mechanism (Xie et al., 2016; Makhouri and Ghasemi, 2018). Therefore, we performed in silico molecular docking of piperine with a protein involved in amyloid processing, apoptosis, and oxidative stress, and suggested interaction of piperine with important amino acid residues. In the present study, in silico studies used was molecular docking approach. Molecular docking is powerful computation tool to understand the structural and chemical basis of ligand-target specificities. The molecular docking results showed the interaction between piperine and specific proteins involved in amyloid processing, apoptosis, and oxidative stress such as BACE1, PSEN1, APAF1, CASPASE3, and CATALASE. The binding affinity of the proteins with piperine was measured by FullFitness score and deltaG (kcal/mol). As these proteins are encoded by specific genes, which express these proteins BACE1, PSEN1, APAF1, CASPASE3, and CATALASE, the gene specific primers were designed and gene expression studies using RT-PCR showed alteration of the gene expression profile in the piperine treated group of the abovementioned genes as compared to control. As the genes control most of the biological function through specific proteins, the molecule which can either bind to protein or alter gene expression can be used for therapeutic intervention in amelioration complex conditions line hyperglycemia induced neurodegeneration process. The gene expression profile in response to the piperine support the docking results and propose a credible viewpoint on the pathways associated with protein responses to piperine binding in AD-related drug targets.

CONCLUSION

In conclusion, piperine demonstrated to possess neuroprotective properties in STZ induced diabetic rodent model as it can be used as an interventional strategy to protect neuronal cells in hyperglycemic conditions. The improvement of HOMA indices, histo-architectures, and downregulation to genes involved in apoptosis and oxidative stress are scientific evidence underlying the protective mechanism.

DATA AVAILABILITY STATEMENT

The authors confirm that the data supporting the findings of this study are available within the article and its supplementary materials.

ETHICS STATEMENT

The animal study was reviewed and approved by IAEC, Department of Zoology, JNVU, Jodhpur, India.

AUTHOR CONTRIBUTIONS

SK designed and conceived the idea of this research work. SK wrote the original manuscript. SC performed all the cell culture and docking experiments, RP, AR, and DK performed all gene expression studies, HR, PK, and PN completed all *in vivo* experiments, SS performed histopathology related experiments. All the authors contributed to writing the manuscript.

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Studies on the Changes of Pharmacokinetics Behaviors of Phytochemicals and the Influence on Endogenous Metabolites After the Combination of Radix Bupleuri and Radix Paeoniae Alba Based on Multi-Component Pharmacokinetics and Metabolomics

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Radix Bupleuri-Radix Paeoniae Alba (RB-RPA) is a classic herb pair, which is commonly used to treat depression by soothing "liver gi stagnation" in the clinic. However, little is yet known concerning the combination mechanism of Radix Bupleuri (RB) and Radix Paeoniae Alba (RPA), their bioactive forms in vivo and the regulatory effects on the organism. The present study aimed to elucidate the changes in multi-component pharmacokinetics (PK) behavior after the combination of RB and RPA by a highresolution full-scan mode of UPLC-HRMS method (a total of 38 components PK profiles were obtained, of which 23 components come from RB and 15 components come from RPA). Moreover, the metabolomics approach was used to analyze the dynamic response of endogenous metabolites intervened by RB-RPA, and the correlation between concentration-time curves of 38 components from RB-RPA and the dynamic response profiles of endogenous metabolites was characterized by Pearson correlation analysis. The results demonstrated that the combination of RB and RPA could significantly improve the bioavailability of five components in RB, and six components in RPA. Besides, metabolomics results indicated that a total of 21 endogenous metabolites exhibited time-dependent changes in response to the RB-RPA administration, of which 12 endogenous metabolites were significantly increased, and nine endogenous metabolites were significantly decreased. Furthermore, correlation analysis results indicated that the components with significantly improved bioavailability after combination such as saikogenin F, saikogenin G, albiflorin, methyl gallate, paeonimetabolin II were significantly positively correlated with picolinic acid, a metabolite with neuroprotective effect; saikogenin F, saikogenin G were significantly positively correlated with itaconic acid, a endogenous metabolite with anti-inflammatory activity; and albiflorin, paeonimetabolin II were significantly positively correlated with α -linolenic acid, a metabolite with strong protective actions on brain functions. These results indicated that the combination of RB and RPA can enhance each other's neuroprotective and anti-inflammatory activities. In this study, A novel and efficient strategy has been developed to analyze the influence of the combination of RB and RPA *in vivo* behaviors by combining multi-component pharmacokinetics with metabolomics, which was contributed to clarifying the scientific connotation of herb-herb compatibility.

Keywords: Radix Bupleuri-Radix Paeoniae Alba herb pair, multi-component pharmacokinetics, metabolomics, correlation analysis, herb-herb compatibility

INTRODUCTION

RB is the dried root of the umbelliferous plant *Bupleurum chinense* DC. It has been widely used in Asia for thousands of years due to its pharmaceutical effects on antipyretic, analgesic, anti-inflammatory and anti-depressant (Ashour and Wink, 2011). The saponins such as saikosaponin A, saikosaponin D were the main active components of antidepressant effect (Tian et al., 2016). RPA is derived from the dried roots of *Paeonia lactiflora* Pall. In "Shennong's Classic of Material Medical," the efficacy of RPA was described in detail. Modern pharmacological studies have found that RPA has a variety of biological activities, such as analgesia, anti-inflammatory, immune-enhancing and

anti-depression effects (Xu et al., 2008). Paeoniflorin and albiflorin were the main active ingredients in the antidepressant effect of RPA (Qiu et al., 2013). RB-RPA was a common herb pair, which was regarded as the core drug pair in Xiaoyaosan, Sinisan and Chaihu-Shugan San which all were classic prescriptions for treating depression, and exerted antidepressant effect by relieving "liver qi stagnation." Herb-herb compatibility is a common form of TCM, it can achieve an optimal effect by obtaining synergy or reducing possible adverse reactions (Zhao et al., 2010). Modern pharmacological studies have shown that the analgesic, anti-inflammatory, and antidepressant effect was significantly improved after the combination of RB and RPA (Wang et al.,

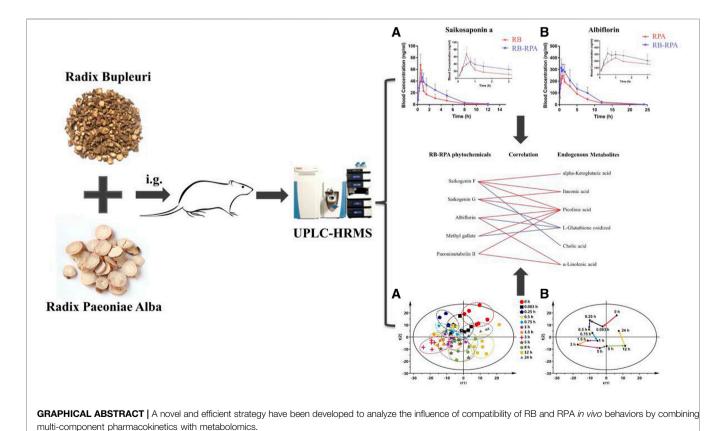


TABLE 1 | The prototype components and their metabolites characterized by UPLC/MS/MS after oral administration of RB-RPA herb pair in rat plasma, and the extracted ion ranges of 38 components.

No.	Name	$t_{ m R}$ /min	Formula	Ion mode	m/z	Source or parent	Extracted ion ranges
P1	Desbenzoylpaeoniflorin	0.972	C ₁₆ H ₂₄ O ₁₀	[M + HCOO] ⁻	421.13408	RPA	421.13405–421.13410
P2	Methyl gallate	3.473	$C_8H_8O_5$	[M-H] ⁻	183.02991	RPA	183.02988-183.02993
P3	Oxypaeoniflorin	4.695	C ₂₃ H ₂₈ O ₁₂	[M-H] ⁻	495.15087	RPA	495.15084-495.15090
P4	Albiflorin	6.658	C ₂₃ H ₂₈ O ₁₁	[M + HCOO]-	525.16021	RPA	525.16019-525.16024
P5	Paeoniflorin	7.693	C ₂₃ H ₂₈ O ₁₁	[M + HCOO] ⁻	525.16029	RPA	525.16026-525.16032
P6	Saikosaponin C	13.856	C ₄₈ H ₇₈ O ₁₇	[M + HCOO] ⁻	971.52109	RB	971.52107-971.52112
P7	Saikosaponin A	15.069	C ₄₂ H ₆₈ O ₁₃	[M + HCOO] ⁻	825.45521	RB	825.45518-825.45523
P8	Saikosaponin B ₂	15.516	C ₄₂ H ₆₈ O ₁₃	[M + HCOO] ⁻	825.45520	RB	825.45518-825.45523
P9	Acetyl-saikosaponin A	16.183	C ₄₄ H ₇₀ O ₁₄	[M + HCOO] ⁻	867.47362	RB	867.47360-867.47370
P10	Saikosaponin D	16.525	C ₄₂ H ₆₈ O ₁₃	[M + HCOO] ⁻	825.45521	RB	825.45518-825.45523
P11	Acetyl-saikosaponin B ₂	16.615	C ₄₄ H ₇₀ O ₁₄	[M + HCOO]	867.47364	RB	867.47360-867.47370
P12	Acetyl-saikosaponin D	17.583	C ₄₄ H ₇₀ O ₁₄	[M + HCOO]	867.47368	RB	867.47360-867.47370
M1	Paeonimetabolin I	9.674	C ₁₀ H ₁₄ O ₄	[M-H] ⁻	197.08117	Paeoniflorin	197.08115-197.08123
M2	Paeonimetabolin II	11.311	C ₁₀ H ₁₆ O ₄	[M-H] ⁻	199.09755	Paeoniflorin	199.09753-199.09758
МЗ	Paeonimetabolin I glucuronide isomer	6.033	C ₁₆ H ₂₂ O ₁₀	[M-H] ⁻	373.11411	Paeoniflorin	373.11408-373.11414
M4	Methylgallic acid glucuronide	6.957	C ₁₄ H ₁₆ O ₁₁	[M-H] ⁻	359.06197	Methyl gallate	359.06195-359.06199
M5	Methylgallic acid sulfate	2.968	C ₈ H ₈ O ₈ S	[M-H] ⁻	262.98679	Methyl gallate	262.98675-262.98682
M6	3,4-di-O-methyl gallic acid sulfate	10.353	$C_9H_{10}O_8S$	[M-H] ⁻	277.00231	Methyl gallate	277.00228-277.00233
M7	Pyrogallol glucuronide	1.284	$C_{12}H_{14}O_9$	[M-H] ⁻	301.05658	Methyl gallate	301.05656-301.05662
M8	Pyrogallol sulfate	6.745	$C_6H_6O_6S$	[M-H] ⁻	204.98135	Methyl gallate	204.98133-204.98138
M9	Methylpyrogallol sulfate	2.082	$C_7H_8O_6S$	[M-H] ⁻	218.99695	Methyl gallate	218.99692-218.99698
M10	Methylpyrogallol glucuronide	1.049	C ₁₃ H ₁₆ O ₉	[M-H] ⁻	315.07209	Methyl gallate	315.07206-315.07213
M11	Prosaikogenin F	14.972	$C_{36}H_{57}O_{8}$	[M + HCOO] ⁻	662.40253	Saikosaponin A	662.40247-662.40257
M12	Saikogenin F	13.123	$C_{30}H_{48}O_4$	$[M-H_2O + H]^+$	455.35191	Saikosaponin A	455.35188-455.35198
M13	Hydroxy-saikogenin F	13.905	$C_{30}H_{48}O_5$	$[M-H_2O + H]^+$	471.34678	Saikosaponin A	471.34674-471.34692
M14	Dihydroxyl-dehydrogenation-saikogenin F	13.021	$C_{30}H_{46}O_{6}$	$[M-H_2O + H]^+$	485.32603	Saikosaponin A	485.32600-485.32606
M15	Hydroxyl-dehydrogenation-saikogenin F	16.142	$C_{30}H_{46}O_{5}$	$[M-H_2O + H]^+$	469.33111	Saikosaponin A	469.33108-469.33118
M16	Dihydroxyl-saikogenin F	13.648	$C_{30}H_{48}O_{6}$	$[M-H_2O + H]^+$	487.34168	Saikosaponin A	487.34164-487.34172
M17	Trihydroxyl-dehydrogenation-saikogenin F	13.336	$C_{30}H_{46}O_{7}$	$[M-H_2O + H]^+$	501.32095	Saikosaponin A	501.32090-501.32099
M18	Saikogenin E	16.086	$C_{30}H_{48}O_3$	$[M-H_2O + H]^+$	439.35692	Saikosaponin C	439.35686-439.35696
M19	Hydroxy-saikogenin E	17.372	$C_{30}H_{48}O_{4}$	$[M-H_2O + H]^+$	455.35182	Saikosaponin C	455.35178-455.35186
M20	Dihydroxyl-dehydrogenation-saikogenin E	16.321	$C_{30}H_{46}O_{5}$	$[M-H_2O + H]^+$	469.33115	Saikosaponin C	469.33108-469.33118
M21	Hydroxyl-dehydrogenation-saikogenin E	16.894	$C_{30}H_{46}O_4$	$[M-H_2O + H]^+$	453.33621	Saikosaponin C	453.33618-453.33625
M22	Dihydroxyl-saikogenin E	14.757	$C_{30}H_{48}O_5$	$[M-H_2O + H]^+$	471.34669	Saikosaponin C	471.34666-471.34676
M23	Prosaikogenin G	17.669	$C_{36}H_{57}O_{8}$	[M + HCOO]	662.40251	Saikosaponin D	662.40247-662.40257
M24	Saikogenin G	16.516	$C_{30}H_{48}O_4$	$[M-H_2O + H]^+$	455.35196	Saikosaponin D	455.35188-455.35198
M25	Prosaikogenin D	15.947	$C_{36}H_{57}O_8$	[M + HCOO]	662.40249	Saikosaponin B ₂	662.40247-662.40257
M26	Saikogenin D	14.544	$C_{30}H_{48}O_4$	$[M-H_2O + H]^+$	455.35193	Saikosaponin B ₂	455.35188-455.35198

P: prototype components absorbed into the plasma; M: metabolites of prototype components; RB: Radix Bupleuri; RPA: Radix Paeoniae Alba.

2016; Li et al., 2021). However, the scientific connotation of RB and RPA combination and the potential theoretical basis of increasing therapeutic effect after combination were unclear. Currently, pharmacokinetic research has become a reliable way to elucidate the synergistic mechanism of herb-herb compatibility, as it can reflect the dynamic changes of the pharmacodynamic substances before and after compatibility (Wang et al., 2012; Zhou et al., 2017).

Recently, we have also analyzed the chemical components in rat plasma after oral administration of RB-RPA herb pair, a total of 55 components were detected in rat plasma, of which 16 were prototype components and 39 were metabolites of prototype components (Yin et al., 2019). The analysis of the chemical profile of RB-RPA in rat plasma makes it possible to conduct a comprehensive PK study. In this work, we employed the Thermo-Fisher Dionex UltiMate 3000 UHPLC-Q Exactive Orbitrap-MS system, with a high-resolution and high-throughput platform to conduct the PK study of 38 marker

compounds (due to the low concentration of the other 17 components, the time points that could be detected were less than six, their PK curves were not available), and the mass spectrum information and extracted ion ranges of the 38 components were listed in **Table 1**. The method was based on a high-resolution full-scan mode, to acquire a comprehensive profile of all ionized components in rat plasma, and previous studies have confirmed the reliability of this analytical method in PK studies (Wang et al., 2019). So, based on the above research, the impact on pharmacokinetic parameters before and after the combination of RB and RPA was analyzed by multi-component pharmacokinetics research method.

Distinct from chemical drugs, the large number and wide concentration range of compounds were present in TCM. Besides, the vast number of compounds were ingested would have a series of regulatory effects in the body (including endogenous metabolites that were significantly regulated in response to the intake of herbal medicines compounds), multi-

compounds interact with multi-targets to achieve a maximal therapeutic effect and could exert a holistic treatment to multi-targets diseases such as depression (Xue and Roy, 2003). Therefore, establishing the evidence-based pharmacokinetics (PK) and pharmacodynamics (PD) research methods for multicomponent TCM was still a difficult issue. It was worth noting that many of today's major diseases (such as diabetes, hyperuricemia, and depression) have a strong metabolic foundation or a definite metabolic cause (Wishart, 2016). Besides, the nutraceutical intervention of multicomponent herbal medicines was regarded as a process in which the plant metabolome interacts with the body metabolome (Xie et al., 2018). Therefore, endogenous metabolites as an indicator of PD become a reliable method to solve this difficult problem (Zhang et al., 2019). At the same time, revealing the dynamic response and interactions between herbal phytochemistry and endogenous metabolites was provided a new opportunity to clarify the holistic and synergistic mechanisms of TCM (Xie et al., 2012). In this study, metabolomics technology was applied to analyze the dynamic response of endogenous metabolites after oral RB-RPA. At the same time, PK-PD correlation analysis was used to comprehensively analyze the effect of "plant metabolome" on "body metabolome" by integrating pharmacokinetics and metabonomics technology.

MATERIALS AND METHODS

Chemicals and Reagents

HPLC grade acetonitrile, methanol, and LC-MS grade formic acid were obtained from Thermo-Fisher Scientific Inc. (United States). Purification of deionized water using the Milli-Q system (Millipore, Billerica, MA, United States). The Chinese Herbal Slices of Radix Bupleuri and Radix Paeoniae Alba were purchased from Anguo Qiao Chinese herbal sliced medicine Co., Ltd. and the batch number were 1710436111 and 1708255131 respectively. Moreover, Traditional Chinese medicines Radix Bupleuri and Radix Paeoniae Alba were authenticated by Prof. Xue-Mei Qin of Shanxi University, which confirmed that Radix Bupleuri is the dried root of the umbelliferous plant Bupleurum chinense DC and Radix Paeoniae Alba is derived from the dried roots of Paeonia lactiflora Pall. Voucher specimens of Radix Bupleuri and Radix Paeoniae Alba were deposited in the Modern Research Center for Traditional Chinese Medicine of Shanxi University, labeled as YZ-2018-0403001 (Radix Paeoniae Alba) and YZ-2018-0403002 (Radix Bupleuri), respectively. Saikosaponin A (batch number BWB50206), saikosaponin D (batch number BWB50210), saikosaponin C (batch number BWB50209), saikosaponin B₂ (batch number BWB50208) and methyl gallate (batch number BWB50638) were purchased from Chengdu Ruifensi Biological Technology Co., Ltd. (Sichuan, China). Paeoniflorin (batch number Y0001856), albiflorin (batch number ASB-00001513-005), oxypaeoniflorin (batch number BWB50094) and glycyrrhizin (IS; batch number 14110717) were purchased from the Chinese National Institute of Pharmaceutical and Biological Products (Beijing, China). The purities of all standards were at least 98%, and all other organic reagents were of analytical grade.

Preparation of Herb Extracts

As described in previous reports (Chen et al., 2020; Li et al., 2021), Radix Bupleuri (3 kg) or Radix Paeoniae Alba (3 kg) were soaked in 70% ethanol (2.4 L) for 1.5 h before extraction. Then Radix Bupleuri or Radix Paeoniae Alba were extracted twice with 70% ethanol under reflux, each time for 1.5 h. The extracts were filtrated and concentrated in vacuo and lyophilized into powders (15.15% yield for Radix Bupleuri, and 11.78% yield for Radix Paeoniae Alba), and then stored at 4°C until use and UPLC-MS analysis.

Besides, to assure the quality of Radix Bupleuri and Radix Paeoniae Alba, the chemical fingerprinting was analyzed by HPLC. For Radix Bupleuri, the saikosaponin A, saikosaponin D, saikosaponin B_2 , and saikosaponin C were identified as chemical markers for quality monitoring; For Radix Paeoniae Alba, the albiflorin, paeoniflorin, oxypaeoniflorin, and methyl gallate were identified as chemical markers for quality monitoring. The representative HPLC was shown in **Supplementary Figure S1** and the content of the eight constituents in herb extracts was shown in **Supplementary Table S1**.

Preparation of Standards, Calibration Standards, and QC Samples

Individual stock solutions ($1.00~{\rm mg\,mL^{-1}}$) of saikosaponin A, saikosaponin D, saikosaponin C, saikosaponin B₂, paeoniflorin, albiflorin, oxypaeoniflorin and methyl gallate were prepared by accurately weighing the required amounts into volumetric flasks and dissolving in methanol. The individual stock solutions were serially diluted with methanol and then mixed to provide working standard solutions of the desired concentrations. The Internal standard (IS) stock solutions of glycyrrhizin ($1.00~{\rm ug\,mL^{-1}}$) were also prepared in methanol, and then diluted with methanol to the desired concentrations of $300~{\rm ng\,mL^{-1}}$.

Calibration standard solutions were prepared by spiking 50 μ L of a mixed standard solution with 150 μ L blank rat plasma to give a desired concentrations: saikosaponin D, saikosaponin C, saikosaponin B₂, and oxypaeoniflorin at 0.1, 0.2, 0.5, 1.0, 5.0, 10.0, 20.0, 50.0, 250.0 ng mL⁻¹; saikosaponin A and methyl gallate at 0.2, 0.4, 1.0, 2.0, 10.0, 20.0, 40.0, 100.0, 500.0 ng mL⁻¹; albiflorin at 0.5, 1.0, 2.5, 5.0, 25.0, 50.0, 100.0, 250.0, 1250.0 ng mL⁻¹; paeoniflorin at 2.0, 4.0, 10.0, 20.0, 100.0, 200.0, 400.0, 1000.0, 5000.0 ng mL⁻¹.

For method validation, QC samples were prepared using three concentration levels of the standard solution in the same manner, with the desired concentrations of saikosaponin D, saikosaponin C, saikosaponin B₂, and oxypaeoniflorin at 0.2, 5.0, 50.0 ng mL^{$^{-1}$}; saikosaponin A and methyl gallate at 0.4, 10.0, 100.0 ng mL $^{-1}$; albiflorin at 1.0, 25.0, 250.0 ng mL $^{-1}$; paeoniflorin at 4.0, 100.0, 1000.0 ng mL $^{-1}$.

Plasma Sample Pretreatment

 $150~\mu L$ of plasma was mixed with $50~\mu L$ of IS solution and $300~\mu L$ methanol-water (1:1, v/v). The above mixtures were vortexed for 2 min, ultrasonicated for 5 min, and then centrifuged at $4^{\circ}C/$ 13,000~rpm for 15 min. The supernatant was separated and evaporated to dryness with a SCIENTZ-50F vacuum centrifugal concentrator (Scientz Biotechnology Co., Ltd., Ningbo, China). The dry extracts were reconstituted in 150~ul

methanol-water (1:5, v/v), vortexed for 2 min, and centrifuged at 4° C/13,000 rpm for 10 min. Finally, transferred 100 μ L to autosampler vials for UPLC-MS analysis.

Animal Handing and Sampling

Male Sprague-Dawley rats, weighing 220 ± 20 g (aged 8 weeks), were provided by the Beijing Vital Laboratory Animal Co., Ltd. (Beijing, China, No. SCXK2018-0011). All of the rats were adapted to the novel experimental environment for 7 days (room temperature 22 \pm 2°C, 55 \pm 5% relative humidity and 12 h light-dark cycle); All rats were free to access the water and food until 12 h before the experiment. The animal study was reviewed and approved by the Experimental Animal Ethical Committee of Modern Research Center for Traditional Chinese Medicine, Shanxi University (animal ethic approval number: SXULL2018018), and all experimental procedures were carried out in accordance with the NIH Guide for the Care and Use of Laboratory Animals. After one week of adaptation, twenty-one rats were divided into three groups randomly, with seven rats in each group: 1) RPA group, were oral administration of Radix Paeoniae Alba extract (45 gherb/kg); 2) RB group, were oral administration of Radix Bupleuri extract (45 g-herb/kg); 3) RB-RPA group, were oral administration of powder mixture of Radix Bupleuri and Radix Paeoniae Alba extracts (containing 45 g-herb/kg Radix Bupleuri and 45 g-herb/kg Radix Paeoniae Alba). The medicinal powders of all groups were dissolved in distilled water at concentrations of 0.53 g/ml for RPA, 0.68 g/ml for RB and 1.21 g/ml for RB-RPA. Each group received intragastric administration with a volume of 10 ml/kg (rat body weight). The dosage of Radix Bupleuri and Radix Paeoniae Alba is equivalent to a 3-fold clinical dosage of component herbs in Xiaoyao San (Chen et al., 2020). The blood samples (0.3 ml) were collected from the ophthalmic venous plexus into heparinized tubes before oral administration and subsequently at 0.083, 0.25, 0.5, 0.75, 1, 1.5, 3, 5, 8, 12, and 24 h after dosing. All rats were free to access the water during the experiment. The blood samples at each time point were collected from seven rats. The blood samples were centrifuged at 4,000 rpm for 10 min and frozen at -80°C until analysis.

UPLC-HRMS Analysis for Herb Extracts and Plasma Sample

Using a Thermo-Fisher Dionex UltiMate 3000 UHPLC system coupled with a Q Exactive Orbitrap-MS (Thermo-Fisher, United States) and Xcalibur workstation (Thermo-Fisher Scientific Inc.,Waltham, MA, United States) to acquire UPLC-HRMS raw data. Chromatographic separation of herb extracts and plasma samples was performed on an Acquity UPLC HSS T3 column (2.1 mm \times 100 mm, 1.8 µm) maintained at 37°C. The flow rate was 0.2 ml/min and the injection volume was 5 µL. The mobile phase consisted of (solvent A) 0.1% formic acid in water (v/v) and (solvent B) 0.1% formic acid in acetonitrile (v/v), the gradient elution conditions for herb extracts and plasma samples were operated under the following program: 0~5.5 min, 5% B; 5.5~9.5 min, 5~15% B; 9.5~13 min, 15~35% B; 13~17 min, 35~60% B; 17~20 min, 60~90% B; 20~22 min, 90% B; 22~23 min, 90~5%B; 23~25 min, 5% B. Mass spectrometry

detection conditions were set as follows: the MS data were acquired under positive and negative ionization modes via heated electrospray ionization (HESI) source. The scan mode was Full Scan and the scan range was set 50–1000 m/z; heater temperature, 300°C; capillary temperature, 330°C; spray voltage, 3.5 kV (positive mode) and 2.6 kV (negative mode); sheath gas velocity, 35 arb; auxiliary gas flow, 10 arb. The Q Exactive Orbitrap-MS has a fast positive and negative ion switching function, which could switch between positive-negative ion modes during the analysis of the same sample. So, we applied the method of switching ion modes in the detection process to quantify all analytes better. Glycyrrhizin was selected as the internal standard because it could be detected in both positive and negative ion modes.

Pharmacokinetics Analysis

UPLC/MS/MS calibration and quantitation data were processed with Xcalibur workstation (Thermo-Fisher Scientific Inc., Waltham, MA, United States). For the eight components with standard reference, calculating their concentrations from the standard curves. For the other 30 components without standard reference, their concentrations were analyzed following the regression equations of homologous compounds (Qiao et al., 2012): paeoniflorin for P1 and M1 to M3; methylgallate for M4 to M10; saikosaponin A for P9 and M11 to M17; saikosaponin C for M18 to M22; saikosaponin D for P12 and M23 to M24; saikosaponin B2 for P11 and M25 to M26. For the PK studies, the maximum concentration (C_{max}), time of maximum plasma concentration (t_{max}), terminal elimination half-life $(t_{1/2})$, areas under the concentration-time curve $(AUC_{0-t} \text{ and } AUC_{0-\infty})$ of each compound were analyzed by a non-compartmental analysis using Drug And Statistics Version 3.0 (DAS 3.0) software (Mathematical Pharmacology Committee, Chinese Pharmacological Society, China).

Analysis of Radix Bupleuri-Radix Paeoniae Alba Herb Pair-Induced Endogenous Metabolites Variations

The UPLC-HRMS raw data were imported to Compound Discoverer 3.0 (Thermo Fisher, United States) for matching and aligning peak data. The parameters were set as follows: mass tolerance, 5 ppm; RT tolerance, 0.05 min; S/N threshold, 10; intensity tolerance, 30%; assignment threshold, 60; mass range, 50–1000 Da. The peak area data of all metabolites obtained from Compound Discoverer 3.0 was normalized by IS (glycyrrhizin) in Microsoft Excel 2013.

To analyze the RB-RPA herb pair-induced endogenous metabolites variations, the acquired data at each time point from Compound Discoverer 3.0 (removal of 55 RB-RPA herb pair metabolites previously identified in rats plasma (Yin et al., 2019)) were imported into SIMCA-P software (version 16.0, Umetrics, Sweden) for multivariate statistical analysis, such as the principal components analysis (PCA), partial least-squares discriminant analysis (PLS-DA) and orthogonal partial least-squares discriminant analysis (OPLS-DA). The altered endogenous metabolites were screened according to the VIP-

value of S-plot (VIP >1) and T-test (p < 0.05). The selected metabolites of LC-MS analysis were identified based on the molecular formula, accurate m/z values, MS/MS fragments, and online databases including KEGG (http://www.kegg.jp), m/z cloud (https://www.mzcloud.org/), PubChem (https://pubchem.ncbi.nlm.nih.gov/), HMDB (http://www.hmdb.ca), Lipid Maps (http://www. lipidmaps.org), and Massbank (http://www.massbank.jp). Meanwhile, based on the investigation of metabonomics and the semi-quantification, the mean value of each altered endogenous metabolite at each time point, representing the average response, was calculated to analyze the relationship of the dynamic response for endogenous metabolites along with the time course.

Correlation analysis of 38 Radix Bupleuri-Radix Paeoniae Alba Herb Pair Phytochemicals in Rat Plasma and Altered Endogenous Metabolites

Pearson correlation analysis was further applied to find the high linear relationship of phytochemicals and altered endogenous metabolites. To analyze the relationship of the dynamic response for endogenous metabolites along with the time course, the mean value of each endogenous metabolite was calculated at each time point (0 h \rightarrow 0.083 h \rightarrow 0.25 h \rightarrow 0.5 h \rightarrow 0.75 h \rightarrow 1 h \rightarrow 1.5 h \rightarrow 3 h \rightarrow 5 h \rightarrow 8 h \rightarrow 12 h \rightarrow 24 h). A new metabolite vector with 12 mean values calculated at 12 different time points, representing the average response was constructed. Pearson correlation analysis to study the correlation between two new metabolite vectors (representing RB-RPA herb pair phytochemicals and altered endogenous metabolites, respectively). The $|\mathbf{r}| \geq 0.8$ and p < 0.05 represented that there was a high correlation between RB-RPA herb pair phytochemicals and altered endogenous metabolites.

Statistical Analyses

All data were expressed as the mean \pm standard deviation (SD). Data were statistically analyzed by SPSS 18.0 software (SPSS Inc., United States) and SIMCA-P 16.0 software (Umetrics, Sweden). PCA and PLS-DA were used to explore altered endogenous metabolites. Statistical analyses from two groups were analyzed using a two-tailed unpaired t-test, and statistical analyses from more groups were analyzed using one-way ANOVA. The p <0.05 were considered statistically significant.

RESULT AND DISCUSSION

Comparison of the Content of Eight Compounds Between Single Extracts and a Mixture of Radix Bupleuri and Radix Paeoniae Alba Extracts

The content of eight compounds in single (RB or RPA) extracts and mixture of RB and RPA extracts were analyzed by UPLC-HRMS. The base peak chromatograms of herb extracts and mixed standards (saikosaponin A, saikosaponin D, saikosaponin C,

saikosaponin B₂, paeoniflorin, albiflorin, oxypaeoniflorin, methyl gallate, and the internal standard) were shown in Supplementary Figure S1. The content of the eight constituents in herb extracts was shown in Supplementary Table S1. The statistical results showed that the content of eight compounds had no statistical difference between single (RB or RPA) extracts and mixture extracts. These results suggested that mixing process of RB and RPA extracts didn't affect the content changed of each component in RB or RPA extracts. Previous studies have shown that codecoction of RB and RPA in vitro can significantly increase the content of paeoniflorin and galloylpaeoniflorin in the RPA extract, and significantly reduce the content of saikosaponin A in the RB extract (He et al., 2018). Therefore, in order to avoid the content changes of prototype compounds caused by co-decocting in vitro, we used mixture of RB and RPA extracts to analyze the impact on pharmacokinetic parameters before and after the combination of RB and RPA.

Validation of the UPLC-MS/MS in vivo Analysis Method

Specificity

The specificity was investigated by comparing extracted-ion chromatograms (XICs) of the blank plasma sample, spiked plasma sample, and a plasma sample after oral administration of RB, RPA, and RB-RPA. As shown in **Supplementary Figure S2**, there were no significant endogenous substances interference peak was observed.

Calibration Curve and LLOQ

The calibration curves, linear ranges, correlation coefficients (r), and LLOQ of the eight analytes were represented in **Supplementary Table S2**. The coefficient of correlation (r²) values greater than 0.995 and the LLOQs varied from 0.1–2.0 ng/ml for all analytes. This suggested that the calibration curves of these analytes showed good linearity within a certain concentration range in rat plasmas.

Matrix Effect and Extraction Recovery

The results of the matrix effect and extraction recoveries of the eight analytes were listed in **Supplementary Table S3**. The extraction recoveries of the eight analytes in rat plasmas at three different concentrations were in range of 81.32–106.83%, and the matrix effects of the analytes were in range of 79.61–111.53%, indicating that there was no significant ion suppression/enhancement in this bioanalytical method.

Precision and Accuracy

Precision and accuracy were evaluated by analyzing QC samples at three different concentrations (low, medium, and high) in six replicates on the same day (intra-day) and on three consecutive days (inter-day), respectively. As shown in **Supplementary Table S4**, the intra- and inter-day precisions values (RSD) ranged from 1.82 to 9.11% and from 2.21 to 11.48%, respectively, and the accuracy values (RE) ranged from -8.11 to 8.12%. The results suggest that this method is feasible.

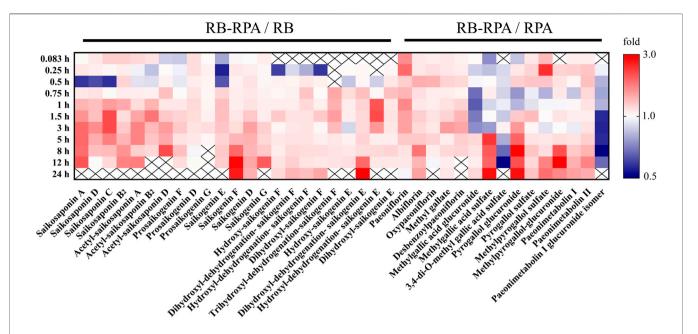


FIGURE 1 Comparison of plasma concentrations to reveal PK interactions. The average plasma concentrations (*n* = 7) between RB-RPA and RB or RPA were compared in heatmap. They were referred to as "X/Y," where X is the Compatibility group and Y is RB or RPA single group. Red color indicates that the ratio is greater than 1, and the blue color indicates that the ratio is less than 1, see color bar scale. "x" means the data was not detected at this time points.

Stability

The stability of the eight analytes during the sample processing and storage procedures was assessed by analyzing five replicates for QC samples at three different concentrations. The results were summarized in **Supplementary Table S5**, which showed that the eight analytes in plasma were all stable at room temperature for 24 h, at autosampler (4°C) for 24 h, three freeze-thaw cycles and 30 days storage at -20° C with values of RE (%) in the range -8.92 to 6.35%.

Pharmacokinetics

Determination of Plasma Concentration of 38 Compounds from "Plant Metabolome"

The validated UPLC-HRMS method was applied to simultaneously determine the plasma concentrations of 38 compounds after oral administration of RB-RPA herb pair in rats, including 12 prototype compounds and 26 metabolized products (**Table 1**). The peak areas of the 38 compounds were extracted from the extracted-ion chromatograms using a mass extraction window centered on the theoretical m/z, which was attributed to the high-resolution and high-throughput acquisition of HRMS. By comparing the plasma concentrations to reveal PK parameters of the 38 compounds before and after combination, we found that the combination of RB and RPA significantly changed the plasma concentrations of 38 compounds compared with the single herbal group (**Figure 1**).

Comparison of Pharmacokinetics of 23 Compounds from RB Before and After Compatibility

The time-concentration curves of 23 compounds from RB before and after combination were shown in **Figure 2**. Furthermore, to clearly observe differences among the 23 compounds from RB before and after combination, the main PK parameters were

calculated using a non-compartment model in DAS 3.0 software, and the results were listed in **Supplementary Table S6**. By comparing the PK parameters (C_{max} , t_{max} , $t_{1/2}$, and $AUC_{0-\infty}$) of 23 compounds between the RB-RPA group and the RB groups, the results showed that the combination of RB and RPA could impact the pharmacokinetic behaviors of 23 compounds from RB (Figure 3). For saikosaponin A and saikosaponin D, the PK profile of administration of RB alone was similar to a previous report (Xu et al., 2012). When saikosaponin A and saikosaponin D were administered in RB-RPA herbs, the C_{max} of saikosaponin A and saikosaponin D were decreased remarkably: from 68.37 \pm 16.95 to 46.47 \pm 12.41, and from 42.84 \pm 11.53 to 26.57 \pm 6.99 ng mL⁻¹, respectively (Figure 3C, Supplementary Table **S6**). In contrast, the $t_{1/2}$ of saikosaponin A and saikosaponin D were longer in the RB-RPA group than the single herbal group, which indicated that combination can extend the residence time of saikosaponin A and saikosaponin D in system circulation (Figure 3B). As a result, the $AUC_{0-\infty}$ of saikosaponin A was significantly improved from 103.55 ± 38.59 to $175.55 \pm$ 45.92 ng mL⁻¹ h after combination (in RB-RBA group), and the $AUC_{0-\infty}$ of saikosaponin D was improved from 69.92 ± 17.38 to 103.56 \pm 33.67 ng mL⁻¹ h (**Figure 3D**). Besides, as for acetyl-saikosaponin D, prosaikogenin F, prosaikogenin G, and dihydroxyl-dehydrogenation-saikogenin E, the $t_{1/2}$ of these compounds were significantly increased after combination, which indicated that combination can extend the residence time of these compounds in system circulation (Figure 3B). As a result, the $AUC_{0-\infty}$ of prosaikogenin F, prosaikogenin G, and dihydroxyl-dehydrogenation-saikogenin E were significantly increased after combination (Figure 3D). As for saikosaponin b₂, when saikosaponin b2 were administered in RB-RPA herbs, the C_{max} increased remarkably: 22.33 \pm 2.99 to 28.19 \pm 5.50 ng mL⁻¹,

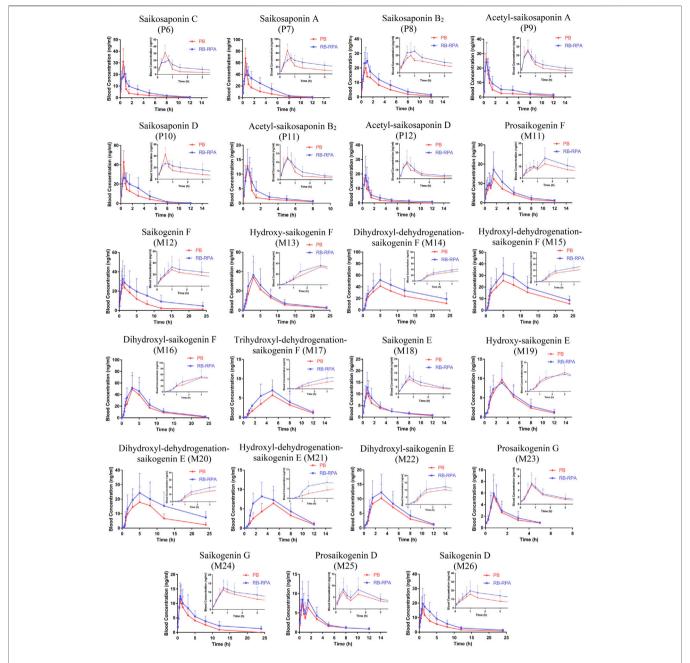


FIGURE 2 | Plasma concentration-time profiles (mean ± SD, n = 7) of 23 compounds from RB after oral administration of the RB (single extract) and RB-RPA (RB and RPA compatibility). The compounds represented by the numbers in **Table 1**.

which indicated that combination can promote the absorption of saikosaponin b_2 . As a result, the $AUC_{0-\infty}$ of saikosaponin b_2 was significantly increased after the combination. However, there was no significant effect on the t_{max} of 23 compounds from RB before and after combination (**Figure 3A**). These results indicated that the combination of RB and RPA played a critical role in improving the bioavailability of five components (saikosaponin A, saikosaponin B₂, prosaikogenin F, prosaikogenin G, dihydroxyl-dehydrogenation-saikogenin E) in RB.

Comparison of Pharmacokinetics of 15 Compounds from RPA Before and After Combination

The time–concentration curves of 15 compounds from RPA before and after combination were shown in **Figure 4**, and the main PK parameters (C_{max} , t_{max} , $t_{1/2}$, and $AUC_{0-\infty}$) were listed in **Supplementary Table S7**. It was clearly observed that the PK parameters of the combination group were remarkably different from those in RPA group (**Figure 5**). Specifically, the PK profile of administration of RPA alone was similar to the previous report

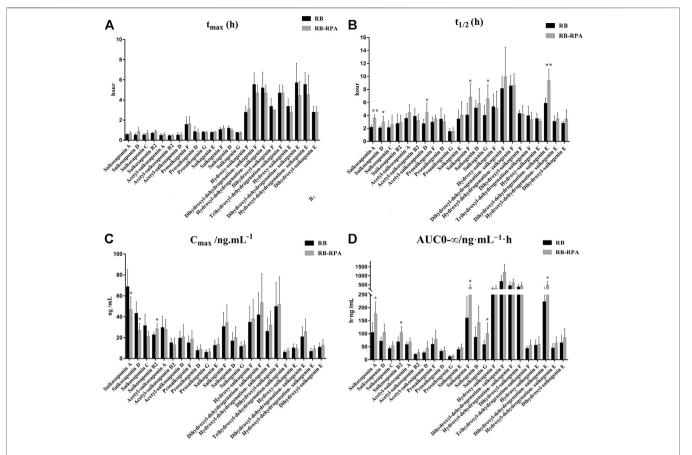


FIGURE 3 | Main pharmacokinetic parameters of 23 compounds from RB in rat plasma after oral administration of the single extract group (RB) and the compatibility group (RB-RPA). **(A)** t_{max} (h); **(B)** $t_{1/2}$ (h); **(C)** C_{max} (ng mL⁻¹); **(D)** $AUC_{0-\infty}$ (ng mL⁻¹ h). All data were expressed as mean \pm SD, (n = 7). *p < 0.05, **p < 0.01 compared with the RB group.

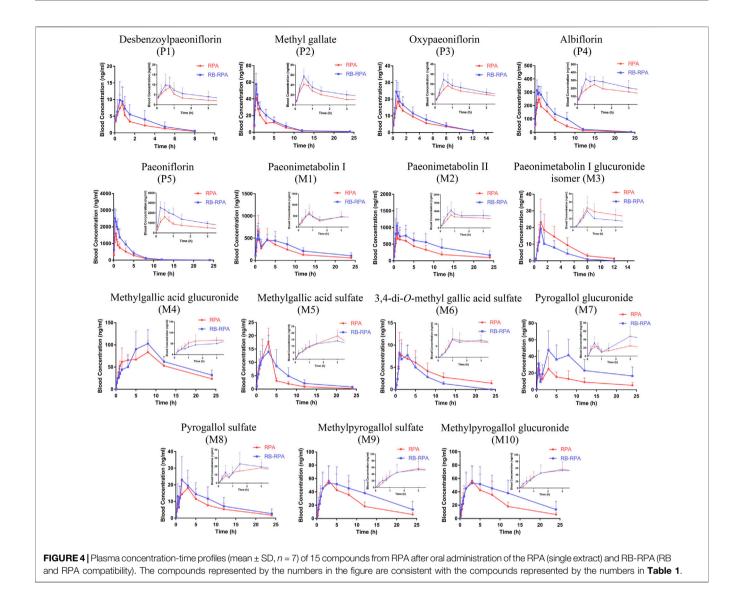
(Gong et al., 2015). However, compared with the administration of RPA alone, co-administration of RB and RPA was significantly increased the $C_{\rm max}$ of paeoniflorin and albiflorin from 1776.42 \pm 513.40 to 2932.12 \pm 385.77, 271.50 \pm 63.29 to 365.94 \pm 41.75 ng mL⁻¹, respectively (Figure 5C, Supplementary Table S7), which indicated that combination can promote the absorption of paeoniflorin and albiflorin. As a result, the AUC₀of paeoniflorin and albiflorin were significantly increased after combination. The results were consistent with previous research that has indicated that saikosaponin A and saikosaponin D could significantly improve the absorption of paeoniflorin and albiflorin in the ileum and colon (Chen et al., 2011), which could be the potential reason to improve the bioavailability of paeoniflorin and albiflorin after combination. As for pyrogallol glucuronide, the C_{max} , $t_{1/2}$, and AUC_{0- ∞} of pyrogallol glucuronide were significantly increased to 140.22, 170.29, and 245.38%, respectively, (Figures 5B-D), which indicated that combination of RB and RPA could improve the bioavailability of pyrogallol glucuronide. Besides, the AUC_{0-∞} of methyl gallate, methylpyrogallol glucuronide, and paeonimetabolin II were significantly increased and 3,4-di-O-methyl gallic acid sulfate was significantly decreased after combination (Figure 5D). These results indicated that the

combination of RB and RPA could significantly improve the bioavailability of six components (paeoniflorin, albiflorin, methyl gallate, pyrogallol glucuronide, methylpyrogallol glucuronide, and paeonimetabolin II) in RPA.

In conclusion, the results demonstrated that the combination of RB and RPA could significantly improve the bioavailability of five components (saikosaponin A, saikosaponin B₂, prosaikogenin F, prosaikogenin G, dihydroxyl-dehydrogenation-saikogenin E) in RB, and improve the bioavailability of six components (paeoniflorin, albiflorin, methyl gallate, pyrogallol glucuronide, methylpyrogallol glucuronide and paeonimetabolin II) in RPA. Besides, improving the bioavailability by the combination of RB and RPA could be summarized into two aspects: improvement in the plasma concentration ($C_{\rm max}$) and prolongation in system circulation ($t_{1/2}$).

Metabolomics

Effect of Radix Bupleuri-Radix Paeoniae Alba Herb Pair Intake on Rat Endogenous Metabolite Endpoints The plasma samples of rats at different time points after oral administration of RB-RPA were analyzed by UPLC-MS/MS, and the base peak intensity (BPI) chromatograms of plasma samples



are shown in Supplementary Figure S3. The metabolomics data acquired from Compound Discoverer 3.0 was imported into SIMCA-P V16.0 for multivariate statistical analysis. The principal component analysis (PCA) was conducted to investigate the trends of endogenous metabolite profiles at different time points after RB-RPA administration. The dynamic response profiles of endogenous metabolites intervened by RB-RPA based on PCA score plots were shown in Figure 6A, and a time-dependent trajectory of endogenous metabolite profiles was shown in Figure 6B. In Figure 6A, each spot represents a plasma sample, and each assembly of samples indicated a specific metabolic profile at different time points. From Figure 6B, endogenous metabolite profiles at different time points after administration were clearly separated from those at the time-point 0 before the RB-RPA intake. The timedependent trajectory showed that endogenous metabolic profiles underwent a significant change from 0 to 24 h, which may be related to changes in plasma concentrations of RB-RPA components. Furthermore, the endogenous metabolite profiles

at 24 h were closed to the pre-dose metabolite profiles, indicating that the metabolic profiles of the subjects showed a recovery trend. Simultaneously, the relative distance calculation between post-dose all time points metabolite profiles and pre-dose metabolite profile from PCA score plot with the average value (x-axis and y-axis) of all samples, to quantify all time points contributions after administration, according to the method described in the literature (Duan et al., 2016), and the results were listed in Supplementary Table S8. As shown in Supplementary Table S8, different relative distance calculation at different time points after administration, indicating that the ability to regulate endogenous metabolic profiles was different, and above all, 3 h after RB-RPA administration displayed the greatest ability to regulate endogenous metabolites as it showed the longest distance calculation. Accordingly, the altered endogenous metabolites associated with RB-RPA were selected by comparing VIP values (VIP >1) and T-test (p < 0.05) between the metabolites at time-point 3 h after the RB-RPA intake (3 h group) and the

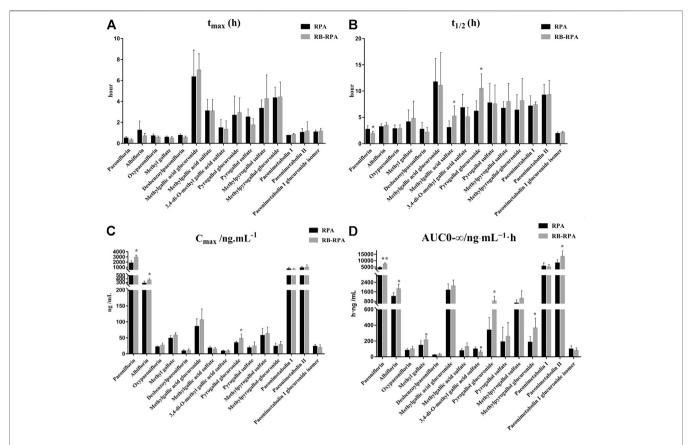


FIGURE 5 | Main pharmacokinetic parameters of 15 compounds from RPA in rat plasma after oral administration of the single extract group (RPA) and the compatibility group (RB-RPA). (A) t_{max} (h); (B) $t_{1/2}$ (h); (C) C_{max} (ng mL⁻¹); (D) $AUC_{0-\infty}$ (ng mL⁻¹ h). All data were expressed as mean \pm SD, (n = 7). *p < 0.05, **p < 0.01 compared with RPA group.

metabolites at time-point 0 h before the RB-RPA intake (0 h group) based on multivariate statistical analysis.

Screening and Identification of Endogenous Differential Metabolites Regulated by Radix Bupleuri-Radix Paeoniae Alba

As mentioned above, the endogenous differential metabolites regulated by RB-RPA were selected by comparing the different variables between the 3 h group and the 0 h group based on multivariate statistical analyses. As shown in Figures 6C-F, The PCA score plots indicated that the 3 h group could be obviously separated from the 0 h group (Figure 6C). This finding indicated that 3 h after the RB-RPA intake significantly altered the metabolic fingerprints of plasma compared with the 0 h group. Using the permutation plot test of the PLS-DA model to check the predictive ability and overfitting of the multivariate statistical analysis model (Figure 6D). The permutation test parameters of R²X, R²Y, and Q² were 0.436, 0.948, and 0.911, respectively. These results showed that the multivariate statistical analysis model had excellent predictive power and had not overfitted. To further enhance the ability of differential metabolite discovery between the 3 h group and 0 h group, the OPLS-DA model was used. The OPLS-DA score plots showed that obvious separation has occurred between the 3 h

group and the 0 h group (Figure 6E). The differential metabolites between the 3 h group and the 0 h group were screened by S-plots and VIP values in the OPLS-DA model (Figure 6F), and VIP >1.0 with p < 0.05 were considered. Besides, the selected differential metabolites were identified based on the molecular formula, accurate m/z values, MS/MS fragments, and online databases. At last, a total of 21 endogenous differential metabolites were screened and identified (Table 2). Compared with the 0 h, 12 endogenous differential metabolites (DL-ornithine, DL-histidine, choline, gamma-aminobutyric acid, L-glutamic acid, valine, alphaketoglutaric acid, L-(-)-asparagine, itaconic acid, picolinic acid, N-acetyl-L-leucine, α-linolenic acid) were significantly increased, and 9 [DL-glutamine, citric acid, L-tyrosine, DLtryptophan, L-glutathione oxidized, thymidine monophosphate, taurochenodeoxycholic acid, lysoPC (18:3), cholic acid] were significantly decreased in 3 h group.

Based on the investigation of metabonomics and the semiquantification, the relative peak areas of endogenous differential metabolites were calculated at various time points before and after administration. The detailed data was listed in **Supplementary Table S9**. Furthermore, Metabonomic response profiles response to RB-RPA intervention at various time points after administration were depicted as a heat map

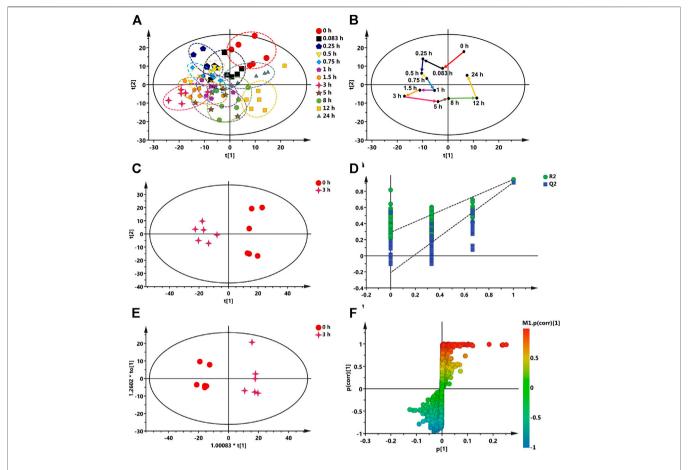


FIGURE 6 | Multivariate data analysis from UPLC-MS/MS. (A) The dynamic response profiles of endogenous metabolites intervened by RB-RPA based on PCA score plots. (B) A time-dependent trajectory of endogenous metabolite profiles at different time points after RB-RPA intake. (C) PCA score plots from 3 h group and 0 h group. (D) PLS-DA model validation diagram. (E) OPLS-DA score plots from 3 h group and 0 h group. (F) S-plot of OPLS-DA.

(**Figure 7**). In heat map, each cell represents the fold change between the two time points for a particular endogenous differential metabolite. These results indicated that 21 endogenous differential metabolites exhibited varying degrees of dynamic changes after RB-RPA administration.

The Potential Link Between Radix Bupleuri-Radix Paeoniae Alba Phytochemicals and the Altered Endogenous Metabolites

The correlation between the RB-RPA concentration-time curves of 38 components and the dynamic response profile of altered 21 endogenous metabolites was presented in **Figure 8**, with positive (red color) and negative (blue color) (p < 0.05, $|\mathbf{r}| > 0.8$) values. Correlation analysis demonstrated that RB-RPA herb pair phytochemicals had an impact on endogenous metabolites. In general, the change of the plasma concentration of endogenous metabolites in response to the alteration of the bioavailability of RB-RPA phytochemicals. As shown in **Figure 8**, most of RB-RPA phytochemicals were positively correlated with DL-ornithine, gamma-aminobutyric acid, valine, alpha-ketoglutaric acid,

itaconic acid, picolinic acid, α-linolenic acid, and were negatively correlated with L-glutathione oxidized and cholic acid.

Besides, to investigate the effects of the combination of RB and RPA on endogenous metabolites, the correlation between the phytochemicals improved bioavailability after combination and endogenous metabolites was summarized. As shown in Figure 9, the components for bioavailability significantly improved after combination such as saikogenin F, saikogenin G, albiflorin, methyl gallate, paeonimetabolin II were significantly positively correlated with picolinic acid; saikogenin F, saikogenin G were significantly positively correlated with itaconic acid; albiflorin, paeonimetabolin II were significantly positively correlated with α-linolenic acid; saikogenin G, albiflorin, methyl gallate were significantly negatively correlated with L-glutathione oxidized; saikogenin F was significantly positively correlated with alphaketoglutaric acid and was significantly negatively correlated with cholic acid. It was worth noting that picolinic acid and α -linolenic acid were endogenous metabolites with a strong neuroprotective effect, and itaconic acid was endogenous metabolites with antiinflammatory activity. These results indicated that the combination of RB and RPA can enhance each other's neuroprotective and anti-inflammatory activities.

TABLE 2 | Altered endogenous metabolites were detected by UPLC-MS/MS.

No.	Metabolites	T _R (min)	m/z	Formula	VIP	HMDB ID	3 h/0 h	Ion mode
1	DL-Ornithine	0.706	133.09723	C ₅ H ₁₂ N ₂ O ₂	1.32	32455	<u></u> †*	[M + H] ⁺
2	DL-Histidine	0.736	156.07683	$C_6H_9N_3O_2$	1.04	00177	↑ *	$[M + H]^{+}$
3	Choline	0.820	104.10671	$C_5H_{13}NO$	1.74	00097	↑**	$[M + H]^{+}$
4	Gamma-Aminobutyric acid	0.856	104.07063	$C_4H_9NO_2$	1.63	00112	↑**	$[M + H]^{+}$
5	L-Glutamic acida	0.860	146.04568	$C_5H_9NO_4$	2.13	00148	↑***	[M-H] ⁻
6	Valine	0.899	118.08636	$C_5H_{11}NO_2$	1.62	00883	↑**	$[M + H]^{+}$
7	DL-Glutamine	0.908	145.06167	$C_5H_{10}N_2O_3$	2.48	00641	J***	$[M-H]^{-}$
8	Alpha-ketoglutaric acid	0.931	145.01433	$C_5H_6O_5$	2.32	00208	↑***	[M-H] ⁻
9	L-(-)-Asparagine	0.941	115.05036	$C_4H_8N_2O_3$	1.03	00168	1 *	$[M-H_2O + H]^+$
10	Citric acid	0.983	191.01963	$C_6H_8O_7$	2.07	00094	J***	[M-H]⁻
11	L-Tyrosine ^a	1.032	182.08116	$C_9H_{11}NO_3$	2.18	00158	J***	$[M + H]^{+}$
12	Itaconic acid	1.062	259.04666	$C_5H_6O_4$	2.52	02092	↑***	[2M-H] ⁻
13	Picolinic acida	1.902	124.03942	$C_6H_5NO_2$	1.96	02243	↑**	$[M + H]^{+}$
14	DL-Tryptophan	3.412	205.09694	$C_{11}H_{12}N_2O_2$	1.51	13609	↓*	$[M + H]^{+}$
15	N-Acetyl-L-leucine	7.195	172.09740	$C_8H_{15}NO_3$	1.72	11756	↑**	[M-H] ⁻
16	L-Glutathione oxidized	7.830	613.15913	$C_{20}H_{32}N_6O_{12}S_2$	1.76	03337	↓**	$[M + H]^{+}$
17	Thymidine 5'-monophosphate	11.572	321.04513	$C_{15}H_{16}O_4P_2$	1.05	01227	↓*	[M-H] ⁻
18	Taurochenodeoxycholic acid	12.272	498.28967	$C_{26}H_{45}NO_6S$	1.33	00951	↓*	[M-H] ⁻
19	Cholic acid	14.329	407.28021	$C_{24}H_{40}O_5$	2.43	00619	J***	[M-H] ⁻
20	α-Linolenic acid	15.936	279.23164	C ₁₈ H ₃₀ O ₂	1.11	01388	<u>†</u> *	[M + H] ⁺
21	LysoPC (18:3)	17.149	518.32404	$C_{26}H_{48}NO_7P$	1.04	10387	 *	[M + H] ⁺

[&]quot;]" means the metabolite significantly decreased or increased in 3 h group compared with 0 h group.

^aValidated with standard.

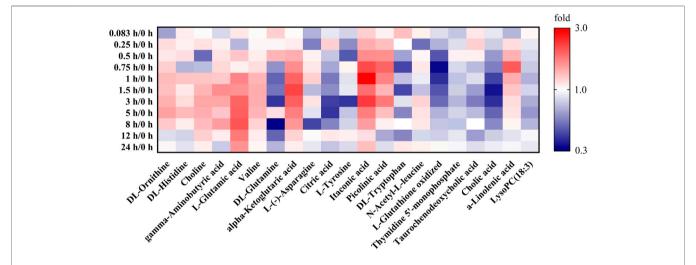


FIGURE 7 | Effect of RB-RPA herb pair intake on rat metabolite endpoints. Each cell in the heat map represents the fold change between at each time points after administration and at time-point 0 before the RB-RPA intake for a particular metabolite. The red color indicates that the ratio is greater than 1, and the blue color indicates that the ratio is less than 1. It visualizes the level of each metabolite at each time points ranging from high (red) over average (white) to low (blue).

Picolinic Acid

Picolinic acid is an end-product of the kynurenine pathway with a strong neuroprotective effect (Lovelace et al., 2017). Recent research has indicated that picolinic acid showed antidepressant effects by decreasing the immobile time of forced swim test and reversing the significant rise in plasma corticosterone level in CUMS-induced depression rats (Dubey et al., 2015). Furthermore, as well as clinically, decreased plasma picolinic acid levels have been demonstrated in depressed patients (Ryan

et al., 2020), and picolinic acid has also been shown to produce significant antidepressant effects in a typical depression (Davidson et al., 2003). Our study demonstrated that the five phytochemicals with improved bioavailability after combination (saikogenin F, saikogenin G, albiflorin, methyl gallate, paeonimetabolin II) were significantly positively correlated with picolinic acid, a metabolite that was significantly downregulated in depressed patients (Colle et al., 2020). Besides, chronic stress can cause imbalances in the kynurenine metabolic pathway and excessively produce the

^{*}p < 0.05, **p < 0.01, ***p < 0.001 compared with 0 h group.

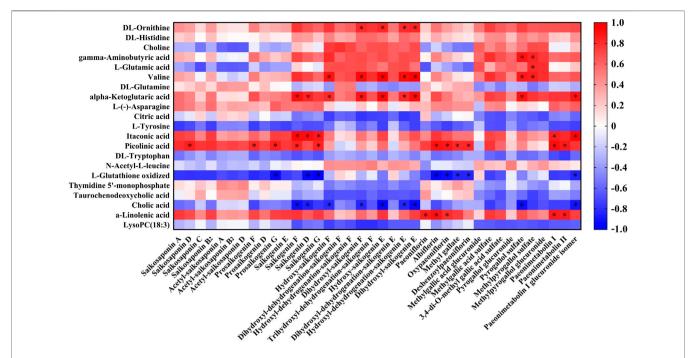
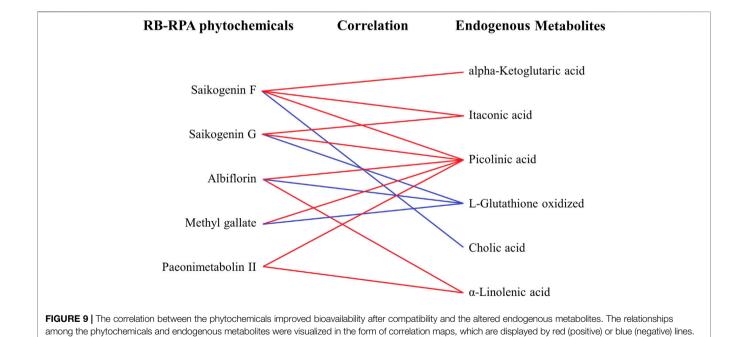


FIGURE 8 | Correlation analysis between the 38 RB-RPA herb pair phytochemicals and the altered 21 endogenous metabolites according to Pearson correlation coefficient. Red color indicated that $|\mathbf{r}|$ was a positive value and blue indicated that $|\mathbf{r}|$ was a negative value. The darker the color, the larger the $|\mathbf{r}|$ value. * represents p < 0.05 and $|\mathbf{r}| > 0.8$.



neurotoxic product quinolinic acid, thereby promoting the occurrence of depressive behavior (Won and Kim., 2016). It was worth noting that as a neuroprotective product, picolinic acid has also been shown to antagonize the adverse effects of quinolinic acid on the nervous system to prevent depression and anxiety symptoms (Grant et al., 2009). These results indicated that these five phytochemicals can inhibit the neurotoxic effects of quinolinic

acid and maintain the balance of the kynurenine metabolic pathway by acting with picolinic acid, thereby avoiding the occurrence of depressive behavior. Besides, several studies have shown that RB, RPA, and their main active ingredients (such as saikosaponins, albiflorin, methyl gallate, etc.) have significant neuroprotective and antidepressant activity (Wang et al., 2016; Li et al., 2017; Li et al., 2018). Therefore, we speculated that the

combination of RB and RPA by increasing the bioavailability of these five phytochemicals, the impact on picolinic acid was strengthened to enhance each other's neuroprotective.

Itaconic Acid

Itaconic acid is a crucial anti-inflammatory endogenous metabolite, which was produced by the decarboxylation of cisaconitate, a tricarboxylic acid cycle intermediate (Michelucci et al., 2013), previous studies have found that itaconate exerts anti-inflammatory effects by inhibiting succinate dehydrogenase (Bordon, 2018). Additionally, recent studies have confirmed that itaconic acid was required for the activation of the antiinflammatory transcription factor Nrf2 by lipopolysaccharide in macrophages, enabling Nrf2 to increase the expression of downstream genes with anti-oxidant and anti-inflammatory capacities (Mills et al., 2018). Further, RB has also been proven to exert anti-inflammatory effects by regulating the Nrf2 signaling pathway (Jia et al., 2019). Our study suggests that the two phytochemicals with improved bioavailability after RB and RPA combination (saikogenin F, saikogenin G) were significantly positively correlated with itaconic acid. The saikogenin F, saikogenin G were deglycosylated metabolites of saikosaponin A and saikosaponin D transformed by intestinal bacteria in the gastrointestinal tract (Shimizu et al., 1985). In addition, related studies speculated that saikosaponins, the main component of RB, was transformed into saikogenins by human intestinal flora, and then exerts pharmacological activity (Liu et al., 2019). These research results indicated that compared to saikosaponin A and saikosaponin D, the pharmacological activity of saikogenin F and saikogenin G in the body may be more significant. And the saikogenin F and saikogenin G maybe activate the Nrf2 signaling pathway by acting on itaconic acid, thereby exerting an anti-inflammatory effect. Meanwhile, saikogenins have also been reported to have anti-inflammatory pharmacological activity (Cheng and Tsai, 1986; Toriniwa et al., 2006), which is in accordance with our research, we speculated that the combination of RB and RRA can enhance the antiinflammatory effect of saikogenin F and saikogenin G.

α-linolenic Acid

The α-linolenic acid is a polyunsaturated omega-3 fatty acid whose metabolism in the body has been well characterized. When α-linolenic acid was ingested, the body converts it to long-chain polyunsaturated fatty acids: eicosapentaenoic acid and docosahexaenoic acid, both of which were considered to exert strong actions on brain functions (Connor, 1999). BDNF is a neurotrophin, it's known for its effects on promoting neurogenesis and neuronal survival, which is significantly associated with depression (Oh et al., 2019). Studies have found that oral consumption of α-linolenic acid increases serum BDNF levels in healthy adults, which may be due to the neuroprotective impact of eicosapentaenoic acid and docosahexaenoic acid on the nervous system (Hadjighassem et al., 2015). Besides, chronic dietary α-linolenic acid deficiency alters dopaminergic and serotoninergic neurotransmission (Delion et al., 1994), which finally accelerates the development of depression. The albiflorin and

paeonimetabolin II were the prototype components and metabolites in RPA, respectively. Our study suggests that the two phytochemicals with improved bioavailability after RB and RPA combination (albiflorin, paeonimetabolin II) were significantly positively correlated with α -linolenic acid. It has been reported that albiflorin, the main active component of RPA, can be used as inhibitors of D-amino acid oxidase in the brain, improved brain function and exerted antidepressant activity (Zhao et al., 2018). In addition, this experiment also found that the combination of RB and RPA can enhance the regulation of α -linolenic acid to enhance the antidepressant activity of RPA. However, it was not clear how RPA and albiflorin can improve brain function and exert antidepressant activity by regulating α -linolenic acid.

CONCLUSION

In conclusion, RB and RPA compatibility could significantly improve the bioavailability of five components in RB, and improve the bioavailability of six components in RPA, which could be summarized into two aspects: improvement in the plasma concentration ($C_{\rm max}$) and prolongation in system circulation ($t_{1/2}$). Furthermore, "plant metabolome" and "body metabolome" correlation analysis results indicated that compatibility of RB and RPA can enhance each other's neuroprotective and anti-inflammatory activities, which provided a research basis for further research on the synergistic pharmacological mechanism of the compatibility of RB and RPA.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding author.

ETHICS STATEMENT

The animal study was reviewed and approved by the Experimental Animal Ethical Committee of Modern Research Center for Traditional Chinese Medicine, Shanxi University.

AUTHOR CONTRIBUTIONS

YZ, XQ, and GD conceived and designed the experiments; CC and QY performed the experiments; CC drafted the manuscript; JT, XG, and XQ reviewed the paper.

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SUPPLEMENTARY MATERIAL

The **Supplementary Material** for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021. 630970/full#supplementary-material.

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Mahuang Decoction Antagonizes Acute Liver Failure via Modulating Tricarboxylic Acid Cycle and Amino Acids Metabolism

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Acute liver failure (ALF) is a serious clinical disorder with high fatality rates. Mahuang decoction (MHD), a well-known traditional Chinese medicine, has multiple pharmacological effects, such as anti-inflammation, anti-allergy, anti-asthma, and antihyperglycemia. In this study, we investigated the protective effect of MHD against ALF. In the lipopolysaccharide and D-galactosamine (LPS/D-GalN)-induced ALF mouse model, the elevated activities of the serum alanine and aspartate transaminases as well as the liver pathological damage were markedly alleviated by MHD. Subsequently, a metabolomics study based on the ultrahigh performance liquid chromatograph coupled with Q Exactive Orbitrap mass spectrometry was carried to clarify the therapeutic mechanisms of MHD against ALF. A total of 36 metabolites contributing to LPS/D-GalN-induced ALF were identified in the serum samples, among which the abnormalities of 27 metabolites were ameliorated by MHD. The analysis of metabolic pathways revealed that the therapeutic effects of MHD are likely due to the modulation of the metabolic disorders of tricarboxylic acid (TCA) cycle, retinol metabolism, tryptophan metabolism, arginine and proline metabolism, nicotinate and nicotinamide metabolism, phenylalanine metabolism, phenylalanine, tyrosine and tryptophan synthesis, as well as cysteine and methionine metabolism. This study demonstrated for the first time that MHD exerted an obvious protective effect against ALF mainly through the regulation of TCA cycle and amino acid metabolism, highlighting the importance of metabolomics to investigate the drug-targeted metabolic pathways.

Keywords: mahuang decoction, acute liver failure, metabolomics, UPLC-Q-exactive-MS, tricarboxylic acid cycle, amino acids metabolism

INTRODUCTION

Acute liver failure (ALF) is a serious clinical disorder that arises from the development of hepatocellular dysfunction, which is predominantly caused by the viral infections (hepatitis A, B and E) in developing world and drug-induced liver injury in developed countries (Bernal and Wendon, 2013; Jiang et al., 2016). To date fatality rates associated with ALF is still as high as 60–80% depending on the disease etiology and patient's access to care (Patterson et al., 2020). Although the liver transplantation is the best choice for the treatment of ALF, it is clinically limited by many factors, such as lack of available liver organs and immune rejection (Nie et al., 2020). Therefore, it is imperative to seek novel effective medicines for ALF disease.

Mahuang decoction (MHD), a famous prescription in *Treatise* on Febrile Disease (Shang Han Lun in Chinese), consists of Ephedrae Herba (Ephedra), Cinnamomi Ramulus (Cassia twig), Armeniacae Semen Amarum (Bitter apricot kernel) and Glycyrrhizae Radix (Prepared licorice), and has been extensively used in treating asthma, cough and cold for thousands of years (He et al., 2018; Huang et al., 2020). Modern research demonstrated that MHD has multiple pharmacological effects, such as anti-inflammation, anti-allergy, anti-asthma, and antihyperglycemia (Zheng et al., 2015). It is reported that Ephedra sinica Stapf, as well as its two main components pseudoephedrine and ephedrine could prevent lethal liver injury by suppressing hepatocyte apoptosis (Yamada et al., 2008; Wu et al., 2014). As Ephedra is the monarch medicine in MHD and is considered to play a leading role in treating the main syndrome of diseases (He et al., 2018), we hypothesized that MHD is an effective therapeutic strategy for ameliorating ALF.

Evaluating the mechanism of pharmacological action of traditional Chinese medicine (TCM) is difficult because of the unclear active components and their possible synergistic actions (Yang et al., 2015). Metabolomics can comprehensively profile the metabolites in the entire organism that alter in responses to the pathophysiological or drug stimuli, identify their related metabolic pathways, and systematically clarify the mechanism of drug actions (Newgard, 2017; Fu et al., 2019). Thus metabolomics may be a powerful approach to unveil the underlying mechanism of MHD. Recently, ultrahigh performance liquid chromatography (UPLC) coupled with a high resolution mass spectrometer (MS) such as Q-Exactive Orbitrap MS are drawing great attention in metabolomics because of the superior peak resolution, selectivity, sensitivity, reproducibility and analysis speed (Fu et al., 2019; Zhong et al., 2019).

In this study, lipopolysaccharide and D-galactosamine (LPS/D-GalN)-induced ALF mice were used to explore the therapeutic benefits of MHD. The underlying mechanism was clarified by the untargeted metabolomics based on UPLC-Q Exactive Orbitrap MS. Our research uncovered for the first time that MHD could ameliorate ALF mainly through the regulation of TCA cycle and amino acids metabolism, providing new understanding of pathological changes and alternative therapeutic strategies for ALF.

MATERIALS AND METHODS

Chemicals and Reagents

Herbs of Ephedra (Ephedra sinica Stapf), Cassia twig (Cinnamomum cassia Presl), Bitter apricot kernel (Prunus armeniaca L.) and Prepared licorice (Glycyrrhiza uralensis Fisch.) were provided by Nanjing Liuhe District Hospital of Traditional Chinese Medicine (Nanjing, China) and were identified by Associate Prof. Junying Zhang from the School of Traditional Chinese Pharmacy of China Pharmaceutical University. Lipopolysaccharide (LPS, from Escherichia coli, O55:B5), D-galactosamine (D-GalN), serotype chlorophenylalanine, amygdalin and trans-cinnamaldehyde were purchased from Aladdin (Shanghai, China). Citric acid, cis-aconitic acid, phenylalanine, tyrosine, tryptophan, valine, arginine, proline, glutamine, pyroglutamic acid, methionine, phenylpyruvic acid, lysine and carnitine were purchased from Shanghai Jingchun Reagent Co., LTD. Lysophosphatidylcholine (LysoPC, 16:0), LysoPC (18:0), and LysoPC (18:2) were obtained from Sigma-Aldrich (St. Louis, MO). Ephedrine hydrochloride, pseudoephedrine hydrochloride and methylephedrine hydrochloride were obtained from National Institutes for Food and Drug Control (Beijing, China). Cinnamic acid was purchased from Nanjing Spring and Autumn Biological Engineering Co., Ltd (Nanjing, China). Glycyrrhizic acid was purchased from Bide Pharmatech Ltd (Shanghai, China). Methanol, acetonitrile, and other reagents were LC/MS grade and obtained from the commercial sources. Water was purified with a Millipore Milli Q-Plus system (Millipore, MA, United States).

Preparation of MHD

The mixture of Ephedra 3 g, Cassia twig 2 g, Bitter apricot kernel 2 g, and Prepared licorice 1 g was immersed in water for 30 min and extracted twice with 120 ml boiling water for 2 h each time. The extract was filtered and the two filtrates were combined and subsequently concentrated to 40 ml to prepare MHD. HPLC analysis of MHD was performed with Shimadzu LC-20AT system (Shimadzu, Kyoto, Japan) on a Welch Ultimate XB-Phenyl column (4.6 \times 250 mm, 5 μ m). The column temperature and flow rate was set at 30°C and 1.0 ml/min, respectively. The mobile phase consisted of 0.05% formic acid-0.05% triethylamine aqueous solution (A) and acetonitrile (B) with the gradient elution program as follows: 0-15 min, 8-10% B; 15–20 min, 10% B; 20–50 min, 10–27% B; 50–55 min, 27–38% B; 55-60 min, 38% B; 60-65 min, 38-8% B; 65-75 min, 8% B. The detection wavelengths were 210, 252, 278 and 291 nm (He et al., 2014). The injection volume was $10 \mu l$. The chromatogram of MHD was presented in Supplementary Figure S1. Ephedrine, pseudoephedrine, methylephedrine, amygdalin, cinnamic acid, cinnamaldehyde and glycyrrhizic acid were found in MHD and identified with each standard sample.

Animals and Treatment

Male ICR mice (25–28 g) were purchased from Comparative Medicine Center of Yangzhou University (Yangzhou, China). All animals were housed in a controlled environment with a 12 h

light/dark cycle with ad libitum access to food and water. The study was conducted following the protocols approved by the Animal Ethics Committee of China Pharmaceutical University. All animals were randomly divided into three groups including the control group (n = 8), model group (n = 15) and MHD group (n = 8). Mice in the model group were given LPS $(10 \mu g/kg)$ and D-GalN (700 mg/kg) intraperitoneally to establish an acute liver failure model (Xia et al., 2014). The MHD group was orally administered with MHD (100 mg/kg, calculated as Ephedra) at 12 h and 30 min before exposed to LPS/D-GalN. The control group was treated with equal amounts of saline. Four mice of the model group and one mouse of the MHD group were excluded because of death. At 8 h after treatment of LPS/D-GalN, blood samples were collected from the retro-orbital plexus, clot at room temperature for 1 h, and then centrifuged at 3000 g for 10 min (4 C). The serum was prepared and stored at −80 C immediately until analysis.

Biochemical Assay

The alanine aminotransferase (ALT) and the aspartate aminotransferase (AST) are important indicators of the liver function (Farooq et al., 2019). ALT and AST in serum were determined using the assay kits purchased from Jiancheng Bioengineering Institute (Nanjing, China) according to the instructions attached to the kits.

Histopathology

After the mice were sacrificed, the livers were collected and fixed in 4% paraformaldehyde. Then the samples were sent to Pathology and PDX Efficacy Evaluation Center of China Pharmaceutical University for haematoxylin and eosin (H&E) staining.

Pretreatment of Serum Sample

Prior to analysis, serum samples were thawed on ice and mixed for 5 s at room temperature. An aliquot of 40 μl serum were added to 160 μl pre-cold methanol containing L-2-chlorophenylalanine (2.5 $\mu g/ml)$ as the internal standard, followed by vortex-mixing for 3 min and then was placed on ice for 20 min. After the mixture was centrifuged at 14000 g for 15 min at 4°C, the supernatant was diluted with 0.1% formic acid at the ratio of 1:1 (v/v) followed by UPLC-Q-Exactive-MS analysis. To verify the repeatability of the LC-MS system, Quality control (QC) samples were prepared by mixing equal aliquots of each sample and were randomly distributed in the real sample sequence (Sangster et al., 2006). In order to avoid the possible signal drift of the mass spectrometer over time, the samples were injected into UPLC-Q-Exactive-MS in a random order.

UPLC-Q Exactive-MS Analysis

The LC-MS analysis was performed with Q-Exactive Orbitrap coupled to a Ultimate $^{\text{TM}}$ 3000 UPLC system (Thermo Fisher Scientific, United States). Analytes were separated on ACQUITY UPLC HSS T3 C18 column (1.8 μm , 2.1 \times 100 mm; Waters, Ireland) at 40 °C. The mobile phase consisted of 0.1% formic acid solution (A) and acetonitrile containing 0.1% formic acid (B). The gradient program was as following: 5% B at

0–2.5 min, 5–95% B at 2.5–18 min, 95% B at 18–21.5 min, 95–5% B at 21.5–22 min, and 5% B at 22–27 min. The flow rate was 0.4 ml/min. The injection volume was 5 μ l. Q Exactive-MS was operated with heated electrospray ionization (HESI)-II. Samples were analyzed under positive mode with full-scan and dd MS². The resolution was 70000; mass-to-charge range was from 60 to 900 m/z; sheath gas, aux gas and sweep gas flow rate were set at 40, 10 and 1, respectively; capillary temperature and aux gas heater temperature were set at 320 C and 350 C, respectively; spray voltage was 3.5 kV; S-lens RF level was 50; maximum IT was 200 ms and AGC target was 3e6 at full MS. For dd MS², the resolution was 17500; maximum IT was 50 ms; AGC target was 1e5; normalized collision energy (NCE) was set at 10, 25, and 40; other parameters were same as full-scan mode.

Data Pre-processing

All the LC-MS raw data were converted to CDF format by Xcalibur 4.2. Data pre-processing, such as peak discrimination, alignment, and matching, were carried out by XCMS package-based R software (Smith et al., 2006). The CentWave algorithm was adopted and algorithm parameters were default settings except for the following: snthresh = 6, peakwidth = c(5, 25), ppm = 30, bw = 5, mzwid = 0.025. The output data matrix contained missing values, which could have a downstream effect on the analysis of the data (Mais et al., 2018). To solve such problem, the variables present in more than 80% of each group were retained (Bijlsma et al., 2006) and the remaining missing values were replaced by a small value that is half of the minimum value in the original data (Mais et al., 2018). After the above steps, the data matrix was normalized by the internal standard.

Multivariate Analysis

The pre-processed data was imported into SIMCA-P 14.1 (Umetrics, Sweden), followed by multivariate data analysis, such as principle component analysis (PCA), partial least squares discrimination analysis (PLS-DA) and orthogonal partial least squares discrimination analysis (OPLS-DA). The outliers and the general clustering trends were analyzed by PCA. The differences among the control group, model group, and MHD group were observed by PLS-DA. OPLS-DA was utilized to examine the metabolic differences between two groups. Besides, all PLS-DA and OPLS-DA models were subjected to the permutation test.

Metabolites Identification and Metabolic Pathway Analysis

Metabolite identification was performed according to our previous report (Tan et al., 2018). Briefly, the quasi-molecular ions were judged according to the positive scanning in MS. The molecular information was obtained from a freely accessible database of HMDB (Wishart et al., 2018), METLIN (Guijas et al., 2018) and KEGG (Kanehisa et al., 2014) within a mass accuracy of 10 ppm. To narrow the scope of target metabolites, the quasi-molecular ions were then subjected to MS/MS analysis. The affected metabolic pathways were analyzed and visualized via MetaboAnalyst (https://www.metaboanalyst.ca/) with identified

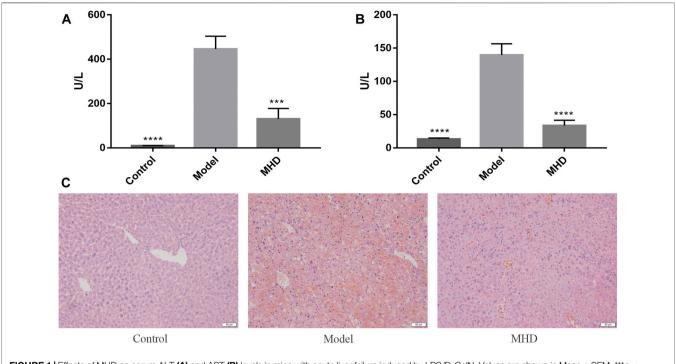


FIGURE 1 | Effects of MHD on serum ALT **(A)** and AST **(B)** levels in mice with acute liver failure induced by LPS/D-GalN. Values are shown in Mean \pm SEM. ***p < 0.001, ****p < 0.0001 vs model group. **(C)** Images of H&E stained liver cells (original magnification ×200).

differential metabolites (Chong et al., 2018, 2019). Finally, 17 available standards were adopted to confirm the identified metabolites.

Statistical Analysis

The normality and homogeneity of variance of all samples were tested by IBM SPSS Statistics 26. One-way ANOVA or Kruskal-Wallis was used to test the statistical differences of the samples according to whether they obey normal distribution and homogeneity of variance. The resultant p values were corrected by Bonferroni correction to ∞/n , where $\infty=0.05$ and n is the number of comparisons in statistical analysis (Berben et al., 2012; Araújo et al., 2018). Adjusted p < 0.05 was considered statistically significant.

RESULTS

Biochemical Assay and Pathological Changes

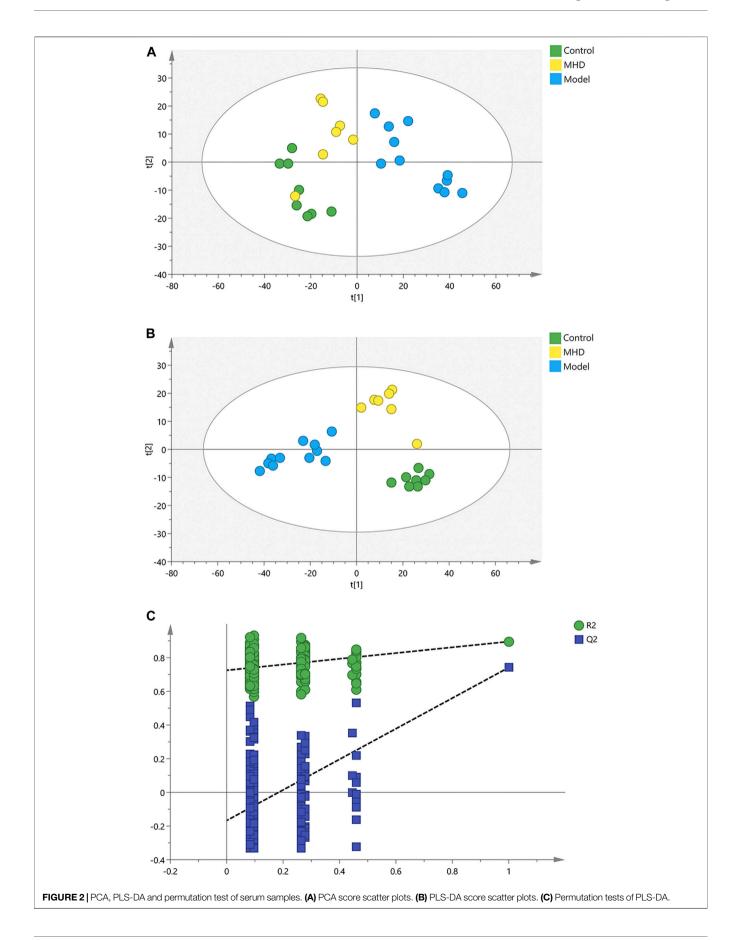
The serum ALT and AST levels of each group are shown in Figures 1A,B, where ALT reflects the degree of liver cell damage and AST reflects the degree of hepatocyte necrosis. The levels of ALT together with AST in the model group were significantly higher than those in the control group, and were similar to the levels reported previously (Wu et al., 2014). Meanwhile, the notably decreased levels of ALT and AST were observed in MHD groups. Consistent with this result, large areas of hepatocytes necrosis were visible in model group by H&E staining, which was remarkably improved by the treatment of

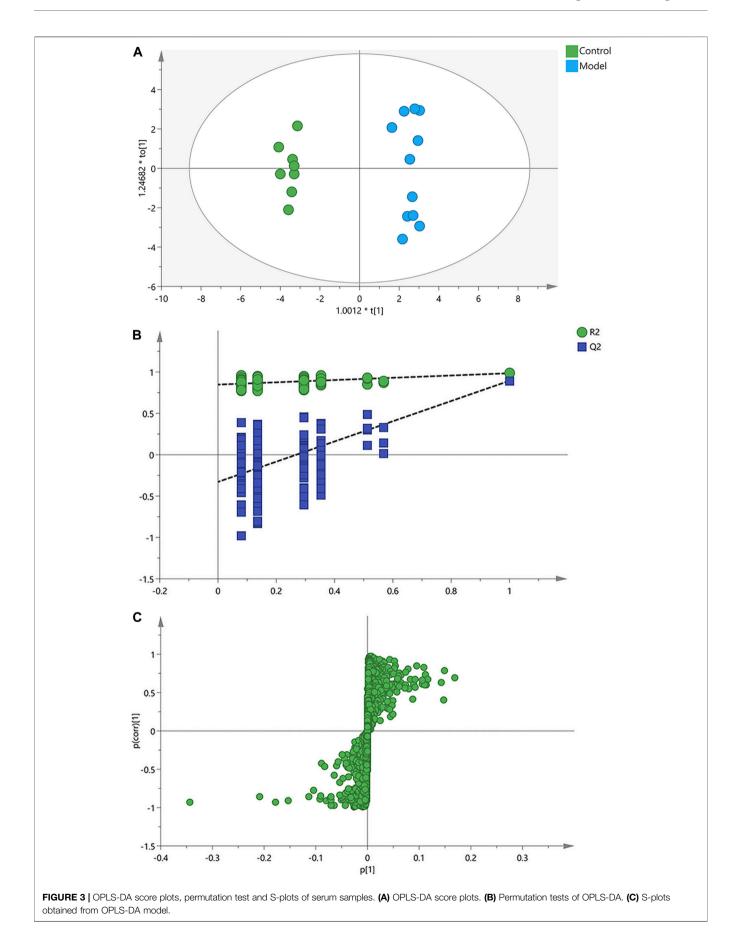
MHD (**Figure 1C**), demonstrating that MHD has a hepatoprotective effect.

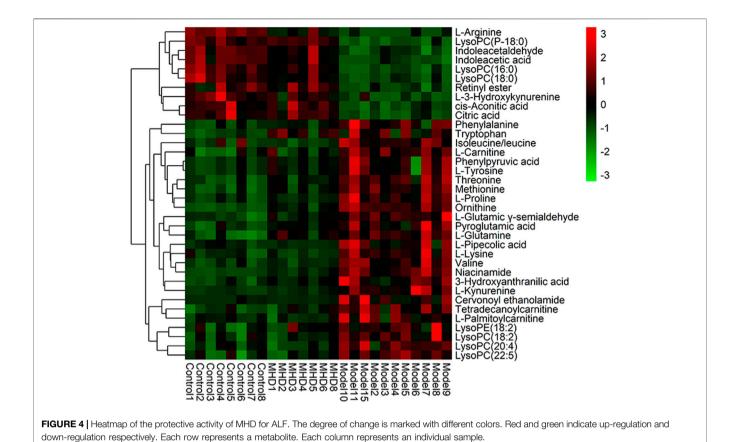
Metabolic Profiling and Multivariate Analysis

The typical total ion current (TIC) chromatogram of UPLC-Q-Exactive MS is shown in **Supplementary Figure S2**. The relative standard deviation (RSD) for the peak intensity of the internal standard was less than 3.0% in QC samples. After peak alignment, filtering and normalization, the RSD of intensity of all peaks in QC samples was calculated. The RSD of 30% covered 88.0% features, indicating that the analytical method had good repeatability. With the RSD less than 30% in QC samples, 7770 molecular features were obtained for further multivariate data analysis.

To analyze the protective effect of MHD, PCA and PLS-DA models were established. An unsupervised PCA model was carried out to observe the tendency of MHD group separated from model group and control group. As shown in **Figure 2A**, a separated trend of the inter-group was observed on the scores plot. The main parameter of PCA, namely R²X value, was greater than 0.4, indicating that the models were well-fitted. As one of the supervised analysis, PLS-DA could ignore intra-group errors as well as random errors, and focus on the analysis of differences between groups. PLS-DA scores plot showed good discrimination power among control, model and MHD groups (**Figure 2B**). The predictive capability of the model was assessed by the internal validation (R²Y = 0.937, Q² = 0.824), suggesting the goodness of fit and predictive capability of the model. A random permutation







test (200 times) was further used to validate the reliability of the PLS-DA model. As R²cum and Q²cum values were lower than the original values of the validation plot (**Figure 2C**), the results were non-overfitting and reliable.

Identification of Differential Metabolites

Afterwards, OPLS-DA was applied to search the differential metabolites between the control and model groups, and a discrimination between groups was (Figure 3A). The predictive capability of the model was assessed by the internal validation ($R^2Y = 0.985$, $Q^2 = 0.893$), suggesting a satisfactory fit with high predictive power. In the random permutation test (200 times), R²cum and Q²cum values in permuted classes were lower than those in original classes, revealing that the OPLS-DA models were not over-fitting (Figure 3B). The S-plot generated from OPLS-DA model was used to find potential biomarkers, since the variables distributed at both ends of the S-plot markedly contribute to the clustering and discrimination (Figure 3C).

Differential metabolites between the model and control groups were identified by using a threshold of variable importance in the projection (VIP) values (VIP>1.0) produced from the OPLS-DA model (Fan et al., 2016). After restricting with univariate statistical analysis (p < 0.05), 36 significantly changed metabolites were designated as biomarkers of ALF (**Table 1**). The MS/MS spectra of these biomarkers together with their proposed fragmentation

pathways are presented in **Supplementary Figure S3**. The relative levels of these biomarkers in each mouse were visualized in **Figure 4**. Compared to the model group, the relative intensity of most biomarkers were reverted by MHD, among which 27 metabolites were significantly regulated (**Figure 5**).

Metabolic Pathways Analysis

To figure out the potential LPS/D-GalN-induced and MHDmodulated metabolic pathways, 36 significantly altered metabolites in ALF model group (vs. control group) and 27 significantly reverted metabolites in MHD group (vs. model group) were imported into MetaboAnalyst 4.0. By using a threshold of the impact-value (≥ 0.10), 11 metabolic pathways were identified to be the potential targets of ALF, including phenylalanine, tvrosine and tryptophan biosynthesis, phenylalanine metabolism, tryptophan metabolism, arginine and proline metabolism, nicotinate and nicotinamide metabolism, retinol metabolism, arginine biosynthesis, tricarboxylic acid (TCA) cycle (citric acid cycle), tyrosine metabolism, alanine, aspartate and glutamate metabolism, as well as cysteine and methionine metabolism (Figure 6A and Supplementary Table S1). MHD-regulated metabolic pathways were identified to be TCA cycle, retinol metabolism, tryptophan metabolism, arginine and proline metabolism, nicotinate and metabolism, nicotinamide phenylalanine phenylalanine, tyrosine and tryptophan synthesis, as well as

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Table 1 | Changes of metabolites in mice with acute liver failure.

Metabolites	Experimental [M + H] ⁺ (m/z)	Retention times (min)	Adduction	Theoretical [M + H] ⁺ (m/z)	MS fragments	Delta (ppm)	Trend	Fold Change	
								CON/M	MHD/M
L-Proline ^a	116.0707	0.673	M + H	116.0706	70.07	1	1	0.6**	0.6*
Valine ^a	118.0863	0.684	M + H	118.0863	72.08, 55.06	0	\downarrow	0.6**	0.7**
Threonine ^b	120.0655	0.653	M + H	120.0655	102.06, 74.06, 60.99	0	\downarrow	0.6****	0.8**
Niacinamide ^b	123.0553	1.000	M + H	123.0553	106.03, 79.02	0	\downarrow	0.3****	0.5***
Pyroglutamic acid ^a	130.0498	0.652	M + H	130.0499	84.04, 70.07, 56.06	1	\downarrow	0.7**	0.8
L-Pipecolic acid ^b	130.0862	0.633	M + H	130.0863	112.04, 84.04	1	\downarrow	0.4*	0.4*
L-Glutamic ?-semialdehyde ^b	132.0656	0.653	M + H	132.0655	114.07, 86.06	1	\downarrow	0.6***	0.8*
Isoleucine/leucine ^b	132.1018	0.765	M + H	132.1019	86.06, 56.97	1	\downarrow	0.8**	0.7*
Ornithine ^b	133.0970	0.553	M + H	133.0972	116.07, 70.07	1	\downarrow	0.2****	0.5*
L-Glutamine ^a	147.0762	0.648	M + H	147.0764	130.05, 102.06, 84.04	1	\downarrow	0.6**	0.9
L-Lysine ^a	147.1126	0.558	M + H	147.1128	130.09, 84.08, 56.05	1	\downarrow	0.6**	0.6**
Methionine ^a	150.0581	0.710	M + H	150.0583	133.03, 104.05	1	1	0.5***	0.7*
3-Hydroxyanthranilic acid ^b	154.0496	1.262	M + H	154.0499	136.04, 109.96, 67.05	2	Ţ	0.5**	0.7
Indoleacetaldehyde ^b	160.0755	1.576	M + H	160.0757	141.92, 131.97	1	1	2.7***	2.0*
L-Carnitine ^a	162.1122	0.647	M + H	162.1125	103.04, 85.03, 60.08	2	Ţ	0.7***	0.8**
Phenylpyruvic acid ^a	165.0544	1.070	M + H	165.0546	147.04, 119.05	1	Ţ	0.6**	0.7
Phenylalanine ^a	166.0860	2.057	M + H	166.0863	149.06, 131.05, 120.08	2	Ţ	0.7**	0.8*
cis-Aconitic acida	175.0234	0.996	M + H	175.0237	157.11, 61.53	2	1	1.7**	1.7**
L-Arginine ^a	175.1187	0.595	M + H	175.1190	158.00, 70.07, 60.06	2	1	10.7****	3.7
Indoleacetic acida	176.0704	1.577	M + H	176.0706	158.00, 106.99	1	1	2.6***	2.0*
L-Tyrosine ^a	182.0809	1.070	M + H	182.0812	165.05, 136.08	2	į	0.6**	0.7
Citric acid ^a	193.0344	0.996	M + H	193.0343	175.03, 133.01, 61.04	1	1	1.7****	1.6****
Tryptophan ^a	205.0968	4.374	M + H	205.0972	188.07, 170.06	2	į	0.8*	1.0
L-Kynurenine ^b	209.0917	1.972	M + H	209.0921	192.07, 120.04, 94.07	2	Ĭ	0.2***	0.4*
L-3-Hydroxykynurenine ^b	225.0865	1.049	M + H	225.0870	207.02, 179.02, 161.01	2	1	5.1**	3.1**
Retinyl ester ^b	303.2311	15.346	M + H	303.2319	285.22, 267.21, 256.88	3	1	2.8***	2.7***
Tetradecanoylcarnitine ^b	372.3099	13.325	M + H	372.3108	313.24, 85.03, 60.08	2	i	0.5**	0.7*
Cervonoyl ethanolamide ^b	373.2728	11.073	M + H	373.2737	355.26, 241.19, 161.13, 81.07	2	Ĭ	0.1**	0.1**
L-Palmitoylcarnitine ^b	400.3412	14.522	M + H	400.3421	341.26, 144.10, 85.03	2	Ĭ.	0.5*	0.6
LysoPE(18:2) ^b	478.2918	14.002	M + H	478.2928	460.28, 337.27	2	Ĭ	0.7*	0.8
LysoPC(16:0) ^a	496.3387	14.260	M + H	496.3398	258.11, 184.07	2	1	2.1****	1.7*
LysoPC(P-18:0) ^b	508.3751	15.304	M + H	508.3762	184.07, 125.00, 104.11, 86.10	2	1	2.5****	2.3****
LysoPC(18:2) ^a	520.3387	14.063	M + H	520.3398	184.07, 104.11	2	i	0.8**	0.8**
LysoPC(18:0) ^a	524.3699	15.761	M + H	524.3711	506.36, 184.07, 86.10	2	1	2.2**	1.6*
LysoPC(20:4) ^b	544.3386	14.115	M + H	544.3398	184.07, 104.11, 86.10, 60.08	2	i	0.7**	0.7**
LysoPC(22:5) ^b	570.3540	14.459	M + H	570.3554	387.29, 184.07,104.11	2	i I	0.7*	0.8*

 $Delta = (abs \ (experimental \ m/z-theoretical \ m/z)/theoretical \ m/z) \times 1000000. \ Trend: \ change \ trend \ of \ contents \ of \ metabolites \ in \ each \ group \ compared \ to \ the \ model \ group. \ Fold \ change: \ relative \ amount \ of \ each \ group \ compared \ to \ the \ model \ group. \ Fold \ change: \ relative \ amount \ of \ each \ group \ compared \ to \ the \ model \ group.$

^aMetabolites validated with standard sample.

^bMetabolites putatively annotated. Abbreviations: LysoPE, lysophosphatidyl ethanolamine; LysoPC, Lysophosphatidylcholine.

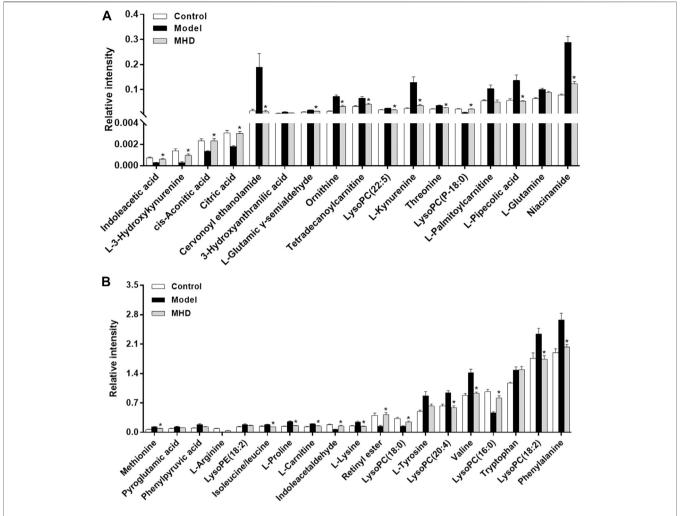


FIGURE 5 | Changes in the relative intensity of target metabolites. Statistical significance was performed using univariate statistical analysis. 27 metabolites were significantly reversed by MHD. Values are shown in Mean ± SEM. *p < 0.05 vs. model group.

cysteine and methionine metabolism (**Figure 6B** and **Supplementary Table S2**). A schematic metabolic network of LPS/D-GalN-induced ALF and MHD modulation were analyzed with the KEGG database (Kanehisa et al., 2014) by relating the major metabolic pathways (**Figure 7**).

DISCUSSION

Mahuang decoction (MHD) has been widely utilized to treat asthma, cough, and exogenous wind-cold (He et al., 2018; Huang et al., 2020). The monarch medicine of MHD, *Ephedra sinica* Stapf, and its two main components pseudoephedrine and ephedrine have been reported to prevent lethal liver injury (Yamada et al., 2008; Wu et al., 2014). Therefore, we hypothesized that MHD has protective effect against ALF.

To verify our hypothesis, the serum transaminase test and histopathology together with a UPLC-Q-Exactive-MS-based metabolomics study were performed to explore the potential efficacy and mechanisms of MHD against ALF. The serum ALT and AST levels in LPS/D-GalN-induced ALF mice were markedly reduced with the treatment of MHD, providing strong evidences for the protective effect of MHD on ALF. Furthermore, a total of 36 metabolites were identified to be ALF relevant biomarkers, among which 27 metabolites were significantly reverted by the treatment of MHD. By constructing the relevant metabolic pathways of these reverted biomarkers, eight metabolic pathways were filtered out to be the most important pathways for the anti-ALF efficacy of MHD, including TCA cycle, retinol metabolism, tryptophan metabolism, arginine and proline metabolism, nicotinate and nicotinamide metabolism, phenylalanine metabolism, phenylalanine, tyrosine and tryptophan synthesis, as well as cysteine and methionine metabolism.

TCA Cycle and Energy Metabolism

The TCA cycle is essential for the aerobic metabolism, which could facilitate the adequate throughput of the substrates derived

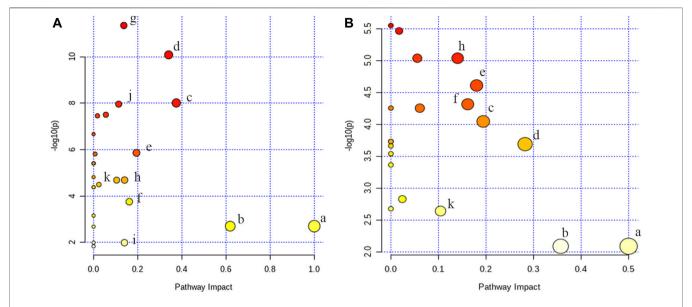


FIGURE 6 | Analysis of metabolic pathways (A) control vs model (B) MHD vs model. a: phenylalanine, tyrosine and tryptophan biosynthesis, b: phenylalanine metabolism, c: tryptophan metabolism, d: arginine and proline metabolism, e: nicotinate and nicotinamide metabolism, f: retinol metabolism, g: arginine biosynthesis, h: TCA cycle, i: tyrosine metabolism, j: alanine, aspartate and glutamate metabolism k: cysteine and methionine metabolism.

from carbohydrates, fatty acids and certain amino acids. The two pivotal intermediates, namely citric acid and cis-aconitic acid, were altered following LPS/D-GalN inducement, suggesting that ALF could perturb TCA cycle. This result is supported by the previous studies (Carvalho et al., 2002; Dabos et al., 2011; Pathania et al., 2020). An unbalanced TCA cycle was indicative of the decreased oxidative metabolism. After treating with MHD, the levels of citric acid and cis-aconitic acid were higher than that in ALF mice, demonstrating that TCA metabolism tended to be normal.

As the principal precursors of β -oxidation substrates and acylcarnitines in serum, the long-chain acylcarnitines (LCAC) mainly come from the liver (Sandor et al., 1990; Jones et al., 2010). The levels of LCAC including tetradecanoylcarnitine and palmitoylcarnitine were significantly increased in ALF group compared to the control group, implying that ALF condition could inhibit the fatty acid oxidation. This finding is supported by the previous studies in which acylcarnitines were elevated under ALF condition (Bi et al., 2013; McGill et al., 2014). The high levels of LCAC in ALF mice may be related to the downregulation of carnitine palmitoyltransferase I (Cpt1) and acyl-CoA thioesterase 1 (Acot1) genes that are involved in the fatty acid β -oxidation pathway (Bi et al., 2013). After the treatment of MHD, the level of tetradecanoylcarnitine was significantly reverted, demonstrating that the modulation of herapeutic fatty acid β -oxidationt is involved in the pharmacological process of MHD.

Branched chain amino acids (BCAAs) are important energy substrates, including valine, leucine, and isoleucine, and they enter the TCA cycle through deamination, decarboxylation, and β -oxidation processes. The serum levels of BCAAs were upregulated in ALF mice, while down-regulated towards normal when treated with MHD. A possible mechanism is that the TCA

cycle in mice is inhibited under the condition of ALF, leading to a reduction of ATP production. Energy compensation may be achieved by consuming BCAAs and accelerating β -oxidation of fatty acids since the level of citric acid and cis-aconitic acid in TCA cycle were elevated but the level of BCAAs and LCAC were reduced after MHD treatment.

Together, these results suggest that the hepatoprotective activities of MHD against ALF are highly likely due to the modulation of the energy metabolism in liver.

Amino Acids Metabolism

The serum levels of aromatic amino acids (AAA) including phenylalanine, tyrosine and tryptophan were elevated in ALF mice. A previous study has implied that the levels of AAA, especially phenylalanine and tryptophan, are good biomarkers of ALF severity, which is probably caused by the inefficient degradation or gluconeogenesis-based conversion of AAA in the damaged liver (Cao et al., 2012). Beside, elevated AAA is closely related with hepatic encephalopathy associated with ALF (Dejong et al., 2007; Wijdicks, 2016). After the treatment of MHD, the serum level of phenylalanine was significantly reverted, suggesting that MHD can promote the recovery of liver function and thus reduce the risk of hepatic encephalopathy.

Consistent with previous reports (Clària et al., 2019; Sekine and Fukuwatari, 2019), the present study observed that tryptophan metabolism is one of the significantly disturbed pathways in ALF mice. This abnormality was regulated by MHD treatment, and similar activity was observed in other TCM such as Yin-Chen-Hao Tang (Liu et al., 2019). Tryptophan and its metabolites play critical roles in many physiological processes, such as inflammation, immune

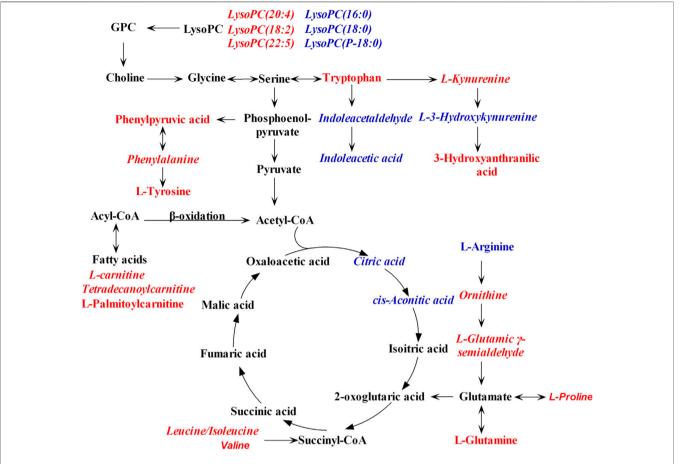


FIGURE 7 | Schematic metabolic network of LPS/D-GalN-induced ALF and MHD modulation based on the KEGG database. Red: the levels of metabolites in model group were up-regulated compared to control group. Blue: the levels of metabolites in model group were down-regulated compared to control group. The italic metabolite names were significantly reversed by MHD treatment. Abbreviations: LysoPC, Lysophosphatidylcholine; GPC, Glycerophosphocholine.

response, and neurotransmission (Cervenka et al., 2017). Free tryptophan is mainly converted to kynurenine with the involvement of microglial indoleamine-2,3-dioxygenase 1, and the process could be stimulated by inflammation (Platten et al., 2019). The substrates of kynurenine pathways increased by kynurenine metabolism will transfer to the central nervous system (CNS) and be degraded locally, which eventually damage the CNS (Müller and Schwarz, 2007). Compared with the control group, the serum level of kynurenine is up-regulated in model group but reverted by MHD, which indicates that MHD may have anti-inflammatory effect.

Moreover, arginine and proline metabolism was disturbed in ALF mice while reverted by MHD. A similar activity was observed in Yin-Chen-Hao Tang (Liu et al., 2019). L-Arginine is an essential amino acid. Catabolic diseases such as cancer and injury will increase the utilization of arginine, leading to arginine consumption. In ALF mice, arginine levels were significantly decreased (>10-fold change, adjusted p < 0.001) and the levels of intermediates of arginine metabolism such as ornithine and L-glutamic- γ -semialdehyde were increased, suggesting that ALF

caused excessive consumption of arginine. With the treatment of MHD, the level of ornithine and L-glutamic- γ -semialdehyde were down-regulated, indicating the disturbance of arginine metabolism was alleviated to a certain extent.

CONCLUSION

In this study, the hepatoprotective activity of MHD against ALF was confirmed by the serum transaminase test and histopathology, and the underlying mechanisms was studied by the UPLC-Q Exactive-MS-based metabolomics. We have identified 36 biomarkers of ALF, among which the abnormalities of 27 metabolites were regulated by the treatment of MHD. Metabolic pathway analysis revealed that the anti-ALF mechanisms of MHD may be mainly attributed to the modulation of metabolic disorders of TCA cycle and amino acids metabolism. To obtain a more complete understanding of MHD, future studies is necessary to find the key factors of the identified metabolic pathways and determine their relationship with the chemical components of MHD.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation, to any qualified researcher.

AUTHOR CONTRIBUTIONS

CW and WL conceived and designed the experiments. QJ, YR, XL, YS and JZ performed the experiment. JL, ZZ and YW assisted the UPLC-Q-Exactive-MS experiments. SW provided the crude herbs. WL and QJ wrote the first draft of the manuscript. CW and LK edited the final manuscript. All authors have read and approved the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.599180/full#supplementary-material.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Anti-Inflammatory and Anti-Arthritic Potential of Standardized Extract of Clerodendrum serratum (L.) Moon

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Aims: Scientific biological evaluation of standardized extracts is becoming one of the central needs for the globalization of customary medication in current times. And to validate the presence of active constituents in crude medicinal extracts, analytical techniques like HPLC and HPTLC are the most suitable authentication systems. In the current study we aimed to standardize and evaluate *Clerodendrum serratum* (L.) Moon (Verbenaceae). For its unique anti-inflammatory and anti-arthritic properties. Evaluation and analysis of the plant, therefore, offers a new platform for the development of the herbal drug and could prove to be a safe and cost effective treatment for arthritis management.

Methods: The aqueous extract of C. serratum, a common plant in the Southeastern Asian region, was used for phytochemical investigation and standardization by HPTLC and HPLC. The standardized HPLC method was further validated by using ICH guidelines. The standardized extract was investigated for anti-inflammatory and anti-arthritic activity. Complete Freund's adjuvant (CFA) model was performed to evaluate the activity. Paw diameter, joint diameter, arthritic score, and body weight was accepted as a parameter for the evaluation of biological activity.

Results: HPTLC method revealed the presence of ursolic acid with an R_f value of 0.38 and the amount quantified was 0.03% w/w. The presence of the bioactive phytochemical was further analyzed and confirmed by HPLC for which the validation was done successfully in accordance with ICH guidelines. The assay content for ursolic acid was found to be 0.059% with relative standard deviation (RSD) <2.5% for specificity and precision with spike recovery between 95–110%. The anti-arthritic activity of aqueous extract exhibited COX-2 and TNF- α inhibition as observed in various parameters like paw edema, arthritic index, and joint diameter. Plant extract showed reclamation of arthritis in regard to body weight, arthritic score, paw edema, and joint diameter. The extract showed significant results for TNF- α and COX-2(ρ < 0.0001). The plant extract also exhibited *in-vitro* anti-inflammatory activity.

Conclusion: The current study established the scientific basis of ethnomedicinal use of the plant for anti-inflammatory purposes and the management of arthritis and can also be used for quality control purposes.

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Tiwari RK, Chanda S, M U, Singh M and Agarwal S (2021) Anti-Inflammatory and Anti-Arthritic Potential of Standardized Extract of Clerodendrum serratum (L.) Moon. Front. Pharmacol. 12:629607. doi: 10.3389/fphar.2021.629607 Keywords: anti-inflammatory, ursolic acid, standardization, HPTLC, arthritic, Clerodendrum serratum

INTRODUCTION

Arthritis and its associated musculoskeletal imbalances is one of the common afflictions, affecting millions of people and greatly restricting their activities of daily living (Baranwal et al., 2012b). It is a common term used by medical practitioners to describe the progressive inflammatory responses to one or more joint structures due to various causes ranging from traumatic, rheumatic, to degenerative concerns resulting in muscular stiffness and restricted physical movements. Further, arthritis commonly affects persons from all age groups, race, sex, and global regions with more than 100 different types, such as juvenile arthritis, rheumatoid arthritis, ankylosing spondylitis, gout, psoriatic arthritis, and osteoarthritis, the last of which is degenerative. Its clinical features in suffering patients may vary from person to person and range from mild pain and swelling to intense forms like complete/partial joint immobility, muscular atrophy, and contractures (Rho et al., 2009). Subsequently, the drug regime includes administration of non-steroidal anti-inflammatory drugs (NSAIDs) to patients as a first line of treatment but its long term usage has led to certain potential adverse reactions, such as gastroduodenal diseases and renal insufficiency (Harirforoosh and Jamil, 2009), that are probably induced by the inhibition of cyclo-oxygenase for reduction in prostaglandin content. Although various types of treatments are available today, like NSAIDs, corticosteroids, and DMARDs, they are mainly used to treat the symptomatic concerns and do not target the pathological origin like membrane stabilizing, protein denaturation, etc. Moreover, treatment by the above available modes can cause serious hepatic damage, gastric bleeding (Craig and Cappelli, 2019), Hospitalization, and death (Rostom et al., 2005).

Therefore, to surpass all these issues and find a more harmless and equally efficacious therapeutic option, researchers are considering plants as a source of medicine. Initially, these plant-based medicinal systems have formed the foundation of folk or ethno medicines, practiced in India and some other parts of the world like China, Africa, and South America. Later a considerable part of this indigenous knowledge was formulated, documented, and eventually passed into organized systems of medicine such as Ayurveda, Unani Siddha, etc. Traditionally plants were used for various therapeutic claims by tribal communities throughout India (Jain and Singh, 2010; Balasankar et al., 2013; Nayak and Dhal, 2013). In our study we have selected the plant *Clerodendrum serratum* (L.) Moon belonging to the family Verbenaceae. This is a deciduous shrub widely distributed in the Western Ghats (Manjunatha, 2004) of India. In Ayurveda, the plant is popularly known as Bharangi (Sanskrit) and customarily called Blue Glory (English). As per the traditional claims, the roots of this plant are a potential source of medicine for ailments such as

allergic disease, body soreness, respiratory illness, infectious disease, dropsy, eye diseases, fever, inflammation, malaria, opthalmia, rheumatism, snakebite, tuberculosis, ulcers, and wounds (Keshavamurthy, 1994). Studies reported various chemical constituents from the plant, like stigmasterol, bis(2-ethylhexyl) phthalate, hispulidin, serratumin A, acteoside, martynoside, serratumoside-A,myricoside, ursolic acid, spinasterol, spinasteryl-β-D-glucopyranoside etc., in various parts of plant including the stem, root, and erial part (Singh et al., 2012; Kumar and Nishteswar, 2013; Padal et al., 2013). The current study was focused on its *in-vitro* anti-inflamatory activity and *in-vivo* arthritis activity by using Complete Freund's adjuvant (CFA) induced arthritis model.

MATERIALS AND METHODS

All the chemicals used in the current study were procured from Sigma Aldrich Co., St. Louis, United States. All other chemicals/solvent adopted were of analytical grade.

Collection and Preparation of Extract

Roots of *C. serratum* L. were collected from Faizabad, Uttar Pradesh, India and taxonomical identification was done at the Department of Agronomy, Aacharya Narendra Dev Agriculture Technical University, Dist. Faizabad, Uttar Pradesh. The prepared brown colored powdered root (100 g) was extracted (decoction) with water (500 ml) at a temperature not exceeding 110°C for 2 h. The extract was strained and lyophilized. The yield of obtained dried extract was 10% w/w.

Standardization of an Extract

Qualitative Estimation by High-Performance Thin Layer Chromatography

The presence of ursolic acid was identified by performing High-performance thin layer chromatography (HPTLC). The solvent system used for the analysis was toluene: ethyl acetate (8:2 v/v) as a binary mobile phase system. For spot detection, anisaldehyde sulfuric acid was used as the spraying reagent. Standard analytical grade of ursolic acid was used as a reference by dissolving in HPLC grade methanol. The obtained concentration was 1,070 μ g/ml, which was further used for preparing the subsequent working standards. Camag Linomat V HPTLC system (Switzerland) equipped with 100 μ l Camag syringe and scanner III was used for the current qualitative estimation. Sample and standard as narrow bands of a width of 3 mm were applied to precoated silica gel aluminum plate 60F-254.

Quantitative Estimation by High-Performance Thin Layer Chromatography

An isocratic HPLC method was developed and validated for the identification of ursolic acid. A prepacked column, C18 $(25~cm\times4.6~mm)~5~\mu m$, with UV detector (210~nm) was used for the current study. The injection volume was $20~\mu l$ and its flow rate was maintained at 0.6~ml/min. Run time for standard and sample were 45~min and the data acquisition was done. For HPLC analytical development studies, methanol and acetonitrile (30:70,~v/v) were selected as the binary mobile phase system. Before using, it was filtered and degassed. Thereafter, the standard solution was prepared by adding 10~mg of ursolic acid in methanol (10~ml) and subjected for sonication. The solution was settled to room temperature and diluted further with the help of diluent up to the mark.

Then the sample solution was prepared by taking 1.5 g of the test sample in iodine flask and adding 25 ml of water followed by 20 min of sonication. Reflux was done for about 30 min in reflux assembly and filtered. The process was repeated twice and the filtrate was evaporated to dryness. The obtained residue was dissolved in methanol and the volume was made up of 10 ml methanol. A further 0.5 ml of this solution was taken into a 10 ml volumetric flask and diluted with methanol. Injection of equal volumes of the standard solution was done and chromatograms were recorded along with measurement of peak area. The percentage of ursolic acid was calculated by using the formula:

$$\%$$
 of Assay = $\frac{At XCsXP}{AsXCu}$

At= Peak area of a test sample, As = Peak area of reference standard, Cs = Concentration of reference standard, Cu = Concentration of test sample, P = Potency of ursolic acid working standard

The developed method was validated according to ICH guidelines (Baranwal et al., 2012a). The parameters adopted for its validation are Linearity, Specificity, Accuracy, Range, Precision, Repeatability, Intermediate precision, Robustness, Limit of Detection, and Limit of Quantification (Manukumar and Umesha, 2015).

Evaluation of Anti-inflammatory Hypotonic Solution-Induced Haemolysis or Membrane-Stabilizing Activity

The evaluation test was performed as per the method reported by Manukumar and Umesha (2015). The extracted sample contains 0.03 ml stock erythrocytes suspension infused with 5 ml hypotonic solution prepared with 154 mM NaCl in 10 mM Sodium Phosphate Buffer at pH 7.4, along with the test sample ranging from 100-500 µg/ml. The blank (without the test samples) and the standard (acetylsalicylic drug) was also treated accordingly. This mixture was incubated at room temperature for 10 min, followed by centrifugation for 10 min at 3,000 rpm. The absorbance of the supernatant was observed spectrophotometrically at 540 nm. The experiment was performed in triplicate. The percentage inhibition of haemolysis was computed by the following formula:

% inhibition of haemolysis = $100 \cdot [(A1 - A2/A1)]$

where: A1 = absorbance of blank; A2 = Absorbance of test and standard sample

Effect of Protein Denaturation

The effect of protein denaturation was performed as per the procedure mentioned below. The concentrations ranging from $100\text{--}500\,\mu\text{g/ml}$ for both test sample and standard acetylsalicylic sample with 1 ml of 1 mM egg albumin solution were incubated at 27°C for 15 min. The mixture was further denatured at 70°C in a water bath for 10 min. The samples were allowed to cool down and observed spectrophotometrically at 660 nm. This experiment was performed in triplicate. Percentage inhibition of denaturation was calculated from the control without sample and standard (Badii and Howell, 2002; Chung et al., 2012). The percentage inhibition of denaturation was done by the below-mentioned formula:

% Inhibition of haemolysis = 100X[(A1 - A2/A1)]

Evaluation of *In-Vivo* Anti-Arthritic Study Complete Freund's Adjuvant Induced Arthritis

For the *in-vivo* anti-arthritic activity, the Complete Freund's Adjuvant (CFA) model was adopted. For this model, Albino Wistar male rats weighing 200 \pm 25 g were considered. The oral route of administration was given to rats placed in different cage groups under a controlled temperature of 22 \pm 2°C conditions with administration of golden feed diet and water to all the animals regularly. The dose adopted was 100 and 200 mg/kg body weight (b.w.). Paw diameter, joint diameter, arthritic score, and body weight were used as parameters for the activity. The histopathological estimation of TNF- α and COX-2 were also performed as confirmative studies. Institutional Animal Ethics Committee (IAEC) approval (Reg No. 1824/PO/ERe/S/15/CPCSEA) as well as Protocol Approval (Reference No. IAEC/PN-16045) were taken before performing the experiments.

In the current study, animals (6 nos.) were divided into five different groups. Group 1 received vehicle normal saline (10 ml/kg) orally before the 30 min waiting period. To group 2, 0.1 ml of CFA (0.05% Mycobacterium butyricum in mineral oil; 10 ml/kg b.w.) and vehicle (10 ml/kg) was injected into the left hind paw (subplantar surface) with the help of a 26 gauge needle. Group 3 received CFA and indomethacin (3 mg/kg b.w.) whereas group 4 and 5 administered samples at a dose of 100 mg/kg b.w. and 200 mg/kg b.w. respectively. For the arthritic evaluations, the paw diameter, joint diameter, arthritic score, and body weight measurements were carried out on the third, seventh, 14th, and 21st days. After completion of the protocol on the 21st day, the blood (terminal) samples were collected and the inflammatory mediators, like TNF-α and COX-2 levels, were estimated from the collected serum using ELISA kit assay for all the assigned groups. The ankle joint tissues were fixed with formalin and preserved for further histopathological studies.

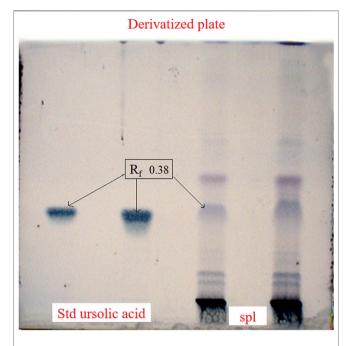


FIGURE 1 | HPTLC chromatogram of ursolic acid standard and plant extract with $R_{\rm f}$ value.

All obtained results were compared and evaluated with the standard (Pincus et al., 2003; Kamal and Baldi, 2015; Ghosh et al., 2016). The statistical analysis was subjected to mean \pm Standard Error Mean (SEM). Differences were considered significant at p < 0.001, or p < 0.01, or p < 0.05 when compared test group vs. control (-ve) group. For numerical results, a one-way analysis of variance (ANOVA) (compare all vs. control) was performed using Graph Pad InStat Version 3 (GraphPad Software).

RESULTS

Qualitative

Estimation by High-Performance Thin Layer Chromatography

The presence of ursolic acid was confirmed by performing the HPTLC from the aqueous extract of $\it C.$ serratum $\it L.$ using standard ursolic acid. The stabilized HPTLC system produced a compact spot of standard ursolic acid with an $\it R_f$ value of 0.38. HPTLC chromatogram of ursolic acid standard and plant extract are shown in **Figure 1.** UV scanning for sample (A) and standard (B,C) were graphically presented in **Figures 2A–C.**

Quantitative Estimation by HPLC and Method Validation as per ICH Guidelines

The statistical analysis was performed by plotting the standard ursolic acid concentration and the peak

responded with a straight line of correlation coefficient 0.998. The observed results showed good recovery within 95–110% when spiked with the standard sample at four different concentrations levels. The developed HPLC method was found to provide repeatable results at various concentrations; thus, the developed protocol was found to be reliable. The sample peak purity was confirmed by comparing with the standards of retention time and peak area. The LOD and LOQ were quantified at 33 $\mu g/ml$ and 0.059% respectively for the ursolic acid of the test sample (extract). The performed analytical development and validation was assured as per the ICH guidelines and graphically presented in **Figure 3** for sample (A) and standard (B).

Evaluation of Anti-inflammatory and Anti-Arthritic

Hypotonic Solution-Induced Haemolysis or Membrane-Stabilizing Activity

Membrane stabilizing activity (8%) at a concentration level of 100 µg/ml was shown in **Figure 4**.

Effect of Protein Denaturation

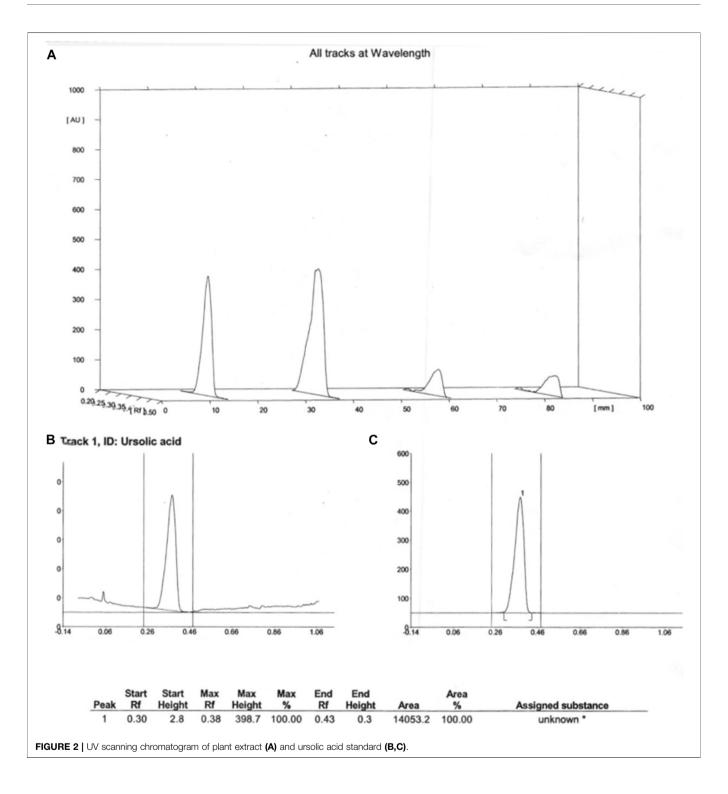
Around 40% of protein denaturation with $100\,\mu g/ml$ concentration was shown in Figure 5.

Evaluation of *In-Vivo* Anti-Arthritic Study

The measured arthritic parameters like paw diameter, joint diameter, arthritic score, and body weight were presented in **Figures 6–9**. Assessment of the blood sample was collected from the terminal parts of the animals. The level of TNF- α and COX-2 was estimated by using ELISA assay (**Figure 10**). The histopathological analysis of ankle joints after 21 days at a dose of 200 mg/kg was shown in **Figure 11**.

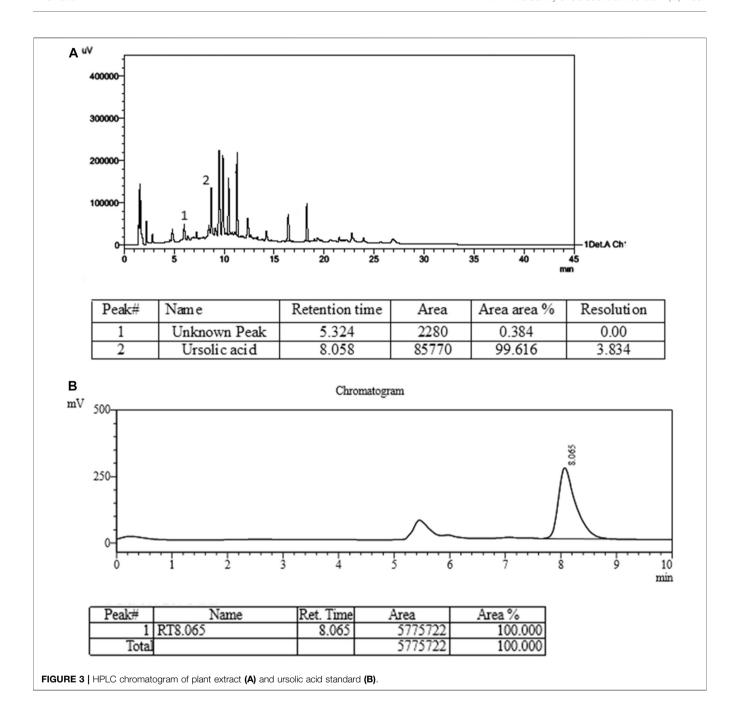
DISCUSSION

Arthritis is a persistent disease that equally affects adults and the elderly. Although the prevalence rate ranges between 0.3 and 1% (World Health Organization, 2020), women are mostly affected. As per Sharon et al., (2017), the high arthritis prevalence rate in low to middle-income countries leads to an inability to meet the daily personal as well as social needs. Fundamental endeavors toward prevention and management of arthritis should be prioritzed. The majority of the manufactured medicines, like NSAIDs (Ghosh et al., 2016), Glucocorticoids (Joseph et al., 2016), DMARDs (Pincus et al., 2003; Donahue et al., 2008; Luo et al., 2013; Kapoor et al., 2014) and certain biologicals (Banse et al., 2015; Brady et al., 2015; Zengin et al., 2017), target the symptoms but not the etiology of the disease with extreme adverse drug effects, whereas the surgical treatments (Krause and Matteson, 2014) can lead to post-operative complexities with mental unacceptance.



The natural product has a significant impact with fewer side effects and co-morbidities. Natural cures could be used to combat the constraints related with current accessible synthetic treatments. The plant Bharangi is a popular folk medicine used for inflammation, rheumatism, and pain. Specialists are considering utilizing the Bharangu plant to improve the symptoms of arthritis.

The identification of metabolites with proper integration of modern scientific techniques in herbal research is an essential step for the global market and also for reproducible results. Thus, both HPLC and HPTLC analytical methods were used in the current study as the most applicable tools for identification and standardization.



In the current study, we focused on the root as a biological source in Ayurvedic Pharmacopoeia of India. Ursolic acid was identified and quantified by HPTLC and HPLC in the aqueous extract of the root. The developed HPLC method was also validated as per ICH guidelines. Shanmuga et al. (2017) likewise quantified the metabolites apigenin and luteolin by reverse phase high-performance liquid chromatography (RP-HPLC) from its leaf extract (Shanmuga et al., 2017). Followed by its analytical analysis, our study focused on its anti-inflammatory and anti-arthritic activity. In our study, it has been found that the presence of secondary metabolites enhances the stability of the biological membranes when

stressed under lysis conditions, considered to be the preliminary investigation involved during the screening of anti-inflammatory activity. The RBC membrane structurally resembles the lysosomal membrane. The protein denaturation of the anti-arthritic property was successfully evaluated using *in-vitro* assessments. Literature (Krause and Matteson, 2014) also supported the use of ursolic acid in inhibition of the release of proinflammatory cytokines TNF- α , IL-2, and IFN- γ . Studies also revealed the presence of β -sitosterol as an anti-arthric potential in ethanolic extract of the leaf of the plant. The methanolic extract demonstrated dual inhibitory effects on arachidonic acid metabolism which is responsible for the

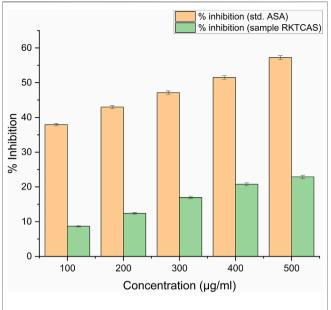


FIGURE 4 | *In-vitro* membrane stabilizing activity showing the possible mechanism of action for the anti-inflammatory activity of aqueous extract of *Clerodendrum serratum* L.

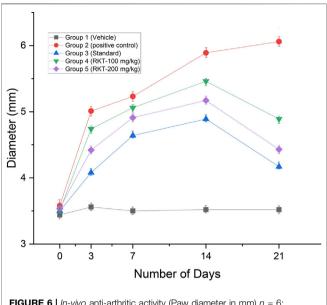
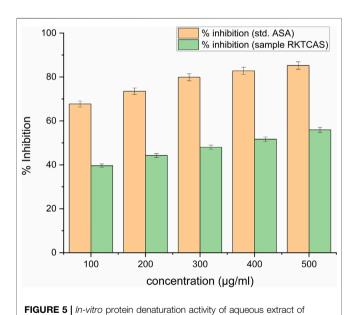


FIGURE 6 | In-vivo anti-arthritic activity (Paw diameter in mm) n = 6; Data = Mean \pm SEM; **p < 0.1 (G2 Vs G4); ***p < 0.001 (G2 vs. G3, G4 and G5).



inhibition of the synthesis of inflammatory mediators released through cyclooxygenase and lipoxygenase pathways (Cargnin and Gnoatto, 2017). Patel et al. (2014) revealed the presence of Apigenin-7-glucoside which further confirmed its anti-inflammatory effects and also claimed pain relief to knee osteoarthritis patients in a randomized controlled clinical trial study (Shoara et al., 2015). Thus the presence of phytochemicals

like ursolic acid, flavonoid, apigenin, and β-sitosterol strongly

Clerodendrum serratum L. against protein denaturation using egg albumin.

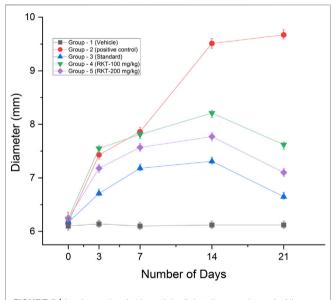
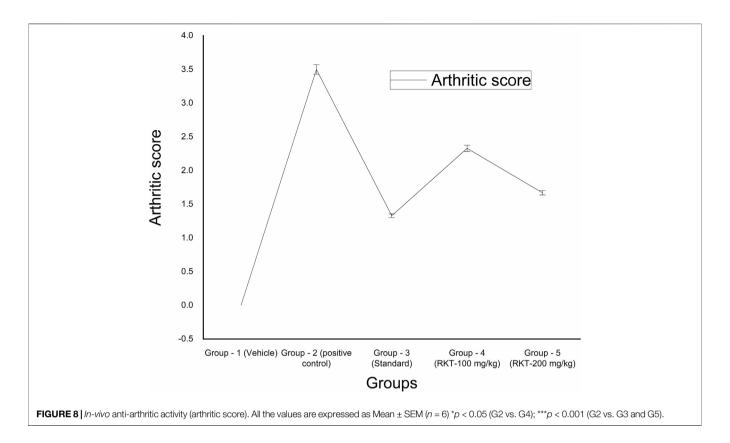


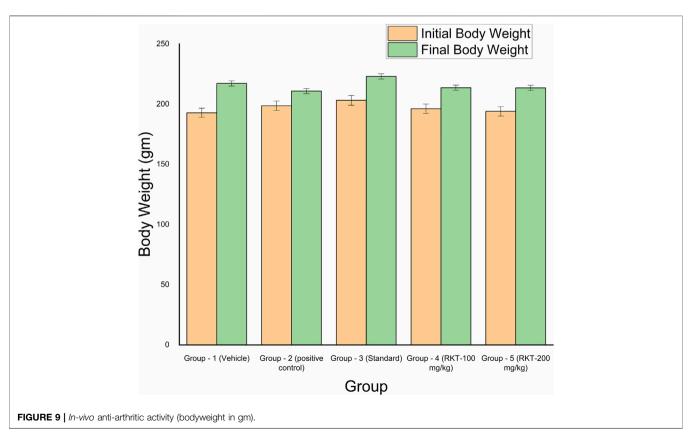
FIGURE 7 | *In-vivo* anti-arthritic activity (joint diameter in mm). All the values are expressed as Mean \pm SEM (n = 6) **p < 0.01 (G2 vs. G4); ***p < 0.001 (G2 vs. G3, G4 and G5).

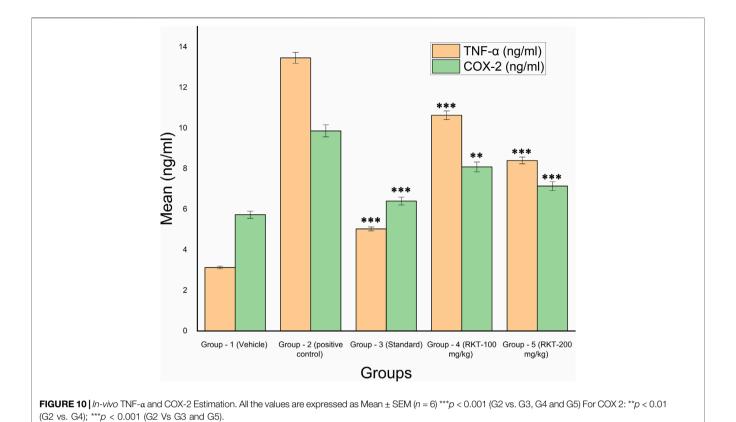
support the traditional use and potentiality of *C. Serratum* as an anti-inflammatory and anti-arthritic.

CONCLUSION

The current study showed that the extract possesses both anti-inflammatory and anti-arthritic activities. The possible mode of action of the anti-arthritic activity of the aqueous extract of C.







HISTOLOGY (Joint Tissue)

Group-1(Vechile)

Group-2(Positive Control)

Group-3 Standard(Indomethacin)

Group-5(RKT-200 mg/kg

Group-4(RKT-100 mg/kg)

FIGURE 11 | Histopathological study of ankle joint at 21 days of treatment after Complete Freund's adjuvant (CFA) injection.

serratum may be mediated by the inhibition of COX-2 and TNF- α . Based on the results, anti-arthritic activity may be due to shielding of a synovial membrane, obstruction of cartilage destruction, and inhibition of vascular permeability. Through our intensive efforts and thorough research, the results confirmed to show favorable arthritis restoration using arthritis parameters and histopathological observations from the selected plant *C. serratum*. The developed HPTLC and HPLC method could be used as an analytical tool for its quality control purpose.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/Supplementary Material, further inquiries can be directed to the corresponding author.

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ETHICS STATEMENT

The animal study was reviewed and approved by the Institutional Animal Ethics Committee (IAEC) (Reg No. 1824/PO/ERe/S/15/CPCSEA; Protocol Approval Reference No. IAEC/PN-16045).

AUTHOR CONTRIBUTIONS

Conceived and design the experiment: RT and UM Conduct experiment: RT, SC, MS and SA Writing of Manuscript: RT, SC, UM and MS Analysis the statistical data and interpretation: RT, SC, UM Manuscript Approval: All authors approved the manuscript.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Pharmacological Evaluation of Safoof-e-Pathar Phori- A Polyherbal Unani Formulation for Urolithiasis

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Ahmad W, Khan MA, Ashraf K, Ahmad A, Daud Ali M, Ansari MN, Kamal YT, Wahab S, Zaidi SMA, Mujeeb M and Ahmad S (2021) Pharmacological Evaluation of Safoofe-Pathar Phori- A Polyherbal Unani Formulation for Urolithiasis. Front. Pharmacol. 12:597990. doi: 10.3389/fphar.2021.597990 Safoof-e-Pathar phori (SPP) is an Unani poly-herbomineral formulation, which has for a long time been used as a medicine due to its antiurolithiatic activity, as per the Unani Pharmacopoeia. This powder formulation is prepared using six different plant/mineral constituents. In this study, we explored the antiurolithiatic and antioxidant potentials of SPP (at 700 and 1,000 mg/kg) in albino Wistar rats with urolithiasis induced by 0.75% ethylene glycol (EG) and 1% ammonium chloride (AC). Long-term oral toxicity studies were performed according to the Organization for Economic Co-operation and Development (OECD) guidelines for 90 days at an oral dose of 700 mg/kg of SPP. The EG urolithiatic toxicant group had significantly higher levels of urinary calcium, serum creatinine, blood urea, and tissue lipid peroxidation and significantly (p < 0.001 vs control) lower levels of urinary sodium and potassium than the normal control group. Histopathological examination revealed the presence of refractile crystals in the tubular epithelial cell and damage to proximal tubular epithelium in the toxicant group but not in the SPP treatment groups. Treatment of SPP at 700 and 1,000 mg/kg significantly (p < 0.001 vs toxicant) lowered urinary calcium, serum creatinine, blood urea, and lipid peroxidation in urolithiatic rats, 21 days after induction of urolithiasis compared to the toxicant group. A long-term oral toxicity study revealed the normal growth of animals without any significant change in hematological, hepatic, and renal parameters; there was no evidence of abnormal histology of the heart, kidney, liver, spleen, or stomach tissues. These results suggest the usefulness of SPP as an antiurolithiatic and an antioxidant agent, and long-term daily oral consumption of SPP was found to be safe in albino Wistar rats for up to 3 months. Thus, SPP may be safe for clinical use as an antiurolithiatic formulation.

Keywords: Urolithiasis, antioxidant, ethylene glycol, ammonium chloride, safoof-e-pathar phori, long term oral toxicity

INTRODUCTION

Urolithiasis is the formation of a stone in the kidney, and it is the most common medical problem in humans. Kidney stones have been reported even before 4000 BC in Egyptian mummies and in remains of old North American Indians dating back to 1,500–1000 BC (Patankar et al., 2008). Kidney stones affect up to 5% of the population, with a lifetime risk of passing a kidney stone in approximately 8–10% of the population (Asplin et al., 1996). Presumably, nearly 12% of the global population is affected by kidney stones, with a higher recurrence rate in males than in females (70–80% vs 47–60%) (Soundararajan et al., 2006).

Urolithiasis is a complex process because stones can originate in any part of the urinary tract and kidney, leading to a deficiency of various vitamins and hormones in the body. The frequency of stones in men is twice as high compared to women, and the prevalence is highest among men aged between 30 and 35 years and among women aged between 35 and 55 years (Sutherland et al., 1985; Srinivas et al., 2012). Kidney stone formation or urolithiasis is a complex process that arises due to differences among promoters and inhibitors in the kidneys (Sathish et al., 2010). Factors affecting stone formation are urinary output (hence, the concentration), concentration of a particular component, urinary pH, and infection or injury within the urinary tract (Michell et al., 1989).

Stones are made up of various components. The first step in the formation of any stone is the supersaturation of urine (Chandhoke, 2002). Calcium oxalate (CaOx) is the principal constituent of most stones, accounting for more than 80% of stones (Moe, 2006), and the remaining 20% of the stone comprises struvite, cystine, uric acid, and other stones (Park and Pearle, 2007). As mentioned, calcium stone formation is caused by supersaturation of the urine with calcium salts forming a stone. Metabolic irregularities such as hypercalciuria, hypocitraturia, hyperoxaluria, hyperuricosuria, and gouty diathesis can change the composition or saturation of urine, increasing the risk of stone formation. Urolithiasis requires preventive and curative therapies because of its high recurrence rate.

Presently, no suitable drugs are available in modern medicine for the prevention and management of kidney stones. Thiazide diuretics and alkali citrate, the most effective hypocalciuric agents, are used to prevent kidney stone formation; however, no allopathic medicine is available for the dissolution or expulsion of the kidney stone (Ikshit et al., 2017). Treatment and management of renal stones relies on surgical techniques, such as extracorporeal shock wave lithotripsy, percutaneous lithotripsy, and transureteral lithotripsy (Mandavia et al., 2013; Mina et al., 2018), These surgeries are complex and expensive and do not affect the recurrence of stones. However, they cause adverse effects including tubular necrosis (Ikshit et al., 2017), hypertension, hemorrhage, and subsequent fibrosis of the kidney (Hardik et al., 2016), which cause cell injury and reappearance of the renal stone (Kaur et al., 2009).

Medicine obtained from herbal sources is a substitute and last resort drug for the prevention and treatment of kidney stones. Several medicinal plants have been used because of their curative and preventive properties against urinary calculi, for example, *Didymocarpous pedicellatus* R. Br (leaf) (Ahmad et al., 2014; Khaling et al., 2014), *Tribulus terrestris* L (fruit and leaves), *Solanum virginianum* L (fruit) (Kumar and Pandey, 2014), and Gokhsuradi churan (an ayurvedic formulation) are commonly and frequently used in traditional medicine in India (Srinivasa et al., 2013).

Traditional medicine provides several alternatives for modern invasive operational treatments in allopathy, for instance, the use of Safoof-e-Pathar phori (SPP) in the treatment of urolithiasis (Anonymous, 1986; Ahmad et al., 2016). SPP, for the treatment of urolithiasis, has been used for a long time in the Unani system of medicine and has been found to be a clinically sound medicine.

In the Unani system of medicine, powdered drugs are termed 'Safoof'. Safoof is an important class of Unani medicinal preparations, which are obtained by powdering and mixing herbs, metals, minerals, and animal products (Dubey et al., 2008). SPP is an Unani poly-herbomineral formulation, and has been used as a medicine for a long time because of its antiurolithiatic activity, as per Unani Pharmacopoeia (Anonymous, 1986). This powder formulation is prepared using plant and mineral constituents such as Didymocarpous pedicellatus R. Br (Gesneriaceae) (Anonymous, 2006; Ahmad et al., 2014; Ahmad et al., 2017), Macrotyloma biflorum var. biflorum (Leguminosae) (Anonymous, 2007a), Rheum webbianum Royle (Polygonaceae) (Anonymous, 2007b; Ahmad W. et al., 2014), Raphanus raphanistrum subsp. sativus (L.) Domin (Brassicaceae), Hordeum vulgare Linn (Poaceae), and potassium nitrate (Ahmad et al., 2013; Ahmad W. et al., 2014; Zaidi and Ahmed, 2016).

Ahmad et al. (2016) reported extensive quality control analysis of SPP for the first time, which comprised phytochemical and physicochemical high-performance analyses, thin-layer chromatography (HPTLC), high-performance chromatography (HPLC), and gas-chromatography coupled to mass spectrometry (GC-MS) fingerprinting profiles, to check the authenticity and to determine the adulterants in this traditional formulation. Quantitative estimation of marker compounds such as emodin (C₁₅H₁₀O₅; 98% purity), chrysophanic acid (C₁₅H₁₀O₄; 98% purity), and alpha-humulene (96% purity) in SPP has been performed using various analytical techniques such as HPTLC, HPLC photodiode array detector, ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry, and GC-MS (Ahmad W. et al., 2014; Ahmad et al., 2015; Ahmad et al., 2016; Ahmad et al., 2019). Additionally, a quality control analysis of individual constituents of SPP (Didymocarpous pedicellatus R. Br, Macrotyloma biflorum var. biflorum, and Rheum webbianum Royle) has been reported (Ahmad et al., 2010; Ahmad et al., 2013; Ahmad W. et al., 2014; Ahmad et al., 2017). Ahmad et al. (2020) reported a comprehensive quality assessment method consisting of HPTLC, HPLC, and GC-MS comparative fingerprinting profiles for SPP and its constituents, using extracts in petroleum ether, chloroform, methanol, and hexane to provide further chemical information. This method can be used for the identification of crude drugs present in other herbal formulations. HPTLC fingerprint profiles of petroleum ether, chloroform, and

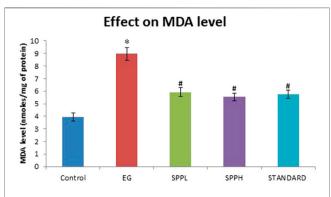


FIGURE 1 | Lipid peroxidation in kidney of rats immunized with EG and AC after treatment with SPP (700 and 1,000 mg/kg b. wt.). Data are expressed as Mean + SD of 6 rats.

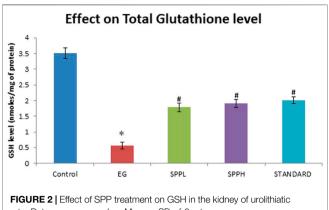
methanol extracts displayed different bands at different wavelengths for SPP and its constituents. Various solvent systems, chemical compositions, and chromatograms are reported by Ahmad et al. (2020). The HPLC finger print profile data showed the presence of 23, 14, 10, and 13 compounds was detected in methanolic extracts of SPP, Didymocarpous pedicellatus R. Br., Macrotyloma biflorum var. biflorum, and Rheum webbianum Royle, respectively, whereas the GC-MS fingerprint profile demonstrated the presence of 22, 51, 28, and 16 metabolites in hexane extracts of SPP, Didymocarpous pedicellatus R. Br., Macrotyloma biflorum var. biflorum, and Rheum webbianum Royle, respectively, which were identified by reviewing NIST and Wiley libraries on the basis of m/z (Ahmad et al., 2020). The formulation and composition used in this study are similar to those described by Ahmad et al. (2020).

To the best of our knowledge, no published scientific evidence is available to prove the effectiveness of SPP in urolithiasis. Hence, this study aimed to investigate phytochemical-based lithotriptic activity of SPP. In addition investigating the therapeutic effects, comprehensive toxicological information on SPP is essential to ensure safety upon use, mainly for long-term use. Therefore, this study was conducted to evaluate the effect of SPP [same formulation as used by Ahmad et al. (2014), Ahmad W. et al. (2014), Ahmad et al. (2015), Ahmad et al. (2016), Ahmad et al. (2019), Ahmad et al. (2020)] on urolithiasis induced by ethylene glycol (EG) and ammonium chloride (AC) in albino Wistar rats and its long-term oral toxicity.

MATERIAL AND METHODS

Plant Material

Crude drugs such as R. webbianum Royle, D. pedicellatus R. Br, and M. biflorum var. biflorum were collected from the local drug market in Khari Baoli, New Delhi, and taxonomic authentication was performed by Dr. H. B. Singh, Ref. NISCAIR/RHMD/1327/ 129, New Delhi.



rats. Data are expressed as Mean + SD of 6 rats.

Method of Safoof-e-Pathar Phori **Preparation**

SPP was prepared as per the process described in Qarabadeen Majeedi. For the 100 g unit formula for SPP preparation, finely powdered plant drugs: Didymocarpous pedicellatus R. Br.50 g, Macrotyloma biflorum var. biflorum12.5 g, Rheum webbianum Royle12.5 g, salts: Hordeum vulgare Linn. 12.5g, Raphanus raphanistrum subsp. sativus (L.), Domin 6.25 g, and potassium nitrate 6.25 g were mixed properly and passed through mesh # 60 to obtain a uniform powder (Table 1). This formulation was prepared in the bioactive natural product laboratory, Jamia Hamdard, New Delhi, and a voucher specimen was submitted to the lab BNPL/SPP/02/2010. The same formulation and composition were used by Ahmad et al. (2014), Ahmad W. et al. (2014), Ahmed et al. (2015), Ahmed et al. (2019), Ahmed et al. (2020).

Chemicals and Apparatus

Biochemical kits for the estimation of calcium, sodium, and potassium were purchased from Span Diagnostics Ltd, Surat, India. All the chemicals were purchased from Sigma Chemicals Co., St Louis, United States, and Hi-media, Mumbai. Apparatus including metabolic cages (INCO, Ambala, India), refrigerated research centrifuge (Remi centrifuge instrument, Mumbai), and UV-spectrometer (model UV 1800; Shimadzu, Japan) were used in the study.

Experimental Animals

Male albino Wistar rats (body weight range 180-220 g) were used for the pharmacological (antiurolithiatic and antioxidant activities) studies, and healthy young adult male and female albino Wistar rats (weighing 125-160 g) were used for the long-term oral toxicity studies. Females were nulliparous and non-pregnant. Animals were procured from the central animal house facility of Jamia Hamdard. The study protocol was approved by the Institutional Animal Ethics Committee (Registration Number 173/CPCSEA and Approval Number 691) following guidelines of the Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA), Government of India.

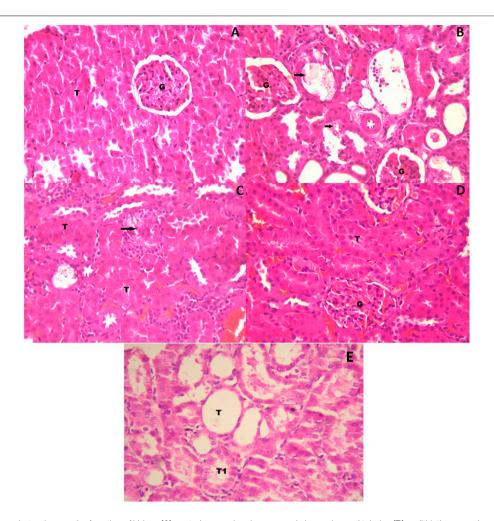


FIGURE 3 | High power photomicrograph of section of kidney (A) control group showing a normal glomerulus and tubules (B) urolithiatic group showing damaged proximal tubules (arrow) with deposits of refractile crystals and loss of tubular epithelium. The distal tubules (DT) are not affected, glomerulus shows no damage (C) urolithiatic group treated with SPP 700 mg/kg/day showing a single damaged proximal tubule (Arrow) with loss of tubular epithelium with several undamaged tubules (T) around it (D) Urolithiatic group treated with SPP 1000 mg/kg/day showing a normal glomerulus and tubules. No evidence of tubular damage was seen in this sample. G = Glomerulus, T = Tubule. (E) But the Neeri standard group's rat kidneys showing a few dilated tubules along with a number of undamaged tubules (HE × 40).

All animals were fed a standard laboratory diet and maintained under standard laboratory conditions (temperature, 22–24°C; relative humidity, 60–70%), standard light and dark cycle, and water *ad libitum*. All the healthy albino Wistar rats were allowed to acclimatize for 1 week prior to the experiment.

Ethylene Glycol- and Ammonium chloride-Induced Urolithiasis

Animals were divided into the following five groups (six animals in each group): control, toxicant, Safoof-e-Pathar phori lower dose (SPPL) treatment group, Safoof-e-Pathar phori higher dose (SPPH) treatment group, and neeri syrup standard group (**Table 1**). To induce CaOx crystal formation, animals were exposed to 0.75% EG with 1.0% AC in their drinking water for 21 days (Bashir and Gilani, 2009). The experimental groups are summarized as follows:

Group I: Normal rats; received vehicle along with simple drinking water for 21 days.

Group II: Toxicant; received 0.75% EG with 1.0% AC in drinking water for 5 days and 0.75% EG for the next 16 days.

Group III: Standard; received 0.75% EG with 1.0% AC in drinking water for 5 days and 0.75% EG for the next 16 days along with the standard drug neeri 2.65 ml/kg/day for all 21 days.

Group IV: SPPL; received 0.75% EG with 1.0% AC in drinking water for 5 days and 0.75% EG for the next 16 days along with SPP at 700 mg/kg/day for all 21 days.

Group 5: SPPH; received 0.75% EG with 1.0% AC in drinking water for 5 days and 0.75% EG for the next 16 days along with SPP at 1,000 mg/kg/day for all 21 days.

For the antiurolithiatic study, fresh suspensions of SPP (700 and $1{,}000 \text{ mg/kg}$; using 0.25% CMC) were administered once daily by oral gavage to the corresponding group of animals for 21 days.

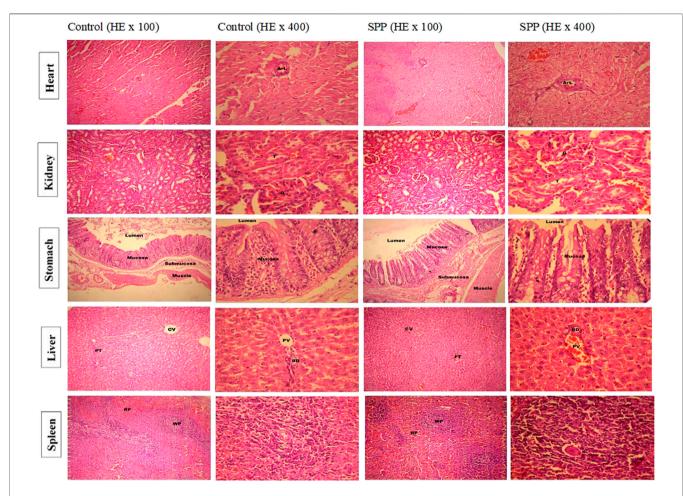


FIGURE 4 | Low and high-power photomicrograph of SPP treated rats showed the normal histological appearance without any significant change in heart, kidney, liver, spleen and stomach compare to normal control rats. Histopathological examination of heart tissue showed normal appearance of cardiac muscle fibers and no evidence of necrosis or myocardial damage is seen. Cardiac muscle fibers with striated cytoplasm and central oval nuclei. A coronary vessel (Art.) cut in cross section is also seen. Histopathological examination of kidney tissues showed normal histopathological appearance of renal parenchyma, glomerular tubule in all treatment groups including control. The histopathological examination of stomach tissues showed normal histological appearance of different layers of stomach walls and mucosa of the stomach showing gastric glands in photomicrographs of all treatment groups including control. Histopathological examination of liver tissues showed normal histological appearance of portal triad (PT), central vein (CV) (100x), bile duct (BD) and portal vein (PV) (400x) in all treatment group including control. The histopathological examination of spleen tissues showed normal histological appearance of white pulp (WP), red pulp (RP) (100x), areas in the splenic parenchyma. Splenic arteriole (SA) and lymphocytes in photomicrographs of all treatment groups including control.

TABLE 1 | Composition of Safoof-e-Pathar phori (Anonymous, 1986).

S. No	Ingredients common name	Ingredients botanical name	Family (part used)	Category	Unit formula per 100 g
	Pathar phori	Didymocarpous pedicellatus R.Br	Gesnericeae (leaves)	Active ingredient	50 g
	Jawakhar desi	Hordeum vulgare L	Poaceae (whole plant)	Active ingredient	12.5 g
	Revand chini	Rheum webbianum Royle	Polygonaceae (Rhizome)	Active ingredient	12.5 g
	Namak turb	Raphanus raphanistrum subsp. sativus (L.) domin	Brassicaceae (Whole plant)	Active ingredient	6.25 g
	Kulthi	Macrotyloma biflorum var. biflorum	Leguminosae (Seed)	Active ingredient	12.5 g
	Shora qalmi	Potassium Nitrate		Active ingredient	6.25 g
				Total	100

Long-Term Oral Toxicity Study

Young adult male and female albino Wistar rats were divided into the following four groups (five rats in each group):

Group I: Normal control (NC); consisting of males receiving vehicle 0.4ml/animal daily for 90days.

Group II: NC; consisting of females receiving vehicle 0.4 ml/animal daily for 90 days.

Group III: SPP (700 mg/kg/day for 90 days); consisting of males.

Group IV: SPP (700 mg/kg/day for 90 days); consisting of females.

For the long-term oral toxicity study, a freshly prepared suspension of SPP (700 mg/kg) was administered daily in the rats for 90 days. The animals were dosed at approximately the same time each day. All animals were observed daily for body weight and mortality throughout the study. Histopathological and biochemical changes in the animals were analyzed at the end of the study period following sacrificing of the animals.

Collection and Analysis of Urine

On the 21st day, animals were kept in a urine collection cage, and urine from the first 3 h of the morning was collected for investigation of crystalluria. All the animals were kept individually in the metabolic cages, and the urine sample at 24 h was collected. The urine samples were acidified by adding a few drops of concentrated HCl and stored at 4°C until further use. Urine was also analyzed for calcium, sodium, and potassium as per the manufacturer's protocol (Span Diagnostics Ltd, Surat, India) (Ikshit et al., 2017)

Hematological and Serum Biochemical Analysis

Blood samples were collected 24 h after the last dose of treatment by puncturing the retro-orbital sinus under a mild anesthetic condition, and the animals were sacrificed by cervical decapitation. In the pharmacological study, hematological parameters such as hemoglobin (Hb), total red blood cells (RBCs), and white blood cells (WBCs) were analyzed in the whole blood. The serum was separated by centrifugation at 1,500 rpm for 15 min in refrigerated research centrifuge and used for the estimation of serum creatinine and blood urea nitrogen (BUN) using commercially available kits (Span Diagnostics Ltd, Surat, India) and the Star-21 plus semi-auto analyzer. In long-term oral toxicity studies, hematological parameters such as Hb, erythrocyte count, total leukocytes and biochemical parameters in the blood serum including serum glutamic oxaloacetic transaminase, serum glutamic pyruvic transaminase, alkaline phosphatase, urea, albumin, bilirubin, total protein, creatinine, uric acid, sodium, and potassium were analyzed using commercially available kits (Span Diagnostics Ltd, Surat, India) as per the manufacturer's protocol.

Histopathological Study of the Kidney, Heart, Liver, Stomach, and Spleen

For investigating the antiurolithiatic activity, the sacrificed animals were dissected after blood sample collection, and only the kidneys were removed and immediately washed with ice-cold saline. After washing with saline, kidneys were preserved for biochemical estimation and fixed in 10% formalin for histopathological studies. For the long-term oral toxicity study, the kidney, heart, liver, stomach, and spleen of animals were dissected. Isolated organs were fixed in 10% neutral buffered formalin, processed in a series of graded alcohol and xylene, and finally embedded in paraffin wax. Histological sections (approximately 5m thickness) were prepared by microtomy and stained with hematoxylin and eosin dye for histological examination. Histological slides were examined under a light microscope at low (10×) and high (40×) magnifications. Statistical Analysis

Results are expressed as mean \pm standard deviation. A two-way analysis of variance followed by a Tukey's test was used for statistical analysis. A p value of <0.05 was considered statistically significant.

RESULTS

Antiurolithiatic Effect of Safoof-e-Pathar Phori on Ethylene Glycol Induced Urolithiasis

The concentrations of urinary calcium, potassium, and sodium in groups I–V are given in **Table 2**. In this study, 0.75% EG (v/v) with 1% AC induced urolithiasis in male rats and resulted in hypercalciuria and hyperoxaluria. The level of urinary calcium was significantly elevated compared with the Normal control (NC) (**Table 2**). However, rats treated with SPPL (700 mg/kg; Group IV) and SPPH (1,000 mg/kg; Group V) demonstrated significantly lower calcium levels and increased potassium and sodium excretion in urine than those in NC (p < 0.01). A decrease in calcium and an increase in potassium and sodium in SPPL and SPPH treated rats were similar to those in Neeri-treated rats (Group III).

Urolithiasis induced by EG and AC caused impairment of renal functions in untreated rats as marked by the increased levels of serum creatinine, uric acid, and urea. Renal function was evaluated by determining the serum creatinine and BUN in EG- and ACinduced urolithiasis and treated rats (Table 2). Levels of serum creatinine and BUN were significantly increased in the toxicant group when compared with the NC, indicating impairment of renal functions. However, SPPL (700 mg/kg) and SPPH (1,000 mg/kg) significantly (p < 0.001) decreased the levels of serum creatinine and BUN excreted by kidneys compared with the toxicant group. Moreover, treatment with SPPL (700 mg/kg) and SPPH (1,000 mg/kg) significantly lowered the elevated serum creatinine level, SPPH showed dose-dependent activity due to maximum decrease in serum creatinine and BUN levels. These results suggested that SPP treatment ameliorates the renal functions compared with urolithiatic control rats. The results of SPP were found to be similar to those of the standard drug neeri.

TABLE 2 | Results of ions estimations in urine of control and urolithiatic group and group treated with Neeri, SPP 700 and 1000 mg/kg oral dose.

Parameter	Group I	Group II	Group III	Group IV	Group V
	Control	Toxicant	Neeri	SPP 700 mg/kg	SPP 1000 mg/kg
Calcium (mg/dl)	4.27 ± 0.12	8.90 ± 0.06 ^a	5.20 ± 0.13 ^b	5.95 ± 0.11 ^b	5.28 ± 0.12 ^b
Potassium (mg/dl)	7.10 ± 0.11	4.40 ± 0.03^{a}	7.20 ± 0.07^{b}	6.80 ± 0.10^{b}	7.41 ± 0.06^{b}
Sodium (mg/dl)	28.2 ± 0.52	10.13 ± 0.85^{a}	28.1 ± 0.41^{b}	25.92 ± 0.47 ^b	29.92 ± 0.62^{b}
Oxalate crystals	Nil	+++	Nil ^b	Nil ^b	Nil ^b
BUN (mg/dl)	19.3 ± 4.5	134.7 ± 14.86 ^a	27.11 ± 6.2 ^b	43.26 ± 3.20^{b}	23.74 ± 2.34^{b}
Creatinine (mg/dl)	0.23 ± 0.02	0.69 ± 0.04^{a}	0.21 ± 0.01^{b}	0.27 ± 0.01^{b}	0.20 ± 0.01^{b}
TBARS (nmoles/mg)	3.95 ± 0.33	8.97 ± 0.51 ^a	5.14 ± 0.14^{b}	5.10 ± 0.37^{b}	5.54 ± 0.29^{b}
GSH (nmoles/mg)	3.51 ± 0.17	0.57 ± 0.11^{a}	3.20 ± 0.09^{b}	2.53 ± 0.04^{b}	2.82 ± 0.08^{b}
RBC (×10 ⁶ /mm ³)	5.88 ± 0.2	6.18 ± 0.3	6.33 ± 0.16	6.23 ± 0.2	6.41 ± 0.3
WBC(×10 ³ /mm ³)	9.7 ± 0.3	10.3 ± 0.2	9.7 ± 0.22	10.1 ± 0.4	10.9 ± 0.2
Hb Content (g/dl)	10.4 ± 0.3	11.7 ± 0.4	11.1 ± 0.31	11.8 ± 0.4	11.3 ± 0.3

ap < 0.001 vs. Control.

The antioxidant parameters were assessed by measuring the malondial dehyde (measured as TBARS) and glutathione (GSH) level. Treatment with EG and AC significantly increased (p < 0.001) the TBARS level and decreased the GSH level in urolithiasis-induced rats compared with NC (**Table 2**). Treatment with SPPL (700 mg/kg) and SPPH (1,000 mg/kg) decreased the TBARS level significantly (**Figure 1**) and improved the GSH concentration (**Figure 2**) compared with the toxicant group.

The crystalluria study revealed the absence of crystals (oxalate crystals) in the rat group treated with standard neeri syrup (2.65 ml/kg), SPPL (700 mg/kg), and SPPH (1,000 mg/kg), which supported the preventive effect of low and high doses of SPP on the induction of urolithiasis. Hematological analysis of various groups of rats showed normal RBC, WBC, and Hb levels and absence of hemolysis in all the groups (**Table 2**).

Figure 3 shows the histopathological examination of the rat kidneys. The histopathological section of the kidneys of rats in the control group exhibited no abnormalities; glomerulus and proximal tubules were normal (Figure 3A). The kidneys of rats in the toxicant group exhibited damaged proximal tubules, with deposits of refractile crystals and loss of tubular epithelium. The distal tubules were not affected, and glomerulus did not show any damage. It exhibited the characteristic signs of stone development on continuous ingestion of 0.75% EG with 1.0% AC (Figure 3B). The kidneys of rats in the urolithiatic group treated with SPPL (700 mg/kg/day) exhibited a single damaged proximal tubule with loss of tubular epithelium with several undamaged tubules around it (Figure 3C), whereas those treated with SPPH 1000 mg/kg/day exhibited a normal glomerulus and tubules. No evidence of tubular damage was observed in this sample (Figure 3D). However, the kidneys of rats in the neeri standard group exhibited a few dilated tubules along with numerous undamaged tubules (Figure 3E).

Long Term Oral Toxicity Study of Safoof-e-Pathar Phori 700 mg/Kg

The long-term oral toxicity study of SPP was performed as per the OECD guideline (OECD, 2020) for 90 days. For determining the

long-term oral toxicity of the animals, observations were noted based on the following aspects: cage side observation of all animals, mortality record, body weight record, hematological observation, and liver and renal function test with histopathological observations of the heart, kidney, liver, spleen, and stomach.

The cage side observation of animals subjected to toxicity was performed based on several parameters on each day up to 90 days, but no abnormality was observed during the complete course of the study. Of the 20 rats, none showed mortality up to 90 days (Table 3). The body weight record of the rats (Table 4) did not exhibit any irregularity in all the treatment groups. Similarly, 13weeks treatment of the rats with 700 mg/kg SPP did not exhibit any significant difference in hematological parameters (Table 5) as well as in liver and kidney function tests (Table 5). There was insignificant variation in the wet weight of vital organs in the SPP (700 mg/kg/day)-treated group compared with the control group, and these results were observed in both male and female rats (Table 5). Histopathological analysis of the heart, kidney, liver, spleen, and stomach in the SPP-treated rats revealed the normal histological appearance of all the organs without any significant change compared with NC rats (Figure 4). Thus, SPP was found to be safe after its oral administration at 700 mg/kg for up to 3 months (90 days).

DISCUSSION

The most commonly used medical therapies in the management of urolithasis include calcium channel blockers, steroids, and α_1 adrenergic blockers (Shekar and Patki, 2011), which exhibit some adverse effects. Some herbal remedies have been used in the management of urinary calculi; however, their efficacy has not been scientifically proven. With the understanding of various pathophysiological functions underlying renal stones and the mechanism of herbal remedies that can play a role in preventing the formation and management of urinary calculi, phytotherapy might be a better alternative in the preventive and curative management of urinary calculi. Oral citrate is the most commonly used medicinal agent in the prevention of urinary

^bP<0.001 vs. Toxicant a denotes that data were compared with normal control and b denotes that data were with toxicant group <0.001.

TABLE 3 | Mortality record of animals in control and treatment group.

Days	Control male	Control female	SPP 700 mg/kg male	SPP 700 mg/kg female
Week 1	-	-	-	-
Week 2	-	-	-	-
Week 3	-	-	-	-
Week 4	-	-	-	-
Week 5	-	-	-	-
Week 6	-	-	-	-
Week 7	-	-	-	-
Week 8	-	-	-	-
Week 9	-	-	-	-
Week 10	-	-	-	-
Week 11	-	-	-	-
Week 12	-	-	-	-
Week 13	-	-	-	-
Mortality	0/5	0/5	0/5	0/5

SPP-Safoof-e-Pathar phori.

TABLE 4 | Body weight records of animals in male and female rats orally treated with SPP 700 mg/kg and control group.

Dose	Mal	e (g)	Fema	Female (g)	
	Control	SPP 700	Control	SPP 700	
0 Week (18/07/2010)	148 ± 13.26	142 ± 11.66	133.43 ± 38.36	128.22 ± 36.55	
Week 1 (25/07/2010)	149 ± 14.96	147 ± 11.66	136.16 ± 38.60	131.97 ± 37.66	
Week 2 (01/08/2010)	158 ± 14.35	157 ± 11.66	142.69 ± 40.84	141.13 ± 40.33	
Week 3 (8/08/2010)	163 ± 14.35	164 ± 11.13	147.69 ± 42.45	147.92 ± 42.20	
Week 4 (15/08/2010)	169 ± 13.56	175 ± 8.94	152.29 ± 43.86	157.41 ± 45.49	
Week 5 (22/08/2010)	173 ± 14.35	183 ± 6.63	156.02 ± 44.83	163.05 ± 47.41	
Week 6 (29/08/2010)	180 ± 12.64	189 ± 6.63	161.88 ± 47.14	169.63 ± 49.74	
Week 7 (5/09/2010)	184 ± 12	195 ± 7.07	166.33 ± 48.60	175.58 ± 51.33	
Week 8 (12/09/2010)	189 ± 10.19	201 ± 8	171.59 ± 50.05	182.41 ± 53.03	
Week 9 (19/09/2010)	196 ± 11.57	209 ± 8	177.71 ± 51.42	189.75 ± 55.29	
Week 10 (26/09/2010)	202 ± 12.08	214 ± 3.74	183.67 ± 53.28	193.97 ± 57.71	
Week 11 (3/10/2010)	208 ± 12.88	221 ± 3.74	190.07 ± 54.88	199.97 ± 59.50	
Week 12 (10/10/2010)	214 ± 13.92	228 ± 4	196.49 ± 56.62	206 ± 61.18	
Week 13 (17/10/2010)	225 ± 12.24	236 ± 3.74	206.85 ± 59.57	214.14 ± 63.64	

calculi (Gurocak et al., 2006). Because of the adverse effects of these agents, alternative management modalities comprising herbal remedies have been significant agents in the treatment (Gurocak et al., 2006). The use of medicinal plants to treat diseases is as old as civilization itself. Plants provide crude drugs, which are used without any modification, and numerous chemical constituents can be used for the synthesis of new drugs with better pharmacological effects (Potterat and Hosttettman, 1995; Zaidi and Ahmad, 2016). Additionally, the World Health Organization (WHO) has highlighted the development and application of herbal and traditional medicines considering their beneficial effects, such as cost-effectiveness and the avoidance of side effects of synthetic medicines. The WHO has estimated that approximately 80% of the population living in the developing countries rely on traditional medicines for their healthcare needs (WHO, 2002).

The present study was performed to evaluate the antiurolithiatic effects of SPP on EG-induced urolithiasis in male Wistar rats used by several investigators. (Bashir and Gilani, 2009; Pareta et al., 2011; Aggarwal et al., 2012; Lin et al., 2012; Nanu et al., 2012; Saeidi et al., 2012; Khan et al., 2016).

EG is a metabolic precursor of oxalate. EG is oxidized to glycolic acid and further to oxalic acid. Administration of EG causes hypercalciuria, leading to urolithiasis. Administration of EG causes hypercalciuria and hyperoxaluria to induce urolithiasis (Verma et al., 2009). AC ingestion, which induces metabolic acidosis, has been used in conjunction with EG to promote the deposition of CaOx crystals in the rat kidneys. Various doses of AC in combination with EG resulted in CaOx depositions in the rat kidneys within 7 days (Khan et al., 2016). After 21 days, crystalluria analysis of rats in the EG-induced urolithiasis group revealed that untreated rats exhibited bigger crystals than treated rats (Bashir and Gilani, 2009). Studies have consistently reported that calculi induced by hyperoxaluria causes an increase in oxalate and a decrease in calcium excretions in the toxicant group (Fan et al., 1999; Park et al., 2007); SPP treatment produced reversible effects in a dose-dependent manner.

Results of the urinary calcium level showed a significant (p < 0.001 vs control) elevation in the toxicant group, whereas sodium and potassium level significantly (p < 0.001 vs control) reduced compared

TABLE 5 | Results of hematological, liver, renal and organ weight assessment of control and SPP 700 mg/kg group.

Test	M	ale	Fer	Female	
	Control	SPP 700	Control	SPP 700	
Erythrocyte count (mill/C.mm)	5.81 ± 0.01	7.30 ± 0.06	5.31 ± 1.59	6.61 ± 1.97	
Hemoglobin (g/dl)	9.84 ± 0.16	13.22 ± 0.08	9.52 ± 2.88	11.70 ± 3.53	
Total leukocytes	11.84 ± 0.10	11.18 ± 0.06	10.49 ± 3.16	10.14 ± 3.04	
Bilirubin (mg/dl)	00.93 ± 0.02	0.88 ± 0.01	00.85 ± 0.25	00.79 ± 0.23	
SGPT (U/L)	30.92 ± 0.66	69.68 ± 0.93	27.69 ± 8.21	63.55 ± 18.89	
SGOT (U/L)	35.26 ± 0.34	67.4 ± 0.61	32.24 ± 9.63	60.95 ± 18.22	
ALP (U/L)	75.11 ± 0.28	25.34 ± 0.53	67.90 ± 20.42	14.73 ± 10.67	
Total Protein(g/dL)	00.13 ± 0.01	04.70 ± 0.08	05.71 ± 1.69	04.26 ± 1.26	
Albumin (g/dl)	03.12 ± 0.14	1.30 ± 0.02	02.77 ± 0.80	01.18 ± 0.35	
Blood Urea (mg/dl)	34.6 ± 1.01	49.22 ± 0.16	31.30 ± 9.19	81.90 ± 124.3	
Creatinin (mg%)	00.73 ± 0.02	00.44 ± 0.01	00.66 ± 0.19	00.40 ± 0.11	
Serum Uric acid(mg/100 ml)	07.06 ± 0.10	08.02 ± 0.11	06.40 ± 1.90	07.27 ± 2.16	
Sodium (meq/L)	143.8 ± 2.31	140 ± 1.41	130.42 ± 38.70	127.03 ± 37.95	
Potassium (meq/L)	04.16 ± 0.13	07.24 ± 0.13	03.69 ± 1.09	06.48 ± 1.93	
Kidney	0.68 ± 0.01	0.69 ± 0.007	0.61 ± 0.18	0.63 ± 0.18	
Spleen	0.31 ± 0.01	0.31 ± 0.01	0.28 ± 0.08	0.29 ± 0.08	
Heart	0.40 ± 0.01	0.41 ± 0.006	0.37 ± 0.11	0.37 ± 0.11	
Liver	2.01 ± 0.08	1.94 ± 0.10	1.87 ± 0.54	1.80 ± 0.51	
Stomach	0.38 ± 0.02	0.37 ± 0.007	0.35 ± 0.10	0.34 ± 0.10	

to the control group. Sodium and potassium levels significantly (p < 0.001 vs toxicant) increased, and calcium levels were decreased in the urine of the rats treated with SPP compared with the toxicant group. Comparison of the SPP and Neeri group showed an insignificant difference. This suggests an increased urinary loss of electrolytes (Hess and Kok, 1996). In urolithiasis, creatinine and BUN accumulate in blood. In this study, we observed that serum creatinine and BUN levels were significantly (p < 0.001 vs control) elevated in the serum of rats with EG- and AC-induced urolithiasis (toxicant group). It is suggested that EG and AC cause renal tubular damage and lower glomerular filtration rate. SPP-treated rats significantly (p < 0.001 vs. toxicant) reduced the BUN and serum creatinine levels compared with the control group at the dose of 700 and 1,000 mg/kg, and these results were similar to those of the standard drug Neeri.

The toxicant group showed a significantly (p < 0.001 vs control) elevated level of TBARS compared to the control group. Lipid peroxidation was measured as a Nano-gram of TBARS per mg of protein level in kidney tissue. Lipid peroxidation is another critical cause of injury that occurs during urolithiasis. Increased TBARS levels due to increased oxidative stress, decreased antioxidant enzymes and GSH levels in kidneys, and impaired kidney functions. Oxalate has been reported as the major stone forming component causing peroxidative injury to the renal epithelial cells (Kato et al., 2007). The SPP treatment protected against various injuries associated with oxidative stress. The biochemical alterations were supported by histopathological interpretations of the kidney (Muthukumar and Selvam, 1998). The urolithiasis toxicant group exhibited the presence of refractile crystals in the tubular epithelial cell and damage to the proximal tubular epithelium, whereas groups treated with SPP along with EG and AC exhibited protection, as evident from the reduction in tubular cell damage and normal kidney histology. Our results suggest that SPP has both protective and preventive effects in rats with EG- and AC-induced urolithiasis, which is consistent with previous studies (Saha

and Verma, 2011). Zaidi and Ahmad (2016) reported that SPP is an effective and safe non-invasive polyherbal remedy for patients with urolithiatic, with no adverse reactions.

Medicinal plants and herbal medicines are progressively required by patients as a source of prescription drugs, in the form of active constituents, in developed and developing countries. They have been shown to possess undeniable and tangible therapeutic benefits with limited toxicity because of their long-term use as traditional medicines. The WHO claims that safety is a critical parameter of herbal medicines in the quality control of healthcare products (Tatke et al., 2012). Toxicity studies are considered to be important during new drug development, keeping in mind that herbal medicines are frequently used indiscriminately without considering their potential side effects, which can vary from mild-severe to life-threatening (World Health Organization, 1987; World Health Organization, 2000). Various herbal preparations have been shown to be beneficial in treating kidney disease; however, the toxicity and safety data for many of these herbal treatments are not available (Tatke et al., 2012).

In this study, the long-term oral toxicity of SPP was evaluated in albino Wistar rats using biochemical, hematological, and histopathological parameters. Weight gain and behavioral activity was similar to the control animals in all single-dosed males and females during the study period. There were no marked abnormal changes observed throughout the study period. Hematology in rats at a single dose of SPP exhibited insignificant differences compared to the control group. Additionally, the functioning of major organs (heart, kidney, liver, spleen, and stomach) was found to be similar to that in the control group. Histopathological examination of the heart, kidney, liver, spleen, and stomach did not exhibit any changes. Oral SPP ingested at 700 mg/kg for up to 3 months resulted in normal growth with no changes in hematological, hepatic, or renal functioning parameters. There was no evidence of abnormal histology. Thus, long-term daily oral consumption of SPP

was found to be safe in Wistar rats, and it may be safe for clinical use as an antiurolithiatic formulation.

CONCLUSION

The results indicated that the administration of the traditional Unani poly-herbomineral formulation SPP reduced and prevented the growth of urinary stones in rats with EGand AC-induced urolithiasis. The toxicity study indicated no serious signs and significant changes in the physical, biochemical, and histopathological hematological, parameters after 90-days administration of (700 mg/kg). SPP was found to be safe for oral administration at 700 mg/kg for up to 3 months. Hence, SPP was observed to be a curative and safe polyherbomineral formulation, useful in the prevention and management of urolithiasis. Further studies at lower dose levels and using extracts of the formulation to reduce the dose are necessary to make it more pharmacologically relevant and to elucidate the mechanism underlying the pharmacological effect of SPP.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article, further inquiries can be directed to the corresponding author.

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ETHICS STATEMENT

The animal study was reviewed and approved by Jamia Hamdard, Institutional Animal Ethics Committee (Registration Number 173/CPCSEA and Approval Number 691) following guidelines of the Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA).

AUTHOR CONTRIBUTIONS

WA: Experimental studies and manuscript preparation MK: Experimental studies and statistical analysis KA: Manuscript editing AA: Review and manuscript editing MD: Review and manuscript editing MA: Critical evaluation of manuscript KY: Literature review SW: Literature review SZ: Formulation preparation SA and MM: Conceived idea of research and data analysis.

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Ramulus Mori (Sangzhi) Alkaloids (SZ-A) Ameliorate Glucose Metabolism Accompanied by the Modulation of Gut Microbiota and Ileal Inflammatory Damage in Type 2 Diabetic KKAy Mice

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Liu Q, Liu S, Cao H, Ji W, Li C, Huan Y, Lei L, Fu Y, Gao X, Liu Y and Shen Z (2021) Ramulus Mori (Sangzhi) Alkaloids (SZ-A) Ameliorate Glucose Metabolism Accompanied by the Modulation of Gut Microbiota and Ileal Inflammatory Damage in Type 2 Diabetic KKAy Mice. Front. Pharmacol. 12:642400. doi: 10.3389/fphar.2021.642400 The novel Traditional Chinese Medicine Ramulus Mori (Sangzhi) alkaloid tablets (SZ-A) are approved by The China National Medical Products Administration for the treatment of type 2 diabetes mellitus (T2DM). However, the extensive pharmacological characteristics and the underlying mechanism are unknown. This study investigated the mechanisms by which SZ-A ameliorates glucose metabolism in KKAy mice, an animal model of T2DM. Diabetic KKAy mice were treated intragastrically with SZ-A once daily for 8 weeks, after which glucose levels, lipid metabolism, gut microbiome, systemic inflammatory factors, luminal concentrations of shortchain fatty acids (fecal samples), and ileal proteomic changes were evaluated. The ileum tissues were collected, and the effects of SZ-A on pathological inflammatory damage were evaluated by hematoxylin and eosin staining, immunofluorescence, and immunohistochemistry. The mRNA and protein expression levels of various inflammatory markers, including monocyte chemoattractant protein-1 and phosphorylated nuclear factor kappa B p65, were detected in the ileum tissues. SZ-A improved glucose metabolism with enhanced insulin response and elevated glucagon-like peptide 1 (GLP-1) nearly 2.7-fold during the glucose tolerance test in diabetic KKAy mice. Gut microbiota analysis demonstrated that SZ-A administration elevated the abundance of Bacteroidaceae and Verrucomicrobia, reduced the levels of Rikenellaceae and Desulfovibrionaceae; and increased the concentrations of fecal acetic and propionic acids

Abbreviations: Ccl11, Chemokine C-C-Motif Ligand 1; Ccl4, Chemokine C-C-Motif Ligand 4; Ccl5, Chemokine C-C-Motif Ligand 5; CXCl1, CXC chemokine ligand 1; CD36, cluster of differentiation 36; 1-DNJ, 1-deoxyno-jirimycin; DAB, 1,4-dideoxy-1, 4-iminod-D-arabinitol; FAG, fagomine; F4/80, adhesion G protein-coupled receptor E1; GLP-1, glucagon-like peptide 1; HbA1c, glycated hemoglobin; IL-1β, Interleukin 1β; IL-5, Interleukin 5; IL-10, Interleukin 10; IL-13, Interleukin 13; IL-1a, Interleukin 1a; IL-6, Interleukin 6; IL-12b, Interleukin 12b; LPS, lipopolysaccharides; MCT1, monocarboxylate transporter-1; MHC II, major histocompatibility complex class II; MCP1, monocyte chemotactic protein 1; NF-κB, Nuclear factor kappa B; SCFAs, short-chain fatty acids; SLC5A8, sodium-coupled monocarboxylate transporter 1; T2DM, type 2 diabetes mellitus; TCM, Traditiona 1 Chinese Medicine; TNFα, tumor necrosis factor α; ZO-1, Zonula Occludens-1.

compared to the diabetic model group. Additionally, SZ-A markedly improved ileal inflammatory injury and pro-inflammatory macrophage infiltration and improved intestinal mucosal barrier function in diabetic KKAy mice. SZ-A also attenuated the levels of circulating endotoxin, pro-inflammatory cytokines, and chemokines in the mice sera. Collectively, SZ-A ameliorated the overall metabolic profile including glucose and lipid metabolism in KKAy mice, which may be associated with an improvement in GLP-1 and insulin secretion, at least in part by modulating the gut microbiome and relieving the degree of ileal and systemic inflammation.

Keywords: ramulus mori (sangzhi) alkaloids, type 2 diabetes, gut microbiome, ileal damage, inflammation

INTRODUCTION

The gut microbiome plays important roles in the regulation of glucose and energy homeostasis. It also plays a critical role in obesity, glycemic control, and type 2 diabetes mellitus (T2DM) (Harris et al., 2012), which is a chronic and multifactorial disease in which diverse physiopathologic mechanisms lead to a persistent state of hyperglycemia. T2DM is fundamentally the result of beta cell and alpha cell dysfunction, and insulin resistance in different tissues of the body (Kahn et al., 2014). T2DM may also be due to the activation of pro-inflammatory mechanisms that involve several factors. Gut microbiota-mediated low-grade inflammation is also involved in the onset and progression of T2DM. Studies in mice and humans have shown that there is dysregulation in the gut microenvironment accompanied by immunological and metabolic dysfunctions in individuals who have T2DM (Ge et al., 2018).

Metabolites derived from the gut microbiota, such as short-chain fatty acids (SCFAs) and lipopolysaccharides (LPS), may act as potent immune modulators (Blaak et al., 2020). During eubiosis, the production of SCFAs is essential for maintaining the integrity of the intestinal barrier as well as for immunogenic tolerance. In addition, effects of SCFAs are not limited to immunomodulatory functions (Salazar et al., 2020), as they can also stimulate the secretion of intestinal peptides that participate in the regulation of appetite and insulin secretion such as glucagon-like peptide 1 (GLP-1) (Grasset et al., 2017). Conversely, in the presence of gut dysbiosis during the progression of T2DM, diet-driven unfavorable microbiota composition can lead to the increased production of pro-inflammatory LPS, which are associated with alterations in gut permeability (Fuke et al., 2019). Subsequently, these inflammatory states might exacerbate the disruption of the mucus layer barrier and increase the epithelial permeability of the small intestine, resulting in elevated LPS levels in the bloodstream, metabolic endotoxemia (Kuti et al., 2020), increased levels of systemic inflammatory mediators, adiposity, obesity, insulin resistance, and hyperglycemia.

Thus, restoration of gut dysbiosis could potentially treat metabolic disorder. Modulation of the intestinal microbiota by interventions has led to a major impact on both the immunological and metabolic functions of the host. In recent years, there has been increasing interest in investigating the use of prebiotics (non-digestible carbohydrates), probiotics (life bacteria), and anti-diabetic drugs for the modulation of gut dysbiosis (Bauer et al., 2018; Hamada et al., 2020). Traditional Chinese Medicine (TCM) has been used to manage T2DM. A large number of studies have shown that the effects of TCM may be, at least

in part, via modulation of gut microbiota (Shao et al., 2020; Xiao et al., 2020; Zheng et al., 2020).

The novel TCM Ramulus mori (Sangzhi) alkaloid (SZ-A) tablets, also known as Sangzhi Zong Shengwujian, is approved by The China National Medical Products Administration (NMPA, formerly known as the China Food and Drug Administration) for the treatment of patients with T2DM (Approve Number Z20200002). The main components of SZ-A powder (materials for SZ-A tablets) include alkaloids, flavonoids, polysaccharides, coumarin, quercetin, resveratrol, amino acids, and organic acids. SZ-A is a group of effective polyhydroxy alkaloids (50% or more by weight) that potently inhibit α-glucosidase, including 1-deoxyno-jirimycin (1-DNJ), fagomine (FAG), 1,4-dideoxy-1, 4-iminod-D-arabinitol (DAB), and other soluble polyhydroxy alkaloids or glycosides with a similar structure (Liu et al., 2019a). In preclinical pharmacological studies, chronic treatment of SZ-A was shown to lower fasting and postprandial blood glucose levels in alloxan-induced diabetic mice and rats. SZ-A has also been shown to reduce the peak of postprandial blood glucose in sucrose/starch loading tests in both healthy and diabetic mice after a single dose through the inhibition of intestinal disaccharidases. Moreover, available evidence from our previous study suggests that SZ-A improves dyslipidemia and glucose-stimulated insulin secretion in high-fat diet-induced obese C57 mice after long-term intragastrical administration (Liu et al., 2019b). These data suggest that the beneficial role of SZ-A may involve multiple mechanisms in addition to α -glucosidase inhibition. Previous studies have systematically investigated the tissue distribution of the three major active alkaloids, and they found that 1-DNJ, FAG, and DAB are mainly found in the gastrointestinal tract, liver, and kidney, respectively (Yang et al., 2017). Therefore, we hypothesized that the anti-diabetic effects of SZ-A may be via regulation of gut microbiota and intestinal metabolites.

In this study, we evaluated the anti-diabetic effects and underlying mechanisms of SZ-A, especially on modulation of gut microbiota, intestinal metabolites, and gut barrier integrity in type 2 diabetic KKAy mice.

MATERIALS AND METHODS

Reagents

SZ-A powder (lot number: 201707008, The total polyhydroxy alkaloid content in SZ-A powder is about 63% by weight, which

was mainly composed of 39% of DNJ, 10.5% of FAG, and 7% of DAB), was kindly provided by the Department of Research & Development of Beijing Wehand-bio Pharmaceutical Co Ltd.

Animal Experimental Design

Animal experiments were performed following the "3R" principles and guidelines for laboratory animals (GB14925-2001 and MOST 2006a) established by the People's Republic of China. The animal protocol used was approved by the Institutional Animal Care and Use Committee of Institute of Materia Medica (Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China). 14-week-old male KKAy mice (30 g) were purchased from Beijing Huafukang Bioscience Co., Ltd (Beijing, China). Animals were maintained at 22 ± 2°C with a 12 h light-dark cycle with free access to food and water. The 14-week-old male KKAy mice were fed with high-fat diets (45% of energy from fat; D12451; Research Diets, United States). And after 4 weeks of high-fat diets feeding, twenty-four KKAy mice were selected and randomly divided into three groups (n = 8) according to the levels of blood glucose, triglyceride, total cholesterol, body weight, and percentage of blood glucose increase at 30 min after oral glucose loading: diabetic model group (DM), SZ-A-low dose-treated group (SZ-A 100, 100 mg/kg), SZ-A-high dose-treated group (SZ-A 200, 200 mg/kg). All mice were treated intragastrically with SZ-A solution or an equivalent volume of water once daily for 8 weeks. After 56 days of treatments, all of the mice were fasted overnight and weighted, then were sacrificed via cervical dislocation. Subsequently, the ileum tissues were isolated, fixed in paraformaldehyde solution.

Blood Glucose, Lipid, and Glycated Hemoglobin Measurements

After 4 weeks of treatment, blood samples (10 µl from each mouse) were collected from tail tips at the baseline and 4 h after fasting. Fasting blood glucose (FBG) and postprandial blood glucose (PBG) levels were measured using the glucose oxidase method (Biosino Bio-Technology and Science Inc., Beijing, China). After 42 days of treatment, all of the mice were fasted for 4 hours with free access to water. Blood samples (20 µl from each mouse) were collected from tail tips. Blood triglycerides, total cholesterol levels, and glycated hemoglobin (HbA1c) levels were assessed using commercial kits (A5911; Homa Biological, Beijing, China).

Oral Glucose-Stimulated Insulin and Glucagon-like Peptide 1 (GLP-1) Secretion Test

To evaluate the response of insulin and GLP-1 secretion after the oral glucose stimulation, oral glucose-stimulated insulin and GLP-1 secretion test were performed after 5 weeks of treatment. All of the 24 mice were fasted overnight and given D-glucose (2 g/kg) intragastrically, and the orbital blood samples were collected at 0 and 15 min after glucose administration. The levels of insulin and active GLP-1 in blood were monitored using

ELISA kits (80-INSMSU-E10; 43-GP1HU-E01; ALPCO, United States).

Gut Microbiota Profiling and Fecal Short-Chain Fatty Acids Analysis

All of the 24 mice were sacrificed and the luminal contents were collected from the ileum (as the fecal samples) and snapfrozen in liquid nitrogen after 40 days at the end of treatment, followed by storage at -80°C. The gut microbiome in feces was assayed and the abundance and diversity of gut microbiota were analyzed using Illumina MiSeq sequencing (Major Bio-Pharm Technology, Shanghai, China) according to the standard protocol as previously described (Li et al., 2020). The sequence data were processed and analyzed on the free online Majorbio I-Sanger Cloud Platform (www.i-sanger. com). SCFAs in these fecal samples were detected based on our previous report (Cao et al., 2020). Briefly, the SCFAs in each sample were assayed by gas chromatography coupled to a mass spectrometer detector (GC-MS) (Agilent Technologies Inc. CA, United States) and quantified using Masshunter quantitative software. Correlation analysis of SCFAs and gut microbiota was performed on the platform of Majorbio I-Sanger Cloud (www.i-sanger.com). R and p values were obtained using Spearman's rank correlation.

Histopathological Evaluation, Immunofluorescence, and Immunohistochemistry Assay of the Ileum

About 4 cm of ileum was fixed in 4% paraformaldehyde to prepare 5 µm paraffin slides. The ileum sections from the 24 mice at the end of experiment were stained with hematoxylin and eosin (H&E) for the analysis of inflammatory changes (n = 8). Histopathological assessment of inflammatory and crypt damages was assessed as previously stated by a light microscope (Dieleman et al., 1998). Six randomly selected fields from each slides were analyzed. The ileum sections were also stained with the first antibodies against F4/80 (ARG22476) and CD11c (n = 5) (ARG59698; Arigo Biolaboratories Corp, Taiwan). For immunohistochemistry analysis, we used Anti-NFκΒ p65 (phospho S536) (ab86299, Abcam, Cambridge, United Kingdom) (n = 5). Images were captured with a Mirax scanner (3DHISTECH, Hungary), and the area of positive points calculated with Image Pro (MediaCybernetics, Rockville, MD).

Cytokines and Chemokines Assay in Serum

Blood was collected when the mice were sacrificed after 40 days at the end of treatment. Serum was prepared followed by centrifuged at 4000 rpm and stored at $-80^{\circ}C_{2}$. The concentration of Endotoxin was determined by ELISA kit, and the concentrations of Interleukin 1 β (IL-1 β), Interleukin 5 (IL-5), Interleukin 10 (IL-10), Interleukin 13 (IL-13), Interleukin 1a (IL-1a), Interleukin 6 (IL-6), Interleukin 12b (IL-12b), Chemokine C-C-Motif Ligand 1 (Ccl11), Chemokine C-C-Motif Ligand 5 (Ccl5) and CXC

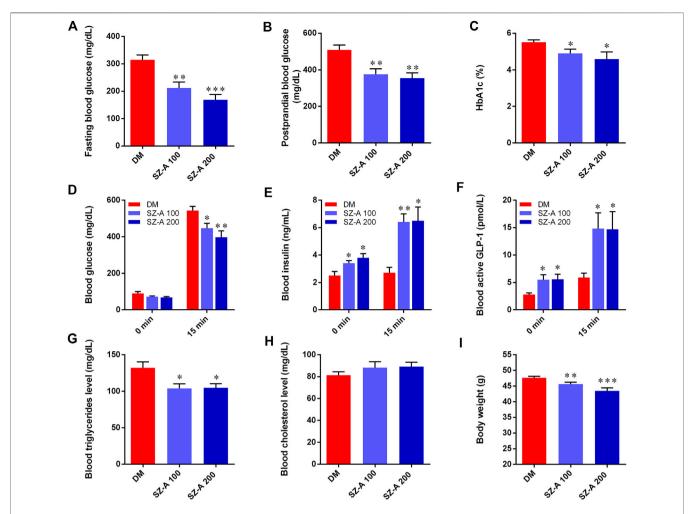


FIGURE 1 | SZ-A ameliorates glucose and lipid metabolism in KKAy mice. **(A)** Fasting blood glucose. **(B)** Postprandial blood glucose. **(C)** Hemoglobin A1c (HbA1c) levels. **(D)** Blood glucose, **(E)** Blood insulin and **(F)** active glucagon-like peptide 1 (GLP-1) levels at 0 and 30 min in oral glucose-stimulated insulin and GLP-1 secretion test. **(G)** Blood triglyceride levels. **(H)** Blood total cholesterol levels. **(I)** Body weight of mice. Data are expressed as mean ± standard error of the mean (SEM), n = 8. *p < 0.00, **p < 0.01, ***p < 0.01, ***p < 0.01, ***p < 0.01, ***D. DM. DM. diabetic model group, SZ-A low-dose-treated group, SZ-A 200, SZ-A-high-dose-treated group.

chemokine ligand 1 (CXCl1) in serum were determined by Luminex liquid suspension chip detection, which was performed by Wayen Biotechnologies (Shanghai, China). The mouse 23-plex Multi-Analyte kit (Bio-Plex suspension Array System; Bio-rad, Hercules, CA, United States) was used following the manufacturer's instructions. The exact protocol was administered according to what had been reported before (Wei et al., 2015).

Western Blotting and Quantitative Real-Time Polymerase Chain Reaction

Ileum tissues were homogenized and lyzed in radioimmunoprecipitation assay buffer, and protein concentrations were determined using a BCA protein quantitation kit. Information of the antibodies are as follow, anti-CD11c (97,585, CST, United States), anti-MHC-II (68,258, CST, United States), anti-MCP1 (ARG56590, Arigo Biolaboratories Corp, Taiwan), anti-SLC5A8 (21433-1-AP), anti-MCT1 (20139-1-AP), and anti-CD36 (18836-1-AP) were from Proteintech Group Inc. Zonula Occludens-1 (ZO-1, 61-7300, Invitrogen, United States), β -Actin antibody (C1313) and secondary antibodies were from (Applygen Technologies Inc., China). Protein levels were normalized to those of β -actin. Quantitative real-time PCR was conducted as previously described. The detailed procedure is presented in the Supplementary Methods. The primer sequences used in this study are shown in **Supplementary Table S1**.

Tandem Mass Tagging Proteomics Analysis

The primary experimental procedures for TMT proteomics analysis include protein preparation, trypsin digestion, TMT labeling, HPLC fractionation, LC-MS/MS analysis, and data analysis. The detailed procedure is presented in the **Supplementary Material**. The TMT proteomics analysis in our research is supported by Jingjie PTM BioLabs.

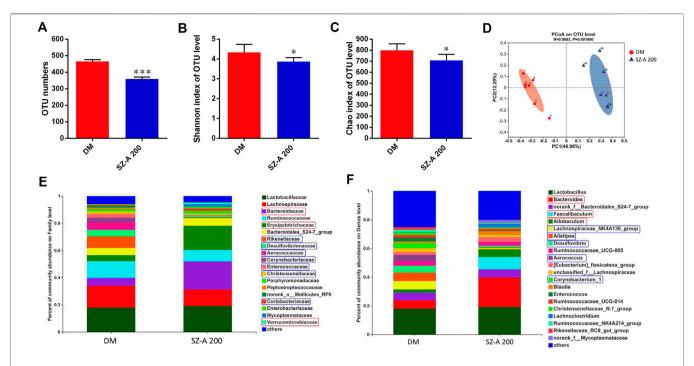


FIGURE 2 SZ-A modulates the composition of gut microbiota of KKAy mice. **(A)** Total OTU numbers. **(B)** Shannon index. **(C)** Chao index. **(D)** PCoA. **(E)** Percentage of community abundance of microbiota at the family level. **(F)** Percentage of community abundance of microbiota at the genus level (upregulated, red box; downregulated, Blue box) data are shown as mean \pm SEM, n = 7. *p < 0.005, ***p < 0.001 vs. DM. DM, diabetic model group, SZ-A 100, SZ-A low-dose-treated group, SZ-A 200, SZ-A-high-dose-treated group.

Statistical Analysis

The data are presented as the mean \pm SEM. Statistical analysis was performed using GraphPad Prism 7.0. Differences in FBG, PBG, insulin, GLP-1, lipid levels, and body weight were assessed using a two-way analysis of variance (ANOVA) with Tukey's test. Data sets involved in two groups or multiple groups were analyzed using unpaired two-tailed Student's t-test or one-way ANOVA depending on the experiments. Differences with p < 0.05 were considered statistically significant.

RESULTS

SZ-A Ameliorates Glucose Metabolism, Enhances the Insulin Response, and Elevates Active GLP-1 Levels During Oral Glucose Tolerance Tests in Diabetic KKAy Mice

After a 4-week treatment, the levels of fasting blood glucose (p < 0.01, p < 0.001) and postprandial blood glucose (p < 0.01, p < 0.01) in both SZ-A-treated groups were significantly decreased compared to the DM group (**Figures 1A,B**). Hemoglobin A1c (HbA1c) levels in SZ-A-treated groups were lower than those in the DM group after a 6-weeks treatment (p < 0.05, p < 0.05; **Figure 1C**), indicating that SZ-A exhibited good glycemic control in the KKAy mice during chronic treatment. As shown in **Figure 1D**, compared to the DM group, both doses of SZ-A significantly reduced blood glucose levels at 15 min after oral glucose loading (p < 0.05, p < 0.01). We further detected the blood

insulin content and active GLP-1 levels as an indication of insulin and GLP-1 secretory function, respectively. As shown in Figures 1E.F. there was no notable increase in blood insulin content and active GLP-1 level in the DM group after oral glucose loading; however, SZ-A-treated groups had increased both insulin content and active GLP-1 levels at both baseline and 15 min after glucose stimulation. SZ-A 100 and SZ-A 200 significantly enhanced insulin secretion nearly 1.73-fold and 1.88-fold from baseline at 15 min after glucose stimulation, respectively (p < 0.01, p <0.05), compared to the DM group (1.11-fold). In addition, both doses of SZ-A elevated active GLP-1 levels nearly 2.7-fold and 2.6-fold at 15 min after glucose stimulation from baseline (p < 0.01, p < 0.05), respectively, compared to the DM group (2.1fold). Moreover, both doses of SZ-A resulted in decreased blood triglyceride levels after 6 weeks (p < 0.05, p < 0.05), and induced significant weight loss compared to the DM group at the end of treatment (p < 0.01, p < 0.001).

SZ-A Modulates Gut Microbiota Profiling and SCFA Concentration in Feces

The effects of high-dose SZ-A (SZ-A 200, 200 mg/kg) on intestinal microbiota composition were examined by Illumina sequencing-based analysis of bacterial 16S ribosomal RNA in fecal samples collected at the end of 8 weeks treatment. Compared to the DM group, the operational taxonomic unit (OTU) numbers were reduced in the SZ-A 200 group (**Figure 2A**; p < 0.001). The Shannon and Chao indices reflect the diversity and richness of

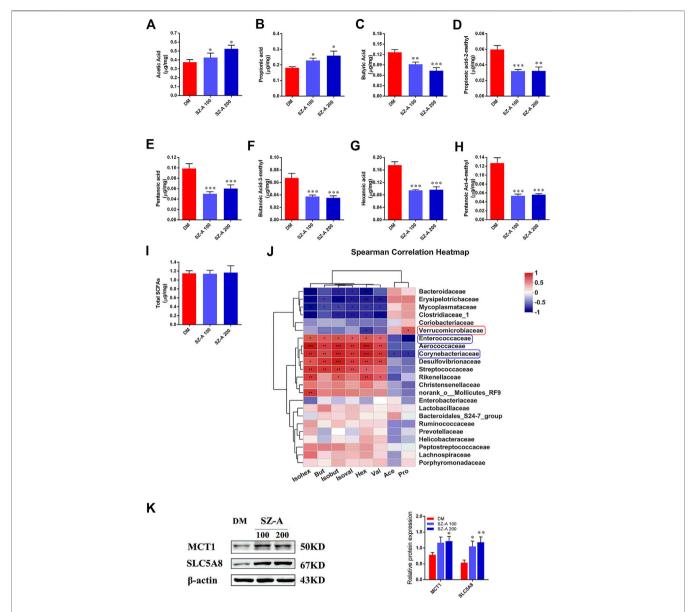


FIGURE 3 | SZ-A alters SCFA composition of fecal samples in KKAy mice. Fecal SCFA concentration, including **(A)** acetic acid, **(B)** propionic acid, **(C)** butyric acid, **(D)** propionic acid-2-methyl, **(E)** pentanoic acid, **(F)** butanoic-acid-3-methyl, **(G)** hexanoic acid, **(H)** pentanoic-acid-4-methyl and **(I)** total SCFAs. **(J)** Correlation analysis of SCFAs and specific microbiota at the family level. The p values are shown in different colors in the diagram. The blue represents negative correlation, and red represents positive correlation. n = 7-8. **(K)** MCT1 and SLC5A8 protein abundance in the ileum tissue. The blots shown are representative images. n = 6. Data are mean \pm SEM, $^*p_0 < 0.05$, $^*p_0 < 0.01$, $^{***}p_0 < 0.01$, $^{**}p_0 < 0.01$

gut microbiota, respectively. As shown in Figures 2B,C, SZ-A diminished the indices of Shannon and Chao (p < 0.05, p <0.05). Unweighted Unifrac principal coordinate analysis (PCoA) based on OTU levels revealed distinct clustering of microbiota composition in each group (Figure 2D). Multivariate analysis of variance of PCoA matrix scores revealed that the microbiota community of mice in the SZ-A 200 group differed from that of the DM group (p < 0.001). Additionally, the bacterial community of SZ-A 200-treated mice differed from that of the DM group. Taxonomic profiling at the family level revealed that SZ-A treatments elevated the abundance of Bacteroidaceae.

Erysipelotrichaceae, and Verrucomicrobia and reduced that of Rikenellaceae, Desulfovibrionaceae, and Aerococcaceae compared with DM mice (Figure 2E). Similar results were also observed at the genus level. SZ-A 200 decreased the abundance of Alistipes, Desulfovibrio, and Aerococcus, and increased the abundance of Bacteroides, Faecalibaculum, and Allobaculum compared with the DM group (Figure 2F). Collectively, these findings indicate that SZ-A 200 modulates the composition of gut microbiota.

Short-chain fatty acids (SCFAs) are generated in the gut by bacterial fermentation of dietary fiber. Fecal SCFA concentrations were quantified to assess the impact of SZ-A on bacterial metabolic

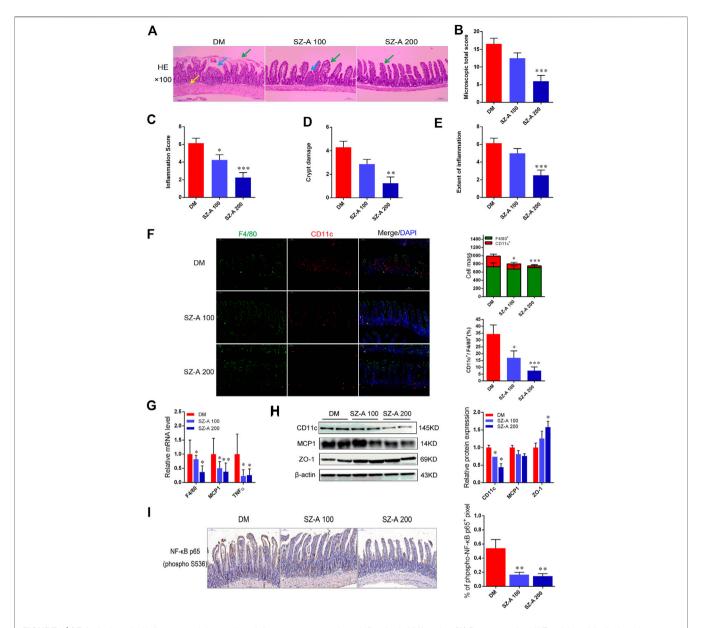


FIGURE 4 | SZ-A alleviates ileal inflammatory injury and pro-inflammatory macrophage infiltration in KKAy mice. (A) Representative H&E staining of the ileal section (scale bar, 200 μm). (B) Histopathological assessment of total score. (C) Inflammation score. (D) Crypt damages score. (E) Extent of inflammation score of ileal sections. (F) Representative F4/80 (green), CD11c (red) and DAPI (blue) immunofluorescence staining of ileum tissues (Scale bar, 100 μm). The histograms indicate quantification of F4/80 (F4/80*) or CD11c (CD11c*) positive cells per field and percentages of CD11c positive cells in macrophages (F4/80*) (n = 5 per group). (G) Real-time PCR analysis of F4/80, MCP1 and TNF-α levels in ileal homogenates (n = 5 per group). (H) CD11c, MCP1 and ZO-1 protein abundant levels. The blots shown were representative images. (I) Sections of the ileum were stained with anti-NF-κB p65 (p-S536), the histograms indicate quantification of p-NF-κB p65 positive area per field (n = 5 per group). Data were mean ± SEM, *p < 0.05, **p < 0.01, ***p < 0.001 vs. DM. DM, diabetic model group, SZ-A 100, SZ-A low-dose-treated group, SZ-A 200, SZ-A-high-dose-treated group.

activity in KKAy mice. The concentrations of acetic (p < 0.05, p < 0.05) and propionic acids (p < 0.05, p < 0.05) were elevated in both SZ-A-treated groups (**Figures 3A,B**), whereas butyric, isobutyric (propionic acid-2-methyl), pentanoic, isopentanoic (butanoic acid-3-methyl), hexanoic, and isohexanoic (pentanoic acid-4-methyl) acids decreased in the SZ-A-treated groups compared to the DM group (**Figures 3C–H**). No significant changes were observed in total SCFA concentration between the SZ-A-treated and DM groups

(Figure 3I). Subsequently, the relationship between fecal SCFAs and intestinal bacterial at the family level was analyzed (Figure 3J). The results showed that *Enterococcaceae* and *Corynebacteriaceae*, *Aerococcaceae*, *Desulfovibrionaceae*, and *Rikenellaceae* were positively correlated with the decreased SCFAs, including butyric, isobutyric, hexanoic, isohexanoic, pentanoic, and isopentanoic acids (Figure 3J). *Enterococcaceae* and *Corynebacteriaceae* abundance was negatively correlated with propionic acid, *Corynebacteriaceae*

showed no correlation with acetic acid, and *Verrucomicrobiaceae* was positively correlated and propionic acid was observed (**Figure 3J**). Several transport systems play a role in the cellular uptake of SCFAs in the gut, including monocarboxylate transporter-1 (MCT1) and sodium-coupled monocarboxylate transporter 1 (SMCT1) (SLC5A8). As the transporters responsible for the entry and transcellular transfer of these bacterial products in epithelium are critical determinants of gut function, we detected MCT1 and SLC5A8 protein expression levels in the ileum tissue after SZ-A treatment in KKAy mice. The results showed that MCT1 and SLC5A8 protein levels in ileum from SZ-A-treated mice were significantly increased compared with the DM group.

SZ-A Alleviates Ileal Inflammatory Injury and Pro-Inflammatory Macrophage Infiltration in KKAy Mice

Considering microbial SCFAs production (especially acetate, propionate, and butyrate) is essential for gut integrity by regulating the mucus production, providing fuel for epithelial cells and effects on mucosal immune function, the histological alteration of ileum tissue were evaluated by hematoxylin and eosin (H&E) staining. As shown in Figure 4A, in the DM group, a dense inflammatory cellular infiltrate was present in the mucosa and submucosa and crypts showed typical shortening. Focal crypts were lost and the surface epithelium was damaged (Figure 4A). Microscopic total score and scores for the three features (inflammation, extent of inflammation, and crypt damage) were given for each group (Figures 4B-E). Inflammation scores were significantly reduced by both doses of SZ-A (p < 0.05, p < 0.001). Moreover, microscopic total score, crypt damage score, and inflammation score were significantly reduced in the SZ-A 200 group (p < 0.001, p < 0.01, and p <0.001). Collectively, long-term SZ-A treatment prevented the development of inflammation and restored ileal barrier integrity in diabetic KKAy mice.

The KKAy mice were fed a high-fat diet (HFD) to induce diabetic syndrome. Given the critical role of M1 macrophages in HFDinduced intestinal inflammation, in parallel to those histological changes, macrophage-specific F4/80 and CD11c expression was measured to verify whether SZ-A treatment was able to modulate macrophage infiltration in the ileum tissue. As shown in Figure 4F, compared to the DM group, fewer pro-inflammatory CD11c-positive macrophages were observed in both doses of SZ-A-treated groups (p < 0.05, p < 0.001). This indicates a reduced inflammatory state after SZ-A treatment, and fully consistent with this result, we found downregulated mRNA expression of F4/80 (p < 0.05, p < 0.05) and multiple pro-inflammatory factors, including MCP1 (p < 0.05, p < 0.01) and TNF- α (p < 0.05, p < 0.05; **Figure 4G**), and also reduced CD11c protein expression in the ileum of SZ-A-treated groups (p < 0.05, p < 0.05; **Figure 4H**), compared to the DM group. Given that inflammation damages gut permeability and integrity, we also detected the protein expression levels of zonula occludens-1 (ZO-1), an intestinal tight junction component. SZ-A 200 markedly elevated ZO-1 protein levels (p < 0.05) compared to the DM group.

Nuclear factor kappa B (NF- κ B) is critically associated with the progression of inflammation and cell proliferation in the

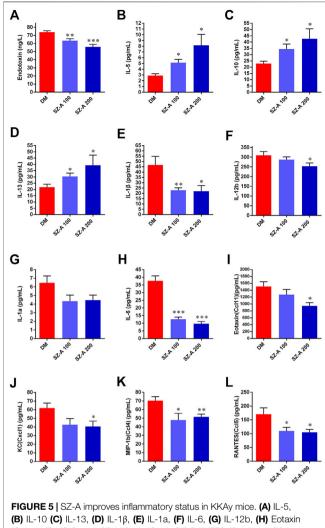


FIGURE 5 | SZ-A improves inflammatory status in KKAy mice. **(A)** IL-5, **(B)** IL-10 **(C)** IL-13, **(D)** IL-1β, **(E)** IL-1a, **(F)** IL-6, **(G)** IL-12b, **(H)** Eotaxin (Ccl11), **(I)** KC(Cxcl1), **(J)** MIP-1b (Ccl4), **(K)** RANTES (Ccl5) and **(L)** Endotoxin. Data are expressed as the mean \pm SEM, n = 8. *p < 0.05, **p < 0.01, ***p < 0.001 p s. DM. DM, diabetic model group, SZ-A 100, SZ-A low-dose-treated group, SZ-A 200, SZ-A-high-dose-treated group.

intestinal mucosa. Therefore, the effects of SZ-A on NF- κ B activity on the ileal mucosa were investigated. The indices of the phosphorylated (p-NF- κ B) p65-positive area were markedly reduced with SZ-A treatment (p < 0.01, p < 0.01; **Figure 4I**). These findings indicate that SZ-A significantly alleviated ileal inflammatory injury and attenuated the inflammatory state induced by pro-inflammatory macrophage infiltration of the ileum tissue in diabetic KKAy mice.

SZ-A Attenuates Endotoxin Content, Pro-Inflammatory Cytokine, and Chemokine Levels in Serum of Diabetic KKAv Mice

Gut dysbiosis not only leads to increased intestinal permeability, but it also results in the translocation of

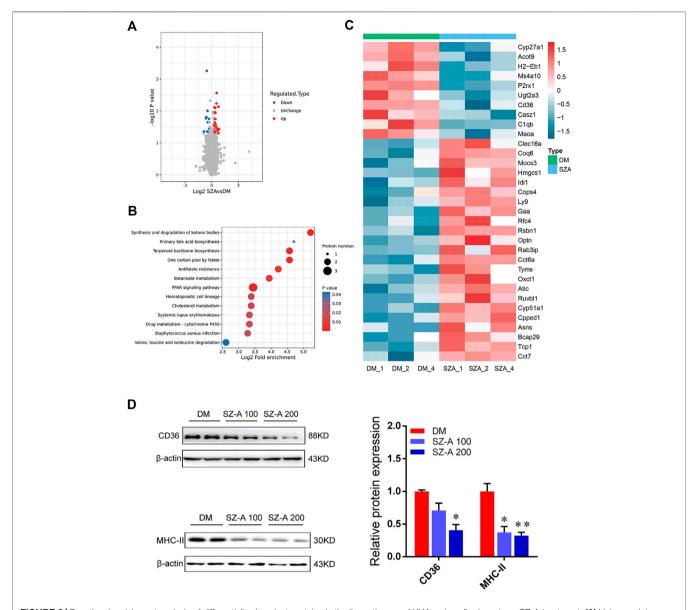


FIGURE 6 | Functional enrichment analysis of differentially abundant proteins in the ileum tissues of KKAy mice after long-term SZ-A treatment. **(A)** Volcano plot shows the differentially abundant proteins in the ileum of SZ-A-treated group (FDR <0.01). Significantly differentially abundant proteins were color-coded: red indicates upregulated proteins, blue shows downregulated proteins. Two clusters consisting of 24 upregulated and 10 downregulated proteins. **(B)** Bubble diagram of enrichment of differentially abundant proteins in KEGG. The results of the first 20 classifications with the most significant enrichment were given in the bubble diagram (ρ < 0.05). **(C)** The heat map from three independent proteomic analyses of testes from the DM and SZA group. **(D)** Validated the downregulated proteins in ileum of DM and SZ-A-treated groups by Western blotting. CD36 and MHC-II protein abundant levels. The blots shown were representative images. Data are mean \pm SEM, n = 6. *p < 0.05, **p < 0.01 vs. DM. DM, diabetic model group, SZA, SZ-A-high-dose-treated group.

bacterial products into circulation, inducing a state of chronic low-grade inflammation, such as LPS in HFD-induced diabetes. Considering the effects of SZ-A on modulating gut microbiota profiling and alleviating ileal inflammatory injury, serum endotoxin content, and levels of cytokines and chemokines were determined after SZ-A treatment of diabetic KKAy mice.

Compared with the DM group, both doses of SZ-A markedly diminished serum levels of the endotoxin content (p < 0.01, p < 0.001; **Figure 5A**), inflammatory cytokines and

also chemokines, such as interleukin 1 β (IL-1 β , p < 0.01, p < 0.05; **Figure 5E**), IL-6 (p < 0.001, p < 0.001; **Figure 5H**), chemokine ligand 4 (CCL4) (p < 0.05, p < 0.01; **Figure 5K**), and CCL5 (p < 0.05, p < 0.05; **Figure 5L**). Additionally, serum levels of IL-12 β (p < 0.05; **Figure 5F**), CCL11 (p < 0.05; **Figure 5J**) were also significantly reduced in the SZ-A 200-treated group. However, serum levels of anti-inflammatory cytokines IL-10 (p < 0.05, p < 0.05; **Figure 5C**) and IL-13 (p < 0.05, p < 0.05; **Figure 5D**) serum were markedly elevated.

Functional Enrichment Analysis of Differentially Abundant Proteins in the Ileum after SZ-A Treatment

Proteomics were used to determine the molecular characteristics of the ileum in the high-dose SZ-A-treated group (SZA) and DM group in KKAy mice. Refer to the supplementary data Supplementary Figure S1, liquid chromatography tandem mass spectrometry identified 208,219 secondary spectra. A total of 42,677 matching effective spectra were obtained. Using a false discovery rate (FDR) < 1% at the peptide and protein levels, 25,060 of the 25,816 peptides were identified as specific, and 4352 of the 5043 proteins were quantifiable (Supplementary Figure S1A). A total of 34 proteins were differentially expressed (fold change >1.2, p < 0.05; Figure 6A) between the DM group and SZA group, of which 24 proteins were upregulated and 10 were downregulated. To determine the characteristics of the differentially expressed proteins, we annotated the subcellular localization, Clusters of Orthologous Group, and Gene Ontology (GO) of the 34 proteins. Annotation of the subcellular localization showed that 44.12% of all identified differentially expressed proteins were localized in the cytoplasm, 14.71% in the plasma membrane, 14.71% in the mitochondria, 11.76% in the nucleus, 8.82% in the extracellular space, and 5.88% in the endoplasmic reticulum (Supplementary Figure S1B). Most differentially abundant proteins participated in and regulated the cellular and metabolic processes (Supplementary Figure S1C). COG functional classification revealed that most of these differentially abundant proteins played a role in posttranslational modification, protein turnover, and chaperones (Supplementary Figure S1D).

Bioinformatics analysis was performed to identify the main biological pathways and functional categories of the differentially abundant proteins (fold change >1.2; p < 0.05). Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis showed that the most significantly altered pathways were involved in primary bile acid biosynthesis, peroxisome proliferator-activated receptor (PPAR) signaling pathway, synthesis and degradation of ketone bodies, and terpenoid backbone biosynthesis (Figure 6B). We identified 34 abundant proteins that were mainly involved in the abovementioned pathways (Figure 6C). These proteins included downregulation of cluster of differentiation 36 (CD36), a protein related to the PPAR pathway; CYP27a1, the representative differentially abundant protein related to primary bile acid biosynthesis; and histocompatibility 2 class II antigen E beta, which is critical in the antigen processing and presentation pathway and is also described as major histocompatibility complex class II (MHC II). The expression level of these key regulators identified via proteomics was also confirmed by Western blotting. The results showed the level of CD36 (SZ-A 200 group; p < 0.05) and MHC II (p < 0.05, p < 0.01) were significantly reduced in SZ-A-treated groups compared to the DM group (Figure 6D), which is consistent with proteomics analysis.

DISCUSSION

In this study, we evaluated the therapeutic efficacy of SZ-A in glucose and lipid metabolism *in vivo* in the diabetic KKAy mice.

We found that SZ-A ameliorated glucose metabolism and enhanced the insulin response to oral glucose tolerance tests and elevated active GLP-1 levels in diabetic KKAy mice. We suspect that the increased glucose-stimulated insulin secretion might be primarily linked to the improved β -cell function after SZ-A treatment, or related to the elevated blood levels of active GLP-1 in KKAy mice. However, the fact that oral (current study) but not intraperitoneal injection of glucose was associated with improved glucose tolerance in KKAy mice after SZ-A treatment indicated the potential involvement of incretin hormones.

GLP-1, an incretin hormone released in response to the ingestion of nutrients, acts as a hypoglycemic hormone to improve postprandial glucose homeostasis by enhancing mealinduced insulin secretion. GLP-1 activity is mediated by the GLP-1 receptor (GLP-1R). GLP-1Rs are highly expressed in pancreatic β-cells and other tissues including neurons in specific central brain regions, the kidney, and the gut tract (Gray et al., 2020). Findings from the clinical trials have also revealed that the administration of GLP-1R agonists (GLP-1RAs) induces weight loss in addition to glucose improvement (Salehi and Purnell, 2019). In our study, we also found that both doses of SZ-A induced significant weight loss at the end of long-term treatment, whereas the glycemic-lowering effects of GLP-1RAs were mainly attributed to endocrine actions at the level of pancreatic islets. Thus, we evaluated changes in α - and β -cell mass or distribution to analyze the functional state of islets after Supplementary SZ-A treatment. In **Figure** immunofluorescence staining showed that the glucagonpositive area was significantly scattered around the islets in the DM group, suggesting the imbalanced distribution of α -cells. SZ-A decreased the ratio of glucagon-positive area and improved the distribution of a-cells.

GLP-1 is predominantly secreted by neuroendocrine L-cells in the gut. L cells, which produce both GLP-1 and peptide YY, are predominantly expressed in the distal ileum. In humans, prebiotic treatment increases microbiome diversity, which in turn may modulate levels of GLP-1 (Grasset et al., 2017). Moreover, with ileal transposition surgery, Lcells located in the transposed ileum are rapidly stimulated by ingested nutrients to produce GLP-1 (Oh et al., 2016). Given the close anatomical proximity, gut microbiota could potentially alter the nutrient-sensing capacity of enteroendocrine cells and subsequent gut peptide release. Additionally, the major components of SZ-A (DNJ, FAG, and DAB) were mainly distributed in the gastrointestinal tract. Therefore, we hypothesized that SZ-A caused the altered active GLP-1 levels, possibly by regulating gut microbiota composition. No study has investigated the effect of SZ-A on the distal ileum microbiota, a site that is crucial for intestinal sensing and absorption of nutrients. Therefore, in this study, we evaluated the interaction between SZ-A and ileal microbiota. Then the effects of SZ-A on the gut microbiota were investigated.

We first characterized the microbiota composition from DM and the high dose-SZ-A treated group (SZ-A 200). Mice were sacrificed and the luminal contents were collected from the ileum (nearly 12 cm distal to the pyloric sphincter). SZ-A increased the abundance of *Bacteroidaceae*, *Erysipelotrichaceae*, and *Verrucomicrobia*. SZ-A also markedly decreased the abundance

of Rikenellaceae, Desulfovibrionaceae, and Aerococcaceae at the family level compared with DM mice (Figure 2E). Similar results were observed at the genus level. SZ-A reduced the abundance of Alistipes, Desulfovibrio, and Aerococcus, and increased the abundance of Bacteroides, Faecalibaculum, and Allobaculum. Bacteroidetes and Verrucomicrobia play crucial roles in producing SCFAs (Harris et al., 2012). We also detected measurable fecal SCFA concentrations in the DM and SZ-Atreated groups, which is consistent with previous studies characterizing the ileal microbiota composition of diabetic KKAy mice. We observed elevated propionate and acetate in the SZ-A-treated groups (**Figures 3A,B**). Propionate and acetate are two of the main SCFAs that are produced by bacteria as a result of resistant starch fermentation. SZ-A-induced microbiota changes facilitated propionate and acetate production in the ileum, which might explain the elevated basal and glucosestimulated blood active GLP-1 levels in diabetic KKAy mice after SZ-A treatment.

The microbiota-derived metabolites in the luminal contents also represent a potential link to expression changes of nutrient sensors, ligand-receptors, or transporters. Figure 3 shows that with the exception of propionate and acetate, other SCFA concentrations in ileal luminal contents were decreased after SZ-A treatment. Several transport proteins are involved in the uptake of SCFAs in the gut, including MCT1 and SMCT1 (SLC5A8). These transporters are critical determinants of the entry and transcellular transfer of SCFAs into intestinal epithelium under physiological conditions and in disease states (Bauer et al., 2018). We detected the protein expression levels of these two transporters. There was significant upregulation in the expression of MCT1 and SMCT1 (SLC5A8) in the ileum of SZ-A-treated groups (Figure 3K), which is consistent with the decreased level of SCFAs following SZ-A treatment. Collectively, we determined a connection between SZ-A action and changes in ileal microbiota to regulate SCFA production, which in turn, affect glucose homeostasis through the regulation of GLP-1 secretion.

LPS is a major component of the cell wall of gram-negative bacteria and is considered an endotoxin when present in the blood. Increased LPS levels can induce a large number of proinflammatory responses and inflammatory cytokine release (Fuke et al., 2019). Of note, among the changes in the gut microbiota of KKAy mice after SZ-A treatment, the decreased abundance of LPS-containing Desulfovibrionaceae was observed. Desulfovbrionaceae is an endotoxin producer and has been linked to gut permeability (Clemente-Postigo et al., 2012). There is increasing evidence of the role of gut microbiota in various inflammatory diseases, especially those affecting gastrointestinal tract inflammation. Additionally, butyrate, propionate and acetate are SCFAs that are produced by bacteria as a result of resistant starch fermentation, and have anti-inflammatory properties (Blaak et al., 2020). Due to these effects of SZ-A on the composition of the gut microbiota, it is speculated that SZ-A treatment might repair the inflammatory damage of intestine by modulating the abundance of LPS and SCFA-producing gut microbiota.

Subsequently, H&E staining was performed on the ileum of KKAy mice after SZ-A treatment. Three different sections were studied for each animal. Histological inflammation was scored by two blinded investigators using a modified scoring system

(Dieleman et al., 1998). Considering the degree of inflammation, the transmural vertical extent of inflammation, and the crypt damage score, related to the percentage of involvement of mucosal surface in each slide. As shown in Figures 4A-E, this finding supported the occurrence of damage of the ileal mucosal barrier in diabetic KKAy mice (DM group) and repaired ileal inflammatory damage after treatment with both doses of SZ-A. LPS production is also responsible for inducing monocyte- and macrophage-mediated inflammation in the intestine (Wang et al., 2020). Gut macrophages, which reside in the connective tissue underlying the gut epithelium, the lamina propria, are considered key players for the maintenance of intestinal homeostasis and inflammation (Yang et al., 2020). We observed that in ileal tissues, the percentage of macrophages (CD11c+/F4/80+) and the cell mass of CD11c-positive monocytes were significantly decreased with both doses of SZ-A compared with the control (Figure 4F). The degree of expression of F4/80, MCP-1, and TNFa mRNA in both SZ-A-treated groups was significantly decreased compared to the DM group. Similarly, the protein levels of CD11c and MCP1 in the ileum were also reduced by SZ-A treatment (Figures 4G,H). The NF-κB signaling pathway was also detected in the ileum. The phosphorylation of p65 and its nuclear translocation were significantly decreased by SZ-A treatment. These results suggest that SZ-A treatment ameliorate ileal inflammatory damage in KKAy mice with down-regulated inflammatory signaling pathways partly via reducing the monocyte recruitment in the iluem.

Over time, major inflammatory signals (e.g., NF-κB-dependent) become activated in diabetic KKAy mice, thereby stimulating proinflammatory cytokine secretion in the small intestine. This inflammatory state might subsequently exacerbate the disruption of the mucus layer barrier and increase epithelial permeability of the small intestine. We observed increased protein levels of the tight junction protein ZO-1 in the SZ-A-treated group, which can reflect the intestinal mucosal barrier function. Our results also confirmed the results that the intestinal mucosal barrier function was improved after treatment of KKAy mice with SZ-A. The persistent inflammatory state not only increases intestinal permeability but also the destruction of tight junction proteins attached to epithelial cells, increasing portal vein and systemic plasma LPS concentrations, and eventually promoting the development of systemic inflammation (Clemente-Postigo et al., 2012). Therefore, we subsequently determined the concentrations of endotoxin and inflammatory cytokines in the serum of KKAy mice. The serum endotoxin levels significantly decreased after both doses of SZ-A treatment, compared to the DM group. The serum levels of inflammatory factors (e.g., IL-1β, IL-6, CCL4, and CCL5) indicated that low-grade inflammation in diabetic KKAy mice decreased after SZ-A treatment, which corresponded to the endotoxin level. Thus, ileal inflammatory damage in the diabetic KKAy mice was positively associated with low-grade inflammation, which was effectively alleviated by SZ-A treatment.

The production of pro-inflammatory cytokines is related to the LPS-induced activation and polarization of macrophage. We observed there was significantly suppressed polarization of macrophages in the ileum after SZ-A treatment in diabetic KKAy mice. The molecular characteristics of the ileal tissues in the high-dose SZ-A and DM groups in diabetic KKAy mice

were investigated through proteomics. Proteomics analysis revealed that monocyte differentiation into intestinal macrophages involves phenotypic changes with MHCII expression was downregulated by SZ-A treatment, which may be responsible for the improvement of ileal inflammatory damage after SZ-A treatment. Beyond that, the representative differentially downregulated abundant proteins related to PPAR pathway and fat digestion and absorption, ileal CD36 expression level was significantly decreased in SZ-A-treated groups (Figure 6D), which might be related to improved blood triglyceride levels.

CONCLUSION

Here, we reported that long-term treatment of SZ-A (8 weeks) is sufficient to alter the microbiota composition in the ileum of diabetic KKAy mice. Our data, together with enriched literature, provide novel mechanistic insights into the role of SZ-A in mediating gut microbial community in ileal inflammatory damage and glucose metabolism.

DATA AVAILABILITY STATEMENT

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found below: NCBI SRA; BioProject ID PRJNA701784. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD024241.

ETHICS STATEMENT

The animal study was reviewed and approved by the Institutional Animal Care and Use Committee of the Institute of Materia

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AUTHOR CONTRIBUTIONS

QL, SL: Conceptualization, Methodology, Software. QL, SL: Data curation, Writing- Original draft preparation. HC, CL, and WJ: Visualization, Investigation. YH, LL, YF, and XG: Software, Validation. ZS and YL: Writing-Reviewing and Editing. SL, ZS: Supervision.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.642400/full#supplementary-material.

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Methanolic Extract of Lysimachia Candida Lindl. Prevents High-Fat High-Fructose-Induced Fatty Liver in Rats: Understanding the Molecular Mechanism Through Untargeted Metabolomics Study

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Fatty liver is one of the most common metabolic syndrome affecting the global population. Presently, limited treatment modalities with symptomatic approach are available for alleviating fatty liver. Traditional and herbal treatment modalities have shown evidence to improve the disease pathology. In the present research work, evaluation of a selected medicinal plant Lysimachia candida Lindl. was carried out to investigate its beneficial effects on fatty liver disease in rats. Male Sprague Dawley (SD) rats were fed with high-fat high-fructose diet to induce fatty liver phenotypes. After induction for 15 weeks, methanolic extract of Lysimachia candida Lindl. (250 mg/kg b. w. p. o.) was administrated to the rats daily for the next 17 weeks. Blood samples were collected at different time points to analyze fasting blood glucose levels and relevant biochemical parameters important for the assessment of metabolic disease phenotypes. Liquid chromatography-mass spectrometry (LC-MS) based metabolomics was done to study the dynamics of metabolic changes in the serum during disease progression and how the medicinally important plant extract treatment reversed the metabolic diseases. Multivariate data analysis approaches have been employed to understand the metabolome changes and disease pathology. This study has identified the interplay of some metabolic pathways that alter the disease progression and their reversal after administration of the plant extract. Different group of metabolites mainly bile acids, fatty acids, carnitines, and their derivatives were found to be altered in the diseased rats. However, all the metabolites identified between control and disease groups are mainly related to lipid metabolism. The results depict that the treatment with the above-mentioned plant extract improves the regulation of aberrant lipid metabolism, and reverses the metabolic syndrome phenotype. Therefore, the present study reveals the potential mechanism of the herbal extract to prevent metabolic syndrome in rats.

Keywords: animal model, herbal extract, LC-MS/MS, bile acids, fatty acids, PPARa

INTRODUCTION

The condition in which surplus lipids accumulate in the hepatocytes is known as fatty liver or hepatic steatosis (Allison, 2004). Accumulation of more than 5% lipids in hepatocytes is known as hepatic steatosis as the human liver does not have much capacity to store lipids (Li et al., 2018). Alcohol, chronic hepatitis C, Wilson's abetalipoproteinemia, and porphyria cutanea tarda are mostly found to be associated with hepatic steatosis. Medications like steroids, tamoxifen, and amiodarone are found to precipitate hepatic steatosis (Allison, 2004). Fatty liver disease can be categorized into two main types: non-alcoholic fatty liver disease (NAFLD) and alcoholic fatty liver disease (AFLD) (Singh et al., 2017). NAFLD is a chronic and progressive disease starting from non-alcoholic fatty liver (NAFL) to hepatic cirrhosis and ultimately leading to hepatocellular carcinoma (Sarkar et al., 2020). As per recent prevalence status, 20-46% of the world population has been stated to suffer from NAFLD (Li et al., 2018) with 15-40% patients in the western countries and 9-40% in Asian countries (Amarapurkar et al., 2007). There are no particular clinical symptoms of NAFLD other than discomfort in the right upper quadrant and fatigue. Some other signs include hepatomegaly, splenomegaly, spider naevi, and palmar erythema, although in most cases, the disease is asymptomatic with no signs of clinical manifestation (Allison, 2004).

NAFL is initiated by the deposition of small lipid droplets in hepatocytes, and overtime accumulation of these lipid droplets triggers lipotoxicity. The circulating cytokines together with elevated hepatic reactive oxygen species induce lobular inflammation, which results in the typical characteristic feature of non-alcoholic steatohepatitis (NASH) called hepatocellular ballooning. At advanced stages, the replacement of hepatic tissue with collagen results in the development of fibrotic scar tissues and leads to hepatic cirrhosis and ultimately hepatocellular carcinoma (Rinella, 2015; Carr et al., 2016; Foulds et al., 2017). The histopathological features of NAFLD are similar to alcoholic hepatic damage. Despite extensive research in understanding the pathophysiology of fatty liver diseases, there are still no targeted treatments available till date. The current treatment modalities for AFLD are identical to what it was 50 years ago i.e., abstinence, nutritional support, and corticosteroids (or pentoxifylline unless steroids are contraindicated). Whereas those for NAFLD include weight loss and co-morbidity management (Singh et al., 2017).

There are several evidences where traditional or herbal remedies are found to be useful in ameliorating several pathological features of fatty liver (Xiao et al., 2013). Based on the evidence to practice in North-east part of India by local people, we have selected a plant known as *Lysimachia candida* Lindl. belonging to the family *Primulaceae* (Yang et al., 2012). The plant is native to the north-east region of India and mainly found in Assam and Manipur states. It is commonly known as

loosestrife or kengoi in Manipuri. It is reported to have some pharmacological activity such as ailment of fever, swelling, fracture of bone, dermatitis, and antifungal activity (Xia et al., 2013). This plant has not been explored for its pharmacological effects on fatty liver disease. We have chosen this plant to explore its beneficial effect on fatty liver and validate this plant in the context of its therapeutic effects.

We have demonstrated that feeding high-fat high-fructose (HFHF) diet to Sprague Dawley (SD) rats over a period of 32 weeks not only induces fatty liver phenotypes such as and histopathological changes but also biochemical differentially regulates the level of several metabolites such as bile acids, unsaturated fatty acids and other metabolites involved in inflammation and homeostasis. Therefore, using the untargeted metabolomics approach, the metabolomic profile of rat serum from all three groups were used to identify the different metabolites involved in disease development and how the reversal of disease happens after the intervention of treatment. We identified various metabolites with the help of liquid chromatography-mass spectrometry (LC-MS) and both the enrichment and the pathway analyses demonstrated that peroxisome proliferator-activated receptor alpha is a central pathway through which Lysimachia candida Lindl. extract may show a beneficial effect on fatty liver.

MATERIALS AND METHODS

Plant Collection and Identification of Bioactive Compounds

The whole plant Lysamachia candida Lindl, were collected from Moirang Kampu, Manipur (Latitude: 25°5'31.995"N to 24°39'45.25"N; Longitude: 94°8'49.324"E to 93°53'47.559"E) in June and July 2017. The Botanical Survey of India, Eastern Regional Centre, Shillong, Meghalaya authenticated the plant (Accession No. 95588). The Lysimachia candida Lindl. plant was air-dried for 2-3 weeks and then pulverized to a fine powder by the electric grinder. Exhaustive extraction was performed in a Soxhlet apparatus for 11 h using methanol (Merck) as a solvent. After which, the extract was concentrated under reduced vacuum pressure at 40°C in a rotary vacuum evaporator. The concentrated extracts were further lyophilized using Eyela Freeze Dryer (FDU-506, United States). 1 kg of fresh plant material yielded 100 g of dry powder losing 90% of moisture content and from extraction 1 kg plant material using methanol as solvent yielded 80 gm of dry extract. The final yield of methanolic extract was 8% w/w. Finally, the lyophilized extract was tested for residual methanol present using GC-MS and stored in a sterile container and placed at -20°C until further use. The stored lyophilized extract did not show the presence of any methanol. The extract was reconstituted in 100% methanol to identify bioactive compounds in LC-MS and LC-MSMS. The Orbitrap Fusion Mass Spectrometer was used to acquire data that is fitted with heated electrospray ionization (HESI) source. Both the negative and positive ions were scanned

at 120,000 resolution in the MS1 mode and 30,000 resolution in the data-dependent MS2 scan mode. The spray voltage of 4,000 and 35,000 V were set for positive and negative modes, respectively. Auxiliary gas and Sheath gas were used and set to 11 and 42, respectively. The Mass scan analyzer was set to scan in the range of 50-1,000 m/z. For MS we have used an automatic gain control target of 200,000 ions with maximum injection time at 80 ms and 20,000 ions were used as an automatic gain control target at a maximum injection time of 60 ms for MSMS analysis. The methanolic extract was separated using HSS T3 column (100 \times 2:1 mm i. d. 1.7 μ m, Waters) in "UPLC Ultimate 3,000" and the temperature was maintained at 40°C. Mobile phase A containing water with 0.1% formic acid and acetonitrile with 0.1% formic acid was used in mobile phase B. The elution conditions were followed as 0 min, 1% B; 1 min, 15% B; 4 min, 35% B; 7 min, 95% B; 9 min, 95% B; 10 min, 1% B; and 14 min, 1% B with flow rate of 0.3 ml/min and 5 µl sample was injected. The data has been processed using Progenesis QI software with an untargeted approach. We have used different libraries of natural products i. e., spectral data matching with mzCloud and MassBank, Global Natural Products Social Molecular Networking (GNPS) for metabolite identification and in-house developed library of compounds based on purchase authentic metabolites standards and predicting the retention time of metabolites not available with us. Metabolites were confirmed through accurate mass, MS/ MS fragmentation and retention time matching.

Animals

To evaluate the potential effect of Lysimachia candida Lindl. on fatty liver, male Sprague Dawley (SD) rats were fed with high-fat high-fructose (HFHF) diet for 32 weeks. The animal protocols were approved by the Institutional Animal Ethics Committee (IAEC) of Translational Health Science and Technology Institute (THSTI), Faridabad, India (Protocol No. BIO-IAEC-3357). The study was performed in AAALAC accredited facility in Bioneeds Pvt. Ltd. Male SD rats aged between 8-12 weeks (200-250 g) was maintained at uniform laboratory conditions in standard steel cages and provided with food and water ad libitum during the study period. Rats were housed under standard laboratory conditions environmentally monitored, air-conditioned room with fresh air supply (12-15 air changes per hour), room temperature 22 ± 3°C and relative humidity 30-70%, with 12 h light and 12 h dark cycle. The temperature and relative humidity were recorded once daily.

Study Design and Sample Collection

The plant extract was evaluated in rats using a curative model. Animals were randomly divided into three groups viz., control group, high-fat high-fructose (HFHF) group, and treatment group. All studies were carried out using six rats (n=6) in each group. In the control group, the rats were fed with a normal chow diet for 32 weeks. At starting rats from the other two groups were fed with a high-fat high-fructose diet (Catalog no. D16030909, Research Diet, Inc. United States) for 15 weeks. After 15 weeks, the animals were selected and randomized into two groups viz., vehicle control (HFHF) and test group (Treatment), based on their fasting blood glucose level. The

dose was selected based on efficacy study, LD50 was measured and it is found that dose is safe until 2.5 gm/kg oral dose. We chose one tenth of the dose as efficacy dose. 0.3% CMC vehicle and the plant extract (250 mg/kg/day) in the same vehicle were administered via oral gavage to the HFHF group and treatment group respectively, for 17 weeks along with HFHF diet. At the end of the study, the blood samples were collected in 2 ml ependroff tubes from the retro-orbital sinus for serum isolation. The animals were sacrificed and the liver was collected at the end of the study. All the serum samples and liver were stored at $-80^{\circ}\mathrm{C}$ immediately for further use.

Bodyweight and Food Intake

Changes in body weight and food intake patterns of rats in all groups were noted throughout the experimental period. The weight of each rat was recorded on day 0 and at weekly intervals throughout the study. The quantity of food consumed by each group was recorded weekly.

Blood Glucose Level

Fasting blood glucose level was measured at day 0 (basal), before test item administration and thereafter once in 2 weeks throughout the experimental period. Animals were fasted overnight (approximately 12–16 h) before the experiment. Blood glucose level was measured using a Code-free glucometer through the tail prick method.

Intraperitoneal Glucose Tolerance Test

Overnight fasted (12 h) rats from all groups were subjected to IPGTT at the end of study period. Freshly prepared glucose load of 2 g/kg of body weight was injected intraperitoneally (i.p.) just before 0 min of the experimental timepoint and a drop of blood was withdrawn from the tail vein by small puncture using a needle. Using a commercially available glucometer, blood glucose level was analyzed at 0, 15, 30, 60, and 120 min after injecting the glucose load.

Biochemical Analysis

Serum and tissue triglycerides (TG) assay (Cayman Chemical, Triglyceride Colorimetric Assay Kit), free fatty acids (FFA) assay (FFA Kit, Biovision), and insulin assay (Insulin Kit, Cayman Chemical) were performed according to the instructions provided by the manufacture. For the hepatic TG, liver tissues of each rat were homogenized in NP-40 lysis buffer and centrifuged at 12,000 g for 30 min at 4°C.

Histopathology

At the end of the experimental period, each animal was sacrificed and tissues were collected and washed by buffered normal saline. Tissues were fixed into 10% formalin solution and then dehydrated through graded alcohol series (70–100%), cleared in xylene, and embedded in paraffin. 5–6 µm thick paraffin sections were cut and stained with hematoxylineosin (H&E) and Masson's trichome (MT). Cryopreserved samples were used for Oil-O-Red (OOR) staining. These slides were investigated and analyzed under a light microscope at 40X and 60X magnification.

Metabolomics Analysis Metabolomics Sample Preparation

Prior to experimentation, the serum samples were thawed at 4°C and kept for 30 min(s). Then, metabolite extraction was carried out by adding 150 µl of ice-cold 100% methanol (LCMS-grade, Merck) in 50 μl serum. The samples were briefly vortexed ~30 s and left on ice for 20 min(s) protein precipitation. Then, samples were centrifuged at 10,000 rpm for 10 min at 4°C. Approximately 150 µl of the supernatant was collected and divided into two microcentrifuge tubes and evaporated to dryness in a vacuum dryer. The samples were stored at -80°C until data acquisition. For reverse-phase chromatography, samples were resuspended in 100 µl of water: methanol (15:85, V/V) and for polar phase chromatography samples were resuspended in 100 µl of water: acetonitrile (50:50, V/V). After brief vortexing, the mixture was centrifuged at 10,000 rpm for 10 min at 4°C. All the supernatants were collected in fresh vials. A Quality Control (QC) sample was prepared by pooling 10 µl from each vial in a microcentrifuge tube (Naz et al., 2017).

Metabolite Measurement

Sample acquisition was done on Dionex Ultimate 3000 RS LC (Thermo Scientific) coupled with Orbitrap fusion MS (Thermo Scientific). Electrospray ionization was used for the better coverage and identification of polar and nonpolar metabolites. Metabolites were separated on reverse phase (C18) and hydrophilic interaction chromatography (HILIC column) in separate runs. The data was acquired in positive and negative ionization modes. The reverse phase column was HSS T3 and the HILIC column was XBridge BEH Amide (Waters Corporation). For, polar compound separation, solvent A was 20 mM ammonium acetate in the water of PH 9.0, and mobile phase B was 100% acetonitrile. The elution gradient starts from 85% B to 10% B over 14 min with a flow rate of 0.35 ml/min. For the reverse-phase, Solvent A was water and B was methanol with 0.1% formic acids added in both. The elution gradient starts with 1% B to 95% B over 10 min with a flow rate of 0.3 ml/min (Yuan et al., 2012; Kumar et al., 2020).

For each sample, injection volume was $5\,\mu l$ and column temperature was kept at $40^{\circ}C$. The MS1 mass scan range was set to 65–1,000 da. The resolution for MS was 120,000 and for MSMS was 30,000. The MSMS analysis was acquired in ddMS2 mode. The flow rate for Auxiliary and Sheath gas was set at 42 arbs and 11 arbs, respectively. The spray voltage was $3.5\,kV$ for positive mode and $3.0\,kV$ for negative mode. The temperature of the vaporizer was $310^{\circ}C$ and the capillary temperature was $300^{\circ}C$. Pool quality control (QC) sample was run after every five samples to monitor signal variation and drift in mass error.

Data Analysis

Metabolomic data analysis was done using compound discoverer (Thermo Scientific) 3.0. Retention time alignment, peak picking, and database search were done in compound discoverer 3.0 with default settings. Metabolite identification was done using the in-house library with retention time, accurate mass, and fragmentation pattern. Additionally, we

used spectral library downloaded from different online databases. All features whose fragmentation score > 30% and retention time were within \pm 0.5 min of the in-house library and a CV score of < 30% in the QC samples were selected for further statistical analysis. The statistical analysis and pathway enrichment analysis were done on freely available online metabolomics data analysis tool, MetaboAnalyst (https://www.metaboanalyst.ca/). One-way analysis of variance (ANOVA) and Bonferroni's test was applied to compare values between control and treated groups using Graph Pad Prism. Results were expressed as mean \pm standard deviation (SD). The values depicting p < 0.05 were considered as statistically significant.

RESULTS

Characterization of Methanolic Extract of Lysimachia Candida Lindl. by Liquid Chromatography-Mass Spectrometry

The methanolic extract of Lysimachia candida Lindl. was characterised LC-ESI-MS/MS. The LC-MS/MS chromatographic profile (both negetaive mode and positive mode) showed the presence of several metabolites which include trans-3-indoleacetic acid. L-phenylalanine, N-methylalanine, dehydrophyto sphingosine, 3-phenyllactic acid, azelate, 3,5 dimethoxycinnamic acid and cinnamic acid (Supplementary Figures S1, S2). All these compounds were identified by MS/MS fragmentation pattern (Supplementary Figure S3A-I).

Effect of Methanolic Extract of Lysimachia Candida Lindl. on Body Weight of High-Fat High-Fructose Diet-Fed Rats

During the experimental period, increase in body weight was observed in all the groups. A substantial increase (p < 0.001) in body weight was observed in HFHF diet-fed animals (**Figures 1A,B**) when compared to normal chow diet animals (Control). Significant (p < 0.001) reduction of body weight gain was observed in HFHF diet-fed animals treated with a dose of 250 mg/kg p. o. methanolic extract of *Lysimachia candida* Lindl. over a period of 17 weeks (**Figures 1A,B**).

Effect of Methanolic Extract of Lysimachia Candida Lindl. on Fasting Blood Glucose Level and Insulin Resistance in the High-Fat High-Fructose Diet-Fed Rats

The study showed that there was an increase in fasting blood glucose levels after 15 weeks of HFHF diet. Fasting blood glucose levels were further increased after 17 weeks of HFHF diet (**Figure 1C**). Oral administration of methanolic extract of *Lysimachia candida* Lindl. to the HFHF-fed animals for 17 weeks showed alleviation in the fasting blood glucose levels (**Figure 1C**).

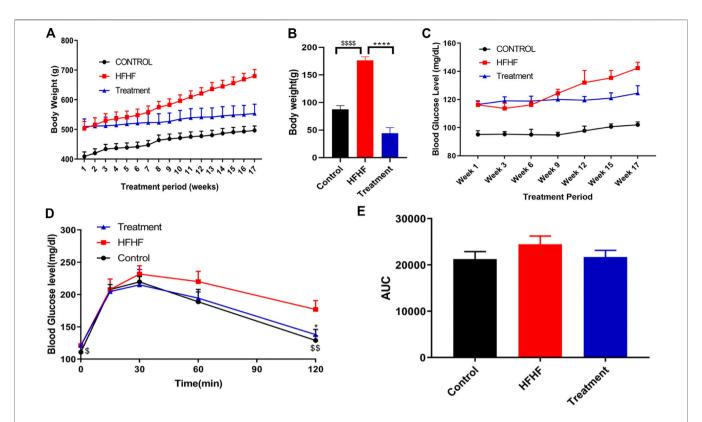


FIGURE 1 | Effect of *Lysimachia candida* Lindl. extract administration on the physical parameters of rats **(A)** Body weight, **(B)** Body weight change, **(C)** Fasting blood glucose, **(D)** IPGTT, **(E)** AUC of glucose level. Data are expressed as mean \pm SD (n = 6) each group, p < 0.0001 **** signifies the statistical difference between HFHF and Treatment, p < 0.05 * signifies the statistical difference between HFHF and Control, p < 0.005 \$\$ signifies the statistical difference between HFHF and Control.

Intraperitoneal glucose tolerance test (IPGTT) was carried out to check insulin resistance of the different experimental groups. As compared to the HFHF group, administration of methanolic extract of *Lysimachia candida* Lindl. prevented the rise in serum glucose levels after 17 weeks of treatment (**Figure 1D**). Similarly, the area under the curve (AUC) of glucose level in the IPGTT also reveals that HFHF groups have a higher area than control whereas treatment with the extract reduced the AUC to that of the Control group (**Figure 1E**).

Effect of Methanolic Extract of Lysimachia Candida Lindl. on Biochemical Parameters of the High-Fat High-Fructose Diet-Fed Rats

To further explore the effectiveness of the *Lysimachia candida* Lindl. extract, biochemical parameters in the HFHF diet-fed rats were monitored. As shown in **Figure 2A**, serum insulin level was markedly increased in the HFHF group compared to the Control and treatment groups at the end of the study. Similarly, the HOMA IR data confirmed that there was remarkable insulin resistance in the HFHF group when compared to the other two groups. The increased levels of serum insulin and HOMA IR were decreased in the treatment group when compared to the HFHF group (**Figures 2A,B**). The increased level of serum and hepatic

triglycerides (TG) in the HFHF group was decreased to the baseline in the treatment group (Figures 2C,D). However, there was no change in the serum of FFA levels among the three groups (Figure 2E). Similar to the change in TG level, increased hepatic FFA was observed in the HFHF group and it decreased after treatment (Figure 2F). Taken together, these data showed that the biochemical parameters were remarkably recovered to baseline in the treatment group although data were not statistically significant.

Effect of Methanolic Extract of Lysimachia Candida Lindl. on Histological Changes in High-Fat High-Fructose Diet-Fed Rats

To examine the histological changes in all the groups, the slides were stained with H&E, Masson's Trichrome stain and Oil-O-Red. H&E-stained liver sections of the control group revealed the normal hepatic structure and no hepatocellular ballooning and degeneration characterized by cell swelling with empty intracellular content, indicating cell necrosis and inflammation. By contrast, the liver histology of the HFHF group showed discernible changes such as increased fat accumulation, as well as ballooning and degeneration of hepatocytes. Interestingly, the liver sections of the treatment group showed no to mild ballooning and degeneration of

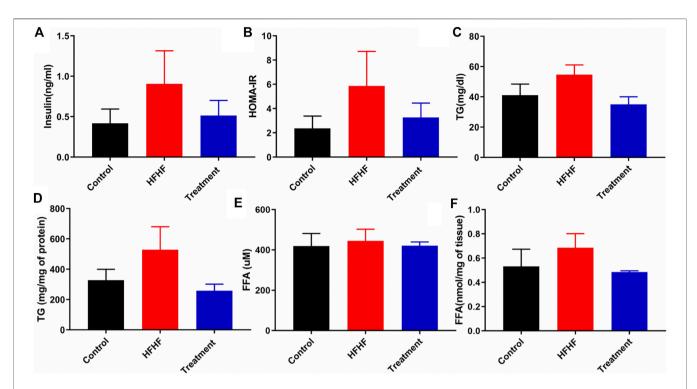


FIGURE 2 | Effect of Lysimachia candida Lindl. extract administration on the serum and liver levels of biochemical parameters of rats (A) Serum insulin, (B) HOMA IR, (C) Serum triglycerides, (D) Liver triglycerides, (E) Serum free fatty acid, (F) Liver free fatty acid. Data are expressed as mean ± SD (n = 6) each group, compared with HFHF group.

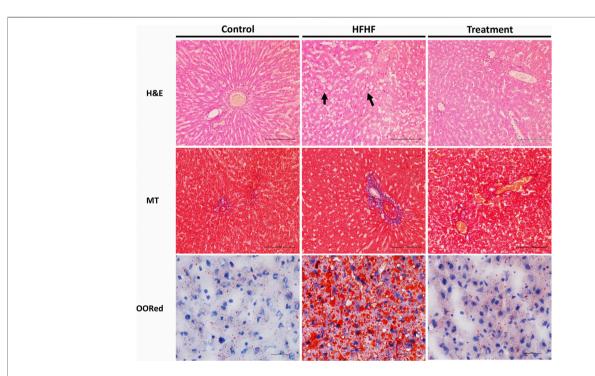


FIGURE 3 | Representative sections of rat liver showing histological alteration in the liver by H&E stain (40X) arrows indicating fat globules, MT stain (40X) indicating fibrosis, and Oil-O-Red stain (60X) indicating the fat accumulation.

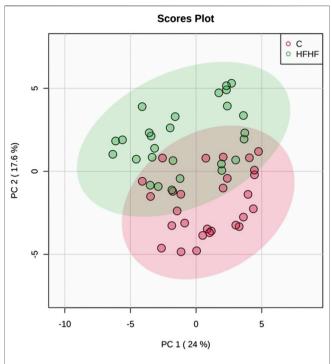


FIGURE 4 Metabolomic analysis of HFHF induced fatty liver. Principal component analysis (PCA) of control and high-fat high-fructose fed rat at different time points.

hepatocytes. It seems to be in the recovery stage as the central vein was found to be slightly dilated but cells were healthy (Figure 3). Masson's Trichrome stained sections did not show much changes in collagen fiber pattern except a little thinning of connective tissue around the portal tracts of HFHF diet-fed animals (HFHF) as compared to control. Interestingly, treatment group animals did not show any such thinning effect (Figure 3). Oil-O-Red staining unveiled huge macrovascular lipid accumulation in all areas of the lobe indicating steatohepatitis in the HFHF group when compared to the Control and Treatment groups. However, *Lysimachia candida* Lindl. extract treatment reduced the lipid droplets to the levels observed in the control group (Figure 3).

Effect of Methanolic Extract of Lysimachia Candida Lindl. on Metabolite Profiling of High-Fat High-Fructose Diet-Fed Rat Serum

To understand the mechanism by which methanolic extract of *Lysimachia candida* Lindl. treatment reverses the disease pathophysiology in high-fat high-fructose (HFHF)-fed rats, we conducted untargeted metabolic profiling using orbitrap fusion mass spectrometry (MS) coupled with ultraperformance liquid chromatography (UPLC). To maximize the coverage of different classes of metabolites and to identify the different classes of metabolites, we have run the rat serum on reverse phase and hydrophilic column. We have identified a total of 155 metabolites in serum samples after combining data from the positive and negative modes (**Supplementary Table**

S1). Principal component analysis (PCA) has clearly indicated a good separation between the control and HFHF rat serum metabolome. As shown in Figure 4, principal component 1 explains 24% of data and principal component 2 explains 17.6% of the data. The third component explains another 10.9% of the data, then fourth and fifth components explain 7.2 and 4.6% of data respectively. Total variation explained by all the five components is 64.3%. Further, we did a clustering analysis of data to visualize the different metabolites in more detail. Comparison among control, HFHF, and treatment have been done by ANOVA and significantly altered metabolites have been shown in the heatmap (Figure 5). Comparison between control and HFHF rat serum metabolites using clustering indicated the change in bile acids, biosynthesis of unsaturated fatty acid, carnitines, and other metabolites involved in the peroxisome proliferator-activated receptors (PPAR) pathways (Figure 5). Interestingly, the expression of these metabolites has been found to be reversed in the Treatment group. The expression of metabolites such as (+/-) 8-hvdroxv eicosapentaenoic acid ((+/-)8-HEPE),pentadecanoic acid, and heptadecanoate was decreased in HFHF group and reversed after the treatment with the plant extract. Similarly, different bile acid levels such as muricholic acid, deoxycholic acid, glycocholic acid, glycochenodeoxycholic acid, and glycodeoxycholic acid were decreased in the serum of HFHF group rats and were found to be normalized after plant extract treatment in early time points (Figure 5). We have also observed that unsaturated fatty acids like linoleic acid and α -eleostearic were decreased in the HFHF group and reversed after treatment (Figure 5). Pathway analysis using metaboanalyst using different metabolites showed that important pathway intervene were linoleic acid metabolism, biosynthesis of unsaturated fatty acids, glycerophospholipid metabolism, and primary bile acid biosynthesis pathway (Figure 6).

DISCUSSION

Non-alcoholic fatty liver disease (NAFLD) is increasingly recognized as a major health problem in developed and developing countries. It includes a spectrum of liver disease ranging from simple steatosis to non-alcoholic steatohepatitis (NASH), advanced fibrosis, and rarely, progression to cirrhosis. NAFLD is associated with several diseases like obesity, insulin resistance, type 2 diabetes mellitus, hyperlipidemia, hypertension, and metabolic syndrome (Bedogni et al., 2005). It has been shown that NAFLD is strongly associated with the features of metabolic syndrome. Insulin resistance is a key pathogenic factor in both NAFLD and metabolic syndrome. Data from experimental and clinical studies indicate that NAFLD may be the hepatic manifestation of metabolic syndrome (Marchesini et al., 2001). There are no drugs i.e., small molecules approved by the FDA to treat NAFLD or NASH. However, few pharmacological modalities have been practiced to ease the associated co-morbidities. Considering the presence of several active biomolecules in herbs and their well-

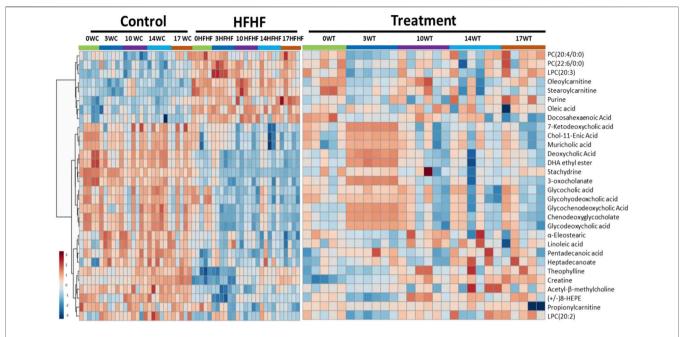
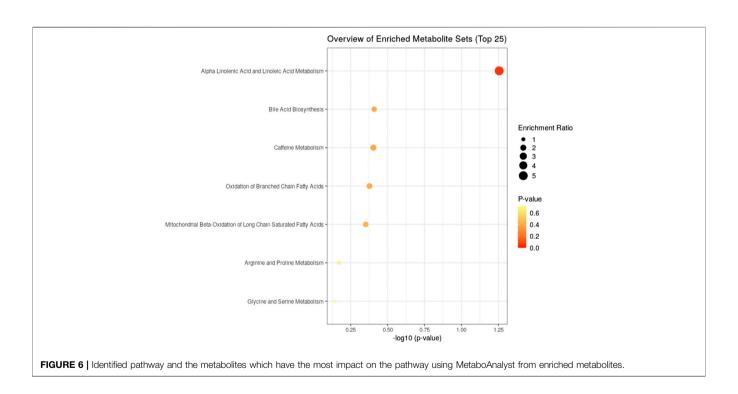


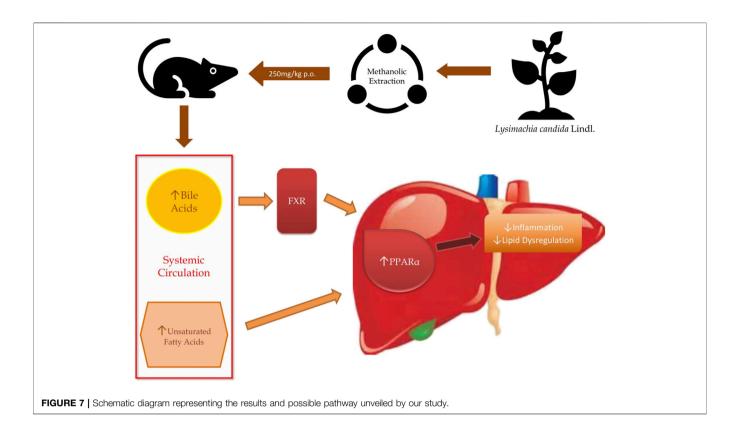
FIGURE 5 | Metabolomic analysis of HFHF-induced fatty liver and the effect of the treatment (Lysimachia candida Lindl.). Heat map analysis of different metabolites depicting the effect of treatment on the altered metabolites. Hot (red) colour indicates high expression and cool (blue) colour represents low expression.



proven role in health and disease, further research is necessary to confirm the therapeutic role of herbs in patient with NAFLD. Few herbal preparations have already found to be beneficial in ameliorating several pathological features of fatty liver (Hong et al., 2006; Park et al., 2006; Bose et al., 2008; Chidambaram et al., 2010). Here, in the present study, we have selected the

plant *Lysimachia candida* Lindl. widely used by the native population of the northeastern region to cure different metabolic disease, to explore its potential role in preventing HFHF-induced fatty liver in SD rats.

Previously, we and others showed that chronic feeding of highfat high-fructose diet causes increase in body weight, insulin



resistance, and hyperglycemia (Nizami et al., 2019). In the present study, we have observed a remarkable increase in body weight in the HFHF group indicating obesity in rats. However, reduction in body weight was observed in high-fat high-fructose diet-fed rats after treatment with methanolic extract of Lysimachia candida, with not much change in its timeline. Similarly, fasting blood glucose (FBG) level was found to be decreased in the treatment group. The data clearly demonstrate that the methanolic extract of Lysimachia candida Lindl. was able to control the FBG levels in the treatment group. The IPGTT curve and its area under the curve reveals that there is an increase in insulin resistance in HFHF group. High levels of insulin were also observed in the HFHF group contrary to the Control group. Insulin resistance in the HFHF was confirmed by the increase in the HOMA IR whereas the treatment with methanolic extract of Lysimachia candida Lindl. alleviated the HOMA IR near to the Control, suggesting its potential activity to combat insulin resistance. To check the lipid levels, we measured the TG and FFAs in both serum and hepatic tissue. We found that the serum and hepatic triglyceride levels were increased in the HFHF group while TG levels decreased in the Treatment group when compared with Control. Hence, again the methanolic extract of Lysimachia candida Lindl. was successfully able to normalize the TG levels in both serum and liver. Similarly, high levels of hepatic FFAs were observed in the HFHF group, which was decreased after treatment. Therefore, the methanolic extract of Lysimachia candida Lindl. is capable of reversing and managing body weight changes, FBG, insulin resistance, TG, and FFA levels.

Histology analysis confirmed the development of fatty liver with early fibrosis. Since Oil-O-Red specifically stains triglycerides together with cholesterol ester, this stain represents the real representation of lipid accumulation (Sarkar et al., 2020). We have observed a high level of lipid deposition in the HFHF group. However, the methanolic extract of *Lysimachia candida* Lindl. administration reduced the fat accumulation similar to the control group. Liver samples from the HFHF group exhibited prominent steatosis, ballooning, and lobular inflammation with mild fibrosis, while the Treatment group unveiled reduced levels of steatohepatitis with no fibrosis. Overall, the histopathology study confirmed the presence of hepatic steatosis, ballooning, lobular inflammation, and perisinusoidal fibrosis in the disease group, which was alleviated in the treatment group.

After confirming the fatty liver phenotype, we wanted to correlate the phenotypic changes in HFHF rats with serum metabolic profiles. The untargeted metabolomic analysis with multivariate data analysis (Principal component analysis) and clustering revealed a clear separation of rat serum metabolome between Control and HFHF groups. Principal component analysis clearly indicates the difference in metabolome in HFHF as compared to control at different time points. Clustering analysis also indicates change in levels of different metabolites in the control and HFHF group. Pathway enrichment analysis of different metabolites suggests a change in linoleic acid metabolism, biosynthesis of unsaturated fatty acids, glycerophospholipid metabolism, and primary bile acid

biosynthesis pathway. Hence, we could infer from our result that high-fat high-fructose diet has altered various metabolites from the normal physiological level. Changes in bile acids, unsaturated fatty acids, carnitines, and other metabolites involved in the peroxisome proliferator-activated receptors (PPAR) pathways were found in HFHF animals. Interestingly, the altered levels of these metabolites have been found to be reversed in the treatment group. PPAR alpha and PPAR gamma are highly expressed in the liver and play a significant role in the synthesis of bile acid and fatty acid uptake (Lee et al., 1995; Mandard et al., 2004). Oxidation of fatty acid and expression of fatty acid transport protein shares a close relationship with nuclear receptor PPARα and PPARγ in liver steatosis (Pyper et al., 2010).

The metabolites serum such hydroxyeicosapentaenoic acid ((+/-)8-HEPE)), pentadecanoic acid, heptadecanoate were downregulated in the HFHF group and interestingly, plant extract treatment has reversed their expression. (+/-) 8-hydroxyeicosapentaenoic acid acts as a ligand of PPAR (Forman et al., 1997; Yamada et al., 2014). For the first time, Yamada et al. demonstrated that orally administered 8-HEPE can activate PPARa, resulting in the decrease of plasma and hepatic TG levels (Yamada et al., 2016). As stated, 8-HEPE is a stimulator of PPARa, hence decrease levels of 8-HEPE can reduce the activation of PPARa and increase the serum and hepatic TG levels as we observed in the HFHF group. However, the methanolic extract of Lysimachia candida Lindl. administration increased the serum 8-HEPE levels similar to the control group. Two fatty acids, pentadecanoic acid (C15) and heptadecanoic acid (C17) were reduced in HFHF group. Epidemiological researches have revealed that plasma concentrations of odd chain saturated fatty acids like pentadecanoic acid and heptadecanoic acid are related to reduced risks for metabolic disorders like type II diabetes and coronary heart disease (Jenkins et al., 2015). Interestingly, the treatment with methanolic extract of Lysimachia candida Lindl. was able to upregulate these odd chain saturated fatty acids levels similar to Control.

Bile acids play a crucial role in maintaining the level of both free and conjugated forms of bile acids in the peripheral circulation. In hepatic disease, levels of bile acids are aberrated especially in synthesis, excretion, and reabsorption of bile acids, which raises the level of total bile acids. Some studies have demonstrated the effect of liver injury on bile acid metabolism (Wang et al., 2012; Beyoğlu and Idle, 2013). A previous study reported that the levels of bile acid were found to be low in carbon tetrachloride (CCl4) induced fatty liver rats (Zhang et al., 2019). When there is a disruption in the bile acid metabolism, it leads to a decrease in the activation of nuclear receptors such as FXR (farnesoid X receptor) and dysregulation in these receptors leads to NAFLD (Parséus et al., 2017; Chen et al., 2019; Liu et al., 2020). Chenodeoxycholic acid, muricholic acid and other cholic acids are primary bile acids produced in the liver as derivatives of cholesterol and secreted in the intestine as taurine and glycine conjugates. These bile acids interact with FXR and regulate glycemia and other metabolic functions (Grabherr et al., 2019). In the present

study, we have found that different bile acids such as Muricholic acid, Deoxycholic Acid, Glycocholic acid, Glycochenodeoxycholic Acid, and Glycodeoxycholic acid were lowered in the serum of HFHF rats. However, their serum levels were normalized after the treatment of the methanolic extract of Lysimachia candida Lindl. especially after 3 weeks. Lower serum levels of bile acids in the HFHF group may reduce the activation of FXR and enhance the fat accumulation in the rat liver which is similar to NAFLD pathologies. Our findings might be working through similar pathway as evidenced in the study by Sun (Sun et al., 2018). Bile acids activate mRNA expression of PPARa via binding of FXR in the PPAR promoter (Pineda Torra et al., 2003). Therefore, it seems that the FXR-PPARa pathway might be involved for the attenuation of fatty liver after the treatment of methanolic extract of Lysimachia candida Lindl (Figure 7).

Unsaturated fatty acids like Linoleic acid and α -Eleostearic acid were lowered in HFHF rats and increased after treatment of the plant extract. Our finding was similar to previous study where it was shown that Linoleic acid, an essential polyunsaturated fatty acid, was declined in non-alcoholic steatohepatitis (NASH) (Puri et al., 2009). α-Eleostearic acid, a PPAR α activator, is lowered in HFHF rats. α -Eleostearic acid also upregulates peroxisomal acyl-CoA oxidase activity and cytochrome P450 4A1 genes in rats, which in turn activates PPARα (Chao et al., 2001). Hence, lower levels of α -Eleostearic acid in HFHF group may cause inactivation of PPARa pathways, and therefore fatty liver pathologies. The methanolic extract of Lysimachia candida Lindl. was able to nullify these pathological features by upregulating α-Eleostearic acid expression and activating PPARα pathways (Figure 7).

Pathway analysis, using metaboanalyst by the exploration of different metabolites confirms that important distrupted pathway are linoleic acid metabolism, biosynthesis of unsaturated fatty acids, glycerophospholipid metabolism, and primary bile acid biosynthesis pathway (**Figure 6**). The summarized pathway of our study is revealed in (**Figure 7**).

Although we have established the link between altered serum metabolites levels and fatty liver phenotypes, there are some limitations of the study. First, there are many different components in the methanolic extract of $Lysimachia\ candida\ Lindl.$ and we have not looked which particular component(s) or compound(s) is activating PPAR α . Secondly, the molecular signaling pathway of PPAR α activation has not been deciphered after the treatment with plant extract.

CONCLUSION

Our study concludes that the methanolic extract of *Lysimachia candida* Lindl. reduces insulin resistance along with fatty liver phenotypes in rats. After analyzing various metabolites and pathways associated with fatty liver, we found that activation of PPAR α by methanolic extract of *Lysimachia candida* Lindl. might be responsible to prevent the high-fat high-fructose induced fatty liver in rats.

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DATA AVAILABILITY STATEMENT

The authors acknowledge that the data presented in this study must be deposited and made publicly available in an acceptable repository, prior to publication. Frontiers cannot accept a article that does not adhere to our open data policies.

ETHICS STATEMENT

The animal study was reviewed and approved by Translational Health Science and Technology Institute (THSTI), Faridabad, India (Protocol No. BIO-IAEC-3357).

AUTHOR CONTRIBUTIONS

JB, BD, and SB did the collection of plants and extraction of the methanolic extract; PK, DK, SB, and BK did animal experimentation; PK, SS, DK, SR, and PD conducted biochemical assays, data analysis, and data interpretation; YK, JA, SG, and NB did metabolomics experiments, metabolomic data analysis, and interpretation; PK, SS, and JA wrote the original manuscript; YK, NT, and SB designed the study,

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interpreted results, reviewed and edited the manuscript. All authors have read and accepted the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.653872/full#supplementary-material.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Transcriptomic and Metabolomic Profiling Reveals the Protective Effect of Acanthopanax senticosus (Rupr. & Maxim.) Harms Combined With Gastrodia elata Blume on Cerebral Ischemia-Reperfusion Injury

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The effects of current treatment strategies used in ischemic stroke are weakened by cerebral ischemia-reperfusion (CIR) injury. Suitable treatment regimens targeting CIR injury are still lacking. Two herbs, namely, *Acanthopanax senticosus* (Rupr. & Maxim.) Harms (ASE) and *Gastrodia elata* Blume (GEB), have been used as traditional Chinese medicine and are indicated in the treatment of stroke and cerebrovascular diseases. However, there are no studies that report the effects of ASE combined with GEB in the treatment of CIR injury. In this study, we used the Zea Longa method to induce CIR injury in male Wistar rats. Results of the pharmacodynamic studies revealed that co-administration of ASE and GEB may improve neuronal injury and prevent neuronal apoptosis by reducing oxidative stress and inflammation, and also help prevent CIR injury. On the basis of our hypothesis, we combined the results from transcriptomic and metabonomic analyses and found that ASE and GEB could prevent CIR injury by targeting phenylalanine, pyrimidine, methionine, and sphingolipid metabolism. Therefore, our study provides the basis for the compatibility and efficacy of ASE and GEB.

Keywords: cerebral ischemia-reperfusion injury, *Acanthopanax senticosus* harms, *Gastrodia elata* blume, transcriptomic, metabonomic

INTRODUCTION

Stroke is a common clinical neurological condition that seriously endangers human health and life. It is the fifth most common cause of death in America (Mozaffarian et al., 2016). The incidence of stroke is high; approximately 7,95,000 individuals, 87% of whom are ischemic, suffer from stroke each year in the United States alone (Lloyd-Jones et al., 2009). Ischemic stroke, the most common variant, affects the nervous system at the morphological and molecular levels. Brain tissue is sensitive to ischemia and hypoxia, and early recovery of blood reperfusion is the primary focus in the clinical management of ischemic strokes (Soares et al., 2009). However, when blood is perfused into the ischemic brain tissue, inflammatory reactions and neuronal death may be intensified owing to the generation of free radicals, calcium overload, and other factors (Bai and Lyden, 2015). Alleviation of

the pathophysiological process of cerebral ischemia-reperfusion (CIR) injury has become a research hotspot worldwide; however, the progress is not satisfactory. The treatment windows of the thrombolytic drugs and neuroprotective agents that are currently used for therapy are narrow and pose challenges during the therapy of stroke (Green, 2008; Boese et al., 2020).

Traditional Chinese medicine (TCM) has a long history in the treatment of stroke. Based on the pathogenesis theory of TCM and the so-called "Syndrome Differentiation and Pattern Diagnosis," most patients who have suffered an ischemic stroke can be grouped as being deficient in Qi and wind movement (Jhong et al., 2013). Therefore, herbs with Oireplenishing, wind-dispelling, and blood-activating effects are frequently used to reverse the damage caused by ischemic stroke (Zhang and Zhao, 2014; Lu et al., 2018). Acanthopanax senticosus (Rupr. & Maxim.) Harms [ASE, Eleutherococcus senticosus (Rupr. & Maxim.) Maxim.] is widely used as a potent Qi supplement to strengthen the spleen as a means to treat cardiovascular diseases (Xie et al., 2015). Gastrodia elata Blume (GEB) is a typical herbal medicine in TCM, which suppresses the hyperactive liver and reduces endogenous wind (Huang et al., 2019). ASE and GEB are herbal medicines that have been widely used for the treatment of ischemic stroke. Using data mining and the Delphi expert questionnaire, Rongrong Zhou was found that ASE-GEB may be a pair of drugs suitable for the treatment of stroke (Zhou et al., 2020). Previous studies have revealed the primary active constituents of ASE to be eleutheroside E (Bai et al., 2011), isofraxidin (Bai et al., 2011), hyperoside (Liu et al., 2012), eleutheroside B (Tohda et al., 2008), and quercetin (Pei et al., 2016), which can inhibit ischemic brain injury and protect against neuritic atrophy and cell death. The main active constituents of GEB include 4-hydroxybenzyl alcohol, gastrodin, and parishin. 4-Hydroxybenzyl alcohol ameliorates ischemic injury by inhibiting the activation of caspase-3 and increasing the expression of Bcl-2 (Yu et al., 2010). Gastrodin ameliorates oxidative stress inflammation by activating the Akt/Nrf2 pathway (Peng et al., 2015). In addition, parishin is mainly degraded to gastrodin in vivo (Tang et al., 2014). ASE and GEB have been abundantly reported in the treatment of CIR injury and nerve protection; however, the combined effect and mechanism of the two drugs are not clear. In this study, we explored the efficacy of ASE combined with GEB for the treatment of CIR injury and attempted to explore the mechanism of action underlying this combination. However, as the multi-component and multitargeting characteristics of TCM play an important role in the efficacy of this combination, the potential mechanism of the combination of ASE and GEB is not clear.

In recent decades, emerging "omics" technologies, including transcriptomics and metabonomics, have immensely improved the ability to study the biochemical changes caused by TCM interventions in biological systems. Metabolomics techniques provide insight into the mechanisms of various physiological conditions and abnormal processes at the systems level of metabolites (Johnson et al., 2016). Transcriptomics studies can be used to perform rapid qualitative and quantitative analysis of mRNA transcripts of up-stream genes (Wang et al., 2009).

Therefore, the integration of transcriptomics and metabonomics is of great significance for comprehensive research to determine the efficacies of and mechanisms of the formulations used as TCM (Du et al., 2018; Wu et al., 2019).

In this study, through the combination of transcriptomic analysis and metabonomics, we revealed the mechanism of the combination of GEB-ASE in alleviating CIR injury in rats.

EXPERIMENTAL APPROACHES

Extraction Methods

Medicinal materials were collected from Heilongjiang Province and identified as the dried roots and rhizomes or stems of Acanthopanax senticosus (Rupr. & Maxim.) Harms (ASE, Eleutherococcus senticosus (Rupr. & Maxim.) Maxim.), and Gastrodia elata Blume (GEB) by Professor Guoyue Zhong of the Jiangxi University of Traditional Chinese Medicine. Voucher specimens (accession number JZ-2017GYZ-CWJ-A2 and JZ-2017GYZ-TM-A3) were deposited in the Center of National Medicine Resource, Jiangxi University of Traditional Chinese Medicine, China.

The plant materials were washed, dried, sliced, and ground to a powder. To prepare the AEGE extract, 500 g of ASE and 500 g of GEB were mixed with 5,000 ml of 70% ethanol, refluxed and extracted for 2 h. The residue was subjected to re-extraction three times using 5,000 ml of ethanol for each subsequent extraction. All fractions were mixed, filtered, concentrated at 60 C using a rotary evaporator and freeze-dried. Lastly, AEGE extract at a concentration of 200 mg/kg was prepared by adding an appropriate volume of 0.5% carboxymethyl cellulose sodium (CMCNa; Xilong Science and Technology Co., Ltd, Shantou, China) solution to the dried extract.

Ethanol extracts of AEGE were analyzed using a Shimadzu UHPLC (ESI) system (Shimadzu, Kyoto, Japan) and an AB **SCIEX** quadrupole time-of-flight mass spectrometer (TripleTOF® 5,600, AB SCIEX, Framingham, MA, USA). The extract was dissolved in methanol and then filtered through a 0.22-um membrane filter. Samples were analyzed using an ACQUITY UPLC C18 column (100 mm \times 2.1 mm, 1.7 μ m, Waters) at 40°C. The mobile phase comprised water containing 0.1% formic acid (A) and acetonitrile (B), and the proportion of mobile phase B was as follows: 2-10%, 0-8 min; 10-20%, 8-16 min; 20-30%, 16-24 min; 30-90%, 24-29 min; 90%, 29–34 min. The injection volume was 1 μ l and the flow rate was 0.3 ml/min. TOF-MS and TOF-MS/MS were performed synchronously. Mass spectra were acquired in the negative ion mode. The parameters were set as follows: turbo spray temperature, 550 C; ion spray voltage floating, -4,500 V; collision gas, -35 eV. The mass range was set at 50-1,250 Da. The obtained data were analyzed using Peak View Software (AB SCIEX, Framingham, MA, United Satets).

Animals and Grouping

Adult male Wistar rats $(240 \pm 20 \text{ g})$ were obtained from Beijing Charles River Co. Ltd (Beijing, China; certification number: SCXK (Jing): 2016-0006). Rats were acclimated for 5 days and

provided access to water and standard laboratory animal diet *ad libitum*. They were randomly divided into four groups as follows: sham, IR, AEGE, and nimodipine (Nim), with 15 rats/group. The AEGE and Nim groups received AEGE (200 mg/kg/d) or Nim (15 mg/kg/d), respectively, orally for 15 days. The sham and IR groups received 0.9% sodium chloride orally for 15 days.

All experimental procedures were performed in accordance with the ethical principles for laboratory animals of the State Key Laboratory (Reference number: BCTG-2016-18). Experiments were reviewed and approved by the Animal Care Committee of the Jiangxi University of Chinese Medicine.

Establishment of IR Model

Rats were anesthetized using an intraperitoneal 10% injection of chloral hydrate (350 mg/kg). Cerebral ischemia-reperfusion injury was established following the method by Longa et al. (1989). Briefly, the external carotid artery was ligated and the common carotid artery was embolized through the internal carotid artery to the middle cerebral artery using a thread coated with silicone at the head end. Two hours after the induction of ischemia, the thread was pulled out to ensure the establishment of reperfusion. Rats in the sham group underwent a similar surgery, but without insertion of the monofilament.

Pharmacodynamics of AEGE

Neurobehavioral Assessment and Evaluation of Cerebral Infarction

After 24 h of reperfusion, the behavioral score of rats was evaluated using a 0–4 point scoring system as follows: no observable neurological dysfunction was marked as 0 points; toe curled up powerless was marked as 1 point; inclined to crawl in the opposite direction was marked as 2 points; turned autonomously to the opposite side upon being stimulated with slight sound was marked as 3 points; fell to the opposite side and had no spontaneous activity for a long time was marked as 4 points.

After neurobehavioral evaluation, the rats were anesthetized using chloral hydrate. Blood was collected from the posterior abdominal aorta. The animals were euthanized by decapitation and the brain tissues were collected.

Brain tissues of 3 rats/group were randomly selected for triphenyl tetrazolium chloride (TTC) staining. The entire brain tissue was sectioned into five 2 mm-thick coronal slices. These sections were incubated at 37 C for 16 min in 1% TTC solution (Solarbio, Beijing, China) and fixed with 4% paraformaldehyde for 3–5 h. The total brain slices and infarcted area were stained and imaged using Image-Pro Plus 6.0 (Media Cybernetics, Bethesda, MD, United states) and the percentage of the infarcted area was calculated.

H&E Staining

The brain tissues of 2 rats from each group were randomly selected for H&E staining. The portion between the root of the crossed optic nerve and the quadrigeminal body of the brain was placed in 4% paraformaldehyde at 4 C for about 24 h. After the fixed brain slices were dehydrated and embedded to prepare continuous paraffin

sections, HE (Solarbio, Beijing, China) staining was performed and the samples were observed using fluorescence microscopy (Leica, Weztlar, Germany).

Biochemical Evaluation

The brain tissues of 7 rats from each group were randomly selected for biochemical evaluation. The blood on the surface of the brain was washed with saline, and the excess saline was blotted using filter paper. Next, the coronal sections around the bregma point were collected (1 mm). Coronal brain tissues were weighed after sectioning. Brain tissue was added to precooled saline in a 1:9 ratio, homogenized, and centrifuged for 10 min (4,000 rpm). The activities of SOD, GSH-Px, and MDA in brain tissue were measured using the respective assay kits (Jiancheng Bioengineering, Nanjing, China). The IL-10, IL-1 β , and TNF- α levels in brain tissue were determined using ELISA (Neobioscience Technology, Shenzhen, China).

Metabolomics Analysis

Plasma Pretreatment and UPLC-Q/TOF-MS Analysis

The plasma samples of 10 rats in the sham, IR, and AEGE group were randomly selected for metabonomics analysis. Blood was collected from the abdominal aorta and loaded into an Eppendorf tube containing heparin sodium. The supernatant was obtained by centrifugation at 4,000 rpm for 10 min. Plasma supernatants were treated with methanol containing 2-chloro-L-phenylalanine (10 μ g/ml) in a 4:1 ratio (methanol: plasma supernatant, v/v, 250 μ l). After centrifugation at 4 C (4,000 rpm, 10 min), the supernatant was collected for analysis. A 50- μ l aliquot of each centrifuged supernatant was uniformly mixed to yield a quality control (QC) sample.

A Shimadzu UHPLC (ESI) system and an AB Sciex quadrupole time-of-flight mass spectrometer (TripleTOF 5600) were used for LC-MS analysis. An ACQUITY UPLC C18 column $(100 \text{ mm} \times 2.1 \text{ mm}, 1.7 \mu\text{m}, \text{Waters})$ was used for all analyses. The mobile phase was a mixture of 0.1% formic acid in water (A) and acetonitrile (B). The proportion of mobile phase B was as follows: 2-30%, 0-3 min; 30-60%, 3-5 min; 60-80%, 5-15 min; 80–100%, 15–16 min; 100%, 16–19 min; 100–2%, 19–20 min; 2%, 20-25 min. The injection volume was 2 μ l, the flow rate 0.3 ml/ min, and the column temperature was 40 C. TOF-MS and TOF-MS/MS were performed synchronously. Mass spectra were acquired in the positive and negative ion modes. The parameters of the positive ion mode were set as follows: ion spray voltage floating, 5,500 V; collision gas, 40 eV. The parameters of the negative ion mode were set as follows: ion spray voltage floating, -4,500 V; collision gas, -40 eV. The turbo spray temperature was 550 C and the TOF-MS mass ranged from m/z 50-1,250 Da.

During analysis of the sample sequence, a QC sample was run after every five injections to validate the analytical methodology (Zhang et al., 2017). QC (n=6) and plasma samples were analyzed using LC-MS. Data quality was evaluated based on the relative SDs (RSDs) of the retention times and intensities of 10 typical peak (including internal standard) of the QC samples.

Data Analysis

Raw data of plasma samples were analyzed using MarkerView 2.0 (AB SCIEX, Framingham, MA, United States). Before chemometric analysis, the data obtained for each sample were normalized using internal standards (2-chloro-L-phenylalanine). The features were subjected to statistical analysis only when detection frequencies of any group reached 100% and the RSD was less than 30%. The missing values were replaced by half minimum of abundances of features. The pre-processed data were analyzed using principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA) using SIMCA 14.1 (Umetrics, Umeå, Sweden). Additionally, the model was considered to qualify when the cumulative values of R2 (score of raw data interpreted by the model) and Q2 (predictive power of the model) were greater than or equal to 0.5; OPLS-DA was performed using a permutation test (200 permutations) to avoid overfitting.

Features with variable importance in projection (VIP) scores >1 in the OPLS-DA model and p-values <0.05 in t-test were selected and their corresponding metabolites identified. Human Metabolome database (HMDB) was used as a tool for the identification of differential metabolites using LC-MS. Associated metabolic pathways were established using the Kyoto Encyclopedia of Genes and Genomes (KEGG) and MetaboAnalyst 3.0, in addition to other online tools.

Transcriptomics Studies

Library Preparation for Transcriptome Sequencing

The brain tissues of 3 rats from the sham, IR, and AEGE groups were randomly selected for transcriptome analysis. Total RNA was extracted from about 150 mg of brain tissue using a MirVana total RNA extraction kit (Ambion, Carlsbad, CA, United Sates). RNA concentration was measured using Qubit® RNA Assay Kit and a Qubit® 2.0 Fluorometer (Life Technologies, Carlsbad, CA, United States). RNA integrity was assessed using an RNA Nano 6,000 Assay Kit of the Bioanalyzer 2,100 system (Agilent Technologies, CA, United States). A total amount of 1.5 μg of RNA per sample was used as the follow-up test material for RNA-sample preparation. Whole transcriptome profiling was performed using NEBNext® Ultra™ RNA Library Prep Kit for Illumina® (NEB, Ipswich, MA, United States) according to the manufacturer's protocol.

Clustering, Sequencing, and Quantification of Gene Expression

Clustering of index-coded samples was performed using a CBOT Cluster Generation system using HiSeq 4,000 PE Cluster Kit (Illumina). Next, RNA sequencing (150 bp, pair-ends) was performed using standard Illumina HiSeq 4000 platform protocols. All downstream analyses were based on clean data with high quality. Gene FPKM was calculated by adding the FPKM of each genome transcript. The differential expression of the two conditions was analyzed using DESeq2R software package (1.26.0). For genes with FPKM values ≥1 in at least one sample, the significantly different expressions between

groups were determined according to the criteria as follows: p < 0.05 and $|\log 2$ FoldChange $| \ge 0.58$.

GO and KEGG Enrichment Analysis of Differentially Expressed Genes

Functional Annotation Bioinformatics Microarray Analysis (DAVID) database (Huang et al., 2009) was used to obtain Gene Ontology (GO) enrichment analysis of DEGs. GO terms (p < 0.05) were considered significantly enriched by DEGs. The enrichment of DEGs in KEGG pathways was tested using KEGG Orthology Based Annotation System v3.0 software; p-values were calculated using one-way ANOVA based on the normalized dataset. KEGG terms (p < 0.05) were considered significantly enriched by DEGs.

Western Blotting

Western blotting was used to determine the protein expression of the key genes measured using transcriptomic analysis. About 100 mg of brain tissue was lyzed with 1 ml of RIPA buffer (Beyotime, Shanghai, China). The protein concentration of the brain homogenate was measured using a bicinchoninic acid assay kit (Thermo Scientific, MA, United States). Protein samples were resolved using sodium dodecyl sulfate polyacrylamide-gel electrophoresis and transferred onto polyvinylidene difluoride membranes (Millipore, Schwalbach, Germany). Then, the proteins were immunoblotted with their corresponding primary and secondary antibodies. A chemiluminescence assay kit was used to determine the intensity of each band using a Tanon 6600 luminous imaging workstation (Tanon, Shanghai, China). Protein expression was determined using Image-Pro Plus 6.0.

Statistical Analysis

All experimental data were analyzed using Student's t-test or one-way ANOVA test with SPSS version 21.0 software (IBM, Armonk, NY, United States) package to calculate statistical significance. p < 0.05 was considered statistically significant.

RESULTS

Identification of Chemical Constituents in AEGE

The total negative ion chromatograms of AEGE are shown in **Supplementary Figure S1**. A total of 18 components were characterized (**Supplemental Table S1**) and their chemical structures are shown in **Supplementary Figure S2**. Four major active components, isofraxidin, eleutheroside E, gastrodin and parishin A, were identified by comparison with the standards, whereas the others were identified by checking their characteristic product ions (**Supplementary Figure S1**).

Pharmacodynamic Effects of AEGE Neurobehavioral Scores and Evaluation of Cerebral Infarction

The neurobehavioral scores of the rats in the IR group were significantly higher (p < 0.05) than those in the sham group. The

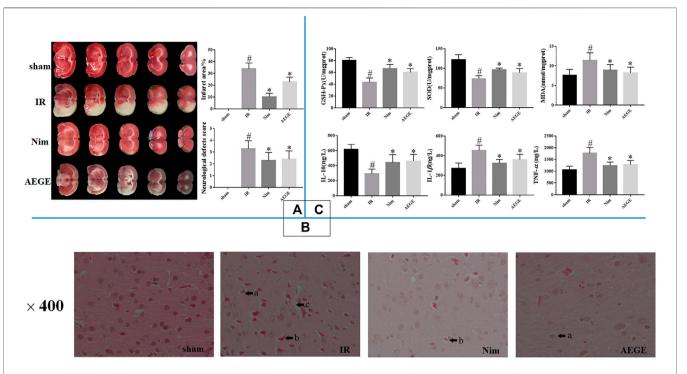


FIGURE 1 | Changes in brain histopathology and biochemical indices in rats with cerebral ischemia-reperfusion injury. **(A)** TTC staining, neurological defects, and infarct area. **(B)** H&E staining. The area marked with an "a" indicates peripheral demyelination; "b" indicates nuclear pyknosis, nerve cell atrophy, and neuronal degeneration; and "c" indicates cytoclasis of the brains in MCAO/R rats. **(C)** Changes in SOD, GSH-Px, MDA, IL-10, IL-1 β , and TNF- α levels in rat brains. Data are expressed as mean \pm SD. "#" represents sham group vs. the IR group (#p < 0.05); "*" represents IR group vs. the AEGE group (*p < 0.05).

cerebral infarction area was consistent with these scores. TTC staining (**Figure 1A**) and scoring scales indicated the successful establishment of the IR model. The rats in the AEGE group showed significantly lower scores (p < 0.05) and infarction areas (p < 0.05) compared to those in the IR group. These findings indicated that AEGE and Nim had a therapeutic effect on nerve injury and CIR injury.

HE Staining

HE staining (**Figure 1B**) showed no neuronal damage or inflammatory cell infiltration in the cerebral cortex of rats in the sham group. However, the ischemic cortex of the brains exhibited cytoclasis, nuclear pyknosis, nerve-cell atrophy, neuronal degeneration, and peripheral demyelination in the IR group. Treatment with AEGE and Nim improved the histopathological features caused due to CIR injury. The neuronal cells were restored to normal, and there were only a few nerve cells that exhibited peripheral demyelination and nerve-cell atrophy.

Biochemical Evaluation

SOD and GSH-Px activity in the brain tissue of IR rats decreased significantly (p < 0.05), whereas there was a significant increase in MDA levels (p < 0.05) compared to the sham group. Compared to that in the IR group, GSH-Px and SOD activity increased significantly (p < 0.05) and MDA level decreased significantly (p < 0.05) in the AEGE group (**Figure 1C**).

In rats with IR injury, IL-10 expression was found to decrease significantly (p < 0.05), and the levels of IL-1 β and TNF- α were significantly elevated (p < 0.05) compared to the corresponding values in the sham group. A significant decrease in TNF- α and IL-1 β levels (p < 0.05) and a significant increase in IL-10 level (p < 0.05) was observed in the AEGE group (**Figure 1C**) compared to that in the IR group. These findings suggested that AEGE may be efficacious in treating cerebral ischemia-reperfusion injury by reducing oxidative stress and inflammation.

Metabolomics Studies

The 10 typical ion peaks in the QC samples showed low RSD in the peak intensity and retention times in the positive and negative ion modes (Supplementary Figure S3; Supplemental Table S3). The clustering of QC samples and significant separation between the sham, IR, and AEGE groups in PCA (Figure 2A) confirmed the robustness and reproducibility of the test method. Moreover, OPLS-DA modes both exhibited well-verifiable parameters (Supplemental Table S4). The permutation test with 200 iterations showed that the OPLS-DA models were not overfitted (Figure 2B).

The metabolites (VIP > 1.0, p < 0.05) were considered as potential differential metabolites. Combined with the primary parent ion information and secondary ion fragment information collected using high-resolution mass spectrometry, differential metabolites were identified by matching Peakview1.2 with the

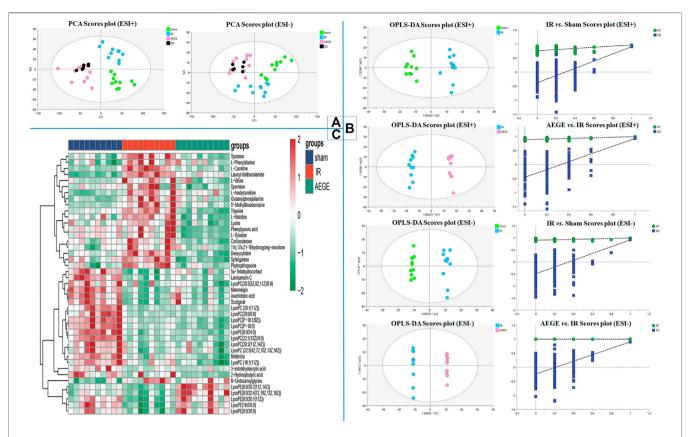


FIGURE 2 | Signatures of plasma metabolism in rats. (A) PCA score plot for the validation of quality control (QC). (B) OPLS-DA and permutation score plots of sham, IR, and AEGE groups. (C) Heatmap of metabolites in the cerebral ischemic injury of rats in the sham, IR, and AEGE groups. Red for higher level and blue for lower level

substance molecules in HMDB, and combined using the standard sample atlas information.

Using this protocol, 43 differential metabolites (Table 1) were identified among the control, model, and AEGE groups. To better capture the changes in metabolism, a heatmap was constructed to represent the graphical view using all groups (Figure 2C). The changes in the levels of observed metabolites were divided into four scenarios as follows: 1) After administration of AEGE, the levels of metabolites, including L-phenylalanine, tyramine, deoxycytidine, sphinganine, 5'methylthioadenosine, corticosterone, thymine, L-histidine, and phytosphingosine, returned to the same level as that in the sham group. 2) The metabolite levels in the IR vs. sham groups were not significantly upregulated or decreased; however, the levels decreased significantly after administration of AEGE. The types of metabolites in this category are more complex and there may be some positive feedback regulation that is considered normal. Examples include phenylpyruvic acid, L-tyrosine, and spermine. 3) The metabolite levels in the IR vs. sham groups were significantly upregulated or decreased; however, these levels were not significantly upregulated or decreased after the administration of AEGE. Examples include 3-indolehydracrylic acid, N-undecanoylglycine, and netilmicin. 4) The metabolite levels in the IR group were significantly

downregulated compared to those in the sham group; however, after the administration AEGE, these levels were still significantly downregulated. This phenomenon was called abnormal regulation. The metabolites mainly comprise lipids and fatty acids, such as LysoPC [20:1 (11Z)/0:0], LysoPC (P-18:0), and LysoPC (P-16:0/0:0).

Forty-three differential metabolites were enriched using the MetaboAnalyst 4.0 database to obtain the enrichment map of the metabolic pathways. The main pathways were identified for the following: phenylalanine, tyrosine, and tryptophan biosynthesis; phenylalanine metabolism; histidine metabolism; sphingolipid metabolism; pyrimidine metabolism; cysteine and methionine metabolism; tyrosine metabolism; steroid-hormone biosynthesis (Supplementary Figure S4). The levels of nine potential biomarkers, including L-phenylalanine, tyramine, deoxycytidine, sphinganine, 5'-methylthioadenosine, corticosterone, thymine, L-histidine, and phytosphingosine were significantly different in the plasma of rats in the IR group (Figure 3).

Transcriptomics Studies

A total of 2,326 DEGs were identified, which included 1,423 upregulated and 903 downregulated genes when the IR and sham groups were compared. A total of 1,453 DEGs were

TABLE 1 | Potential biomarkers of cerebral ischemic injury post-treatment with AEGE.

M/Z	Rt	Formula	Name	Adduct	HMDB	IR vs. sham	AEGE vs. IR
100.0756	2.02	C ₅ H ₁₁ NO ₂	L-Valine	+H-H ₂ 0	HMDB0000883	1	
120.0806	2.01	C ₈ H ₁₁ NO	Tyramine	+H-H ₂ 0	HMDB0000306	↑***	J***
127.0498	1.74	$C_5H_6N_2O_2$	Thymine	+H	HMDB0000262	1***	J***
146.059	1.92	C ₉ H ₇ NO	Lysine	+H	HMDB0000182	1 *	1***
147.0443	1.22	C ₉ H ₈ O ₃	Phenylpyruvic acid	+H-H ₂ 0	HMDB0000205	1	
162.1109	0.92	C ₇ H ₁₅ NO ₃	L-carnitine	+H	HMDB0000062		1****
178.0595	0.84	$C_6H_9N_3O_2$	L-Histidine	+Na	HMDB0000177	1***	J***
182.08	1.2	C ₉ H ₁₁ NO ₃	L-Tyrosine	+H	HMDB0000158	1	
188.0698	6.75	C ₁₁ H ₁₁ NO ₃	3-Indolehydracrylic acid	+H-H ₂ 0	HMDB0059765	<u></u>	1
203.2234	0.81	C ₁₀ H ₂₆ N ₄	Spermine	+H	HMDB0001256	1	***
204.1232	1.22	C ₉ H17NO ₄	L-acetylcarnitine	+H	HMDB0000201		<u></u> *
226.1788	15.89	C ₁₃ H ₂₅ NO ₃	N-Undecanoylglycine	+H-H ₂ 0	HMDB0013286	· 1	Ì
250.0795	1.21	C ₉ H ₁₃ N ₃ O ₄	Deoxycytidine	+Na	HMDB0000014		1***
288.2544	9.05	C ₁₆ H ₃₃ NO ₃	Lauroyl diethanolamide	+H	HMDB0032358		
295.1275	3.3	C ₁₄ H ₁₈ N ₂ O ₅	Glutamylphenylalanine	+H	HMDB0029156		1.***
298.0962	2.72	C ₁₁ H ₁₅ N ₅ O ₃ S	5'-methylthioadenosine	+H	HMDB0001173		
302.3049	8.96	C ₁₈ H ₃₉ NO ₂	Sphinganine	+H	HMDB0000269	· 1	**
318.3026	8.98	C ₁₈ H ₃₉ NO ₃	Phytosphingosine	+H	HMDB0004610		
329.2121	7.06	C ₂₁ H ₃₀ O ₄	Corticosterone	+H-H ₂ 0	HMDB0001547		1.***
347.2222	7.05	C ₂₁ H ₃₂ O ₅	11b,17a,21-trihydroxypreg-nenolone	+H-H ₂ 0	HMDB0006760		<u></u> *
476.3109	9.42	C ₂₁ H ₄₁ N ₅ O ₇	Netilmicin	+H	HMDB0015090	***↑	Ì
506.3621	10.18	C ₂₆ H ₅₂ NO ₆ P	LysoPC [P-18:1 (9z)]	+H	HMDB0010408	***↑	Ĭ
508.3734	11.45	C ₂₆ H ₅₄ NO ₆ P	LysoPC(P-18:0)	+H	HMDB0013122	***↑	ĺ*
522.3512	10.58	C ₂₆ H ₅₂ NO ₇ P	LysoPC [18:1 (11Z)]	+H	HMDB0010385	<u> </u>	Ì
546.3526	15.24	C ₂₈ H ₅₂ NO ₇ P	LysoPC [20:3 (5Z,8Z,11Z)/0:0]	+H	HMDB0010393	<u></u> *	ĺ
548.3694	11.46	C ₂₈ H ₅₄ NO ₇ P	LysoPC [20:2 (11Z,14Z)]	+H	HMDB0010392	Ţ	i
550.3856	13.13	C ₂₈ H ₅₆ NO ₇ P	LysoPC [20:1 (11Z)]	+H	HMDB0010391	J***	Ť
552.3995	15.09	C ₂₈ H ₅₈ NO ₇ P	LysoPC(20:0/0:0)	+H	HMDB0010390	J***	1
566.4153	16.61	C ₂₉ H ₆₀ NO ₇ P	LysoPE (0:0/24:0)	+H	HMDB0011497	J***	ĺ
570.3534	11.46	C ₃₀ H ₅₂ NO ₇ P	LysoPC [22:5 (4Z,7Z,10Z,13Z,16Z)]	+H	HMDB0010402	1	Ť
578.4174	15.68	C ₃₀ H ₆₀ NO ₇ P	LysoPC [22:1 (13Z)/0:0]	+H	HMDB0010399	J***	Ţ
103.0406	1.59	$C_4H_8O_3$	2-Hydroxybutyric acid	-H	HMDB0000008	1	<u></u> *
164.0702	2.00	C ₉ H ₁₃ NO ₃	L-phenylalanine	-H ₂ O-H	HMDB0000068	<u>†</u>	1*
303.2339	14.95	C ₂₀ H ₃₂ O ₂	Arachidonic acid	-H	HMDB0001043	J***	1
347.221	15.26	C ₂₁ H ₃₄ O ₅	5a-Tetrahydrocortisol	+H-H ₂ 0	HMDB0000526		·
353.1403	14.55	C ₂₁ H ₂₂ O ₅	Lansiumarin C	-H	HMDB0034838	J***	· 1
371.2212	14.95	C ₂₃ H ₃₂ O ₄	Scutigeral	-H	HMDB0030012	J***	i
403.1574	14.94	C ₂₅ H ₂₄ O ₅	Mammeigin	-H	HMDB0030785	Ĭ***	1
480.3112	10.16	C ₂₃ H ₄₈ NO ₇ P	LysoPE (18:0/0:0)	-H	HMDB0011130		<u>;</u>
504.3122	9.84	C ₂₅ H ₄₈ NO ₇ P	LysoPE [0:0/20:2 (11Z,14Z)]	-H	HMDB0011483	1	
506.3291	10.95	C ₂₅ H ₅₀ NO ₇ P	LysoPE [0:0/20:1 (11z)]	-H	HMDB0011482	Ĭ	^***
508.3408	12.78	C ₂₅ H ₅₂ NO ₇ P	LysoPE (0:0/20:0)	-H	HMDB0011481	Ĭ	
528.3108	9.61	C ₂₇ H ₄₈ NO ₇ P	LysoPE [0:0/22:4 (7Z,10Z,13Z,16Z)]	-H	HMDB0011493	Ĭ	

^{*}p < 0.05.

identified, of which 507 were upregulated and 946 were downregulated when the AEGE and IR groups were compared; among them, the expression levels of 494 genes were restored after treatment with AEGE. All genes were used to construct volcano maps (**Figure 4A**). It was found that many genes were upregulated in the IR group, whereas, after treatment with AEGE, the expression of most genes was significantly downregulated. The general trend in the number of DEGs is shown in **Figure 4B** and was classified using the KEGG database. Following AEGE administration, the expression levels of amino acid-, carbohydrate-, and lipid-related genes partially returned to a level similar to that of the sham group.

The cellular processes and functions of the significantly altered genes can be understood by using the GO database. At the level of biological processes, genes were involved in the positive regulation of apoptosis. At the level of cellular components, the significantly changed genes mainly existed in the cytoplasm. At the molecular-function level, the genes were involved in the positive regulation of ATP binding, protein homodimerization, and identical protein binding (Supplementary Figure S5).

The KEGG database was used to analyze the biological pathways mediated by the identified genes in more depth. A total of 116 pathways were found to be significantly enriched when the sham and IR groups were compared (**Supplemental**

^{**}p < 0.01.

^{***}p < 0.001.

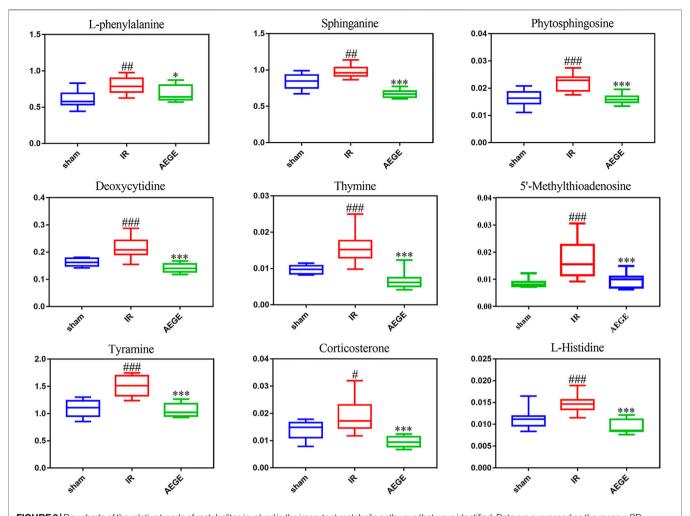


FIGURE 3 | Box charts of the relative trends of metabolites involved in the important metabolic pathways that were identified. Data are expressed as the mean \pm SD. "#" represents sham group vs. the IR group (#p < 0.05, ##p < 0.01, ###p < 0.001); "*" represents IR group vs. the AEGE group (*p < 0.05, ***p < 0.001).

Table S5), whereas 28 pathways were found to be significantly enriched when the AEGE and IR groups were compared (**Supplemental Table S6**). Combined with metabonomic analysis, we found that the pathways of the DEGs were well associated with those of the metabolites produced during phenylalanine, pyrimidine, methionine, and sphingolipid metabolism. When the control, model, and AEGE groups were compared, the expression of six genes, including Tk1, Pold1, Rrm2, Pah, Mtap, and LOC100912604, was found to be restored (**Figure 4C**). Compared to the sham group, the expression levels of Hpd, Ddc, Degs2, Sgpp2, Asah2, Nme6 decreased significantly, whereas that of Sphk1 was significantly upregulated in the IR group. Following AEGE treatment, the expression of *AK9* was significantly upregulated compared to that in the IR group.

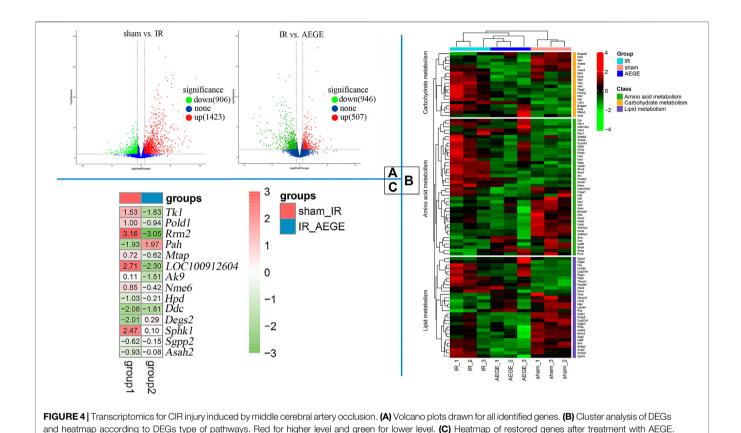
Validation of Changes in Protein Expression

Integrated analysis indicated that the treatment of CIR with AEGE is related to phenylalanine, pyrimidine, methionine, and

sphingolipid metabolism. The protein expression of the key genes in rat brains was evaluated using western blotting (**Figure 5**). Compared to the sham group, the expression level of Pold1, Tk1, Mtap, Rrm2, and Pah increased significantly, whereas that of LOC100912604 decreased significantly in the brain tissue of rats in the IR group. After the administration of AEGE, the protein levels returned to a level similar to that in the sham group. The protein expression of the key genes analyzed using western blot was highly consistent with the results obtained using transcriptomics analysis.

DISCUSSION

Several studies have reported that oxidative stress and inflammation lead to apoptosis, autophagy, and necrosis after CIR. The decreased activities of SOD and GSH-Px and the increased levels of MDA in the brain tissue of IR rats may lead to weakened activity of antioxidant enzymes in



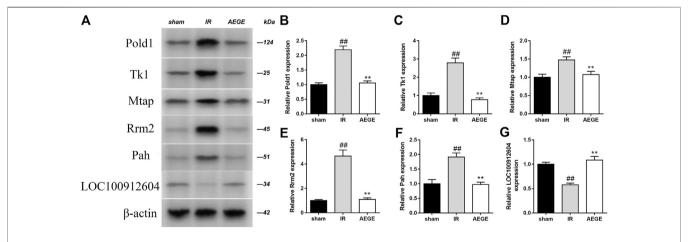


FIGURE 5 | Determination of protein levels in brain tissue of rats in the sham, CIR, and AEGE groups. Expression of Pold1 (A,B), Tk1, (A, C), Mtap (A,D), Rrm2 (A,E), Pah (A,F), and LOC100912604 (A,G) on the indicated group were detected using western blotting. Results are expressed as mean \pm SD for three individual experiments which, were performed in triplicate for each condition. "#" represents sham group vs. the IR group (##p < 0.01); represents IR group vs. the AEGE group (**p < 0.01).

the rat brain, which in turn can disrupt the balance between the antioxidant enzyme system and free oxygen radicals (Zhan and Yang, 2006). The activities of inflammatory cytokines, IL- 1β and TNF- α , in the brain tissue of IR rats increases significantly, whereas that of IL-10 decreases significantly.

This results in the induction of neutrophil adhesion, migration, and activation, and leads to an increase in inflammation and destruction of the brain tissue (Zhang et al., 1998). Therefore, it is believed that rats administered AEGE as a prophylactic might be less susceptible to CIR

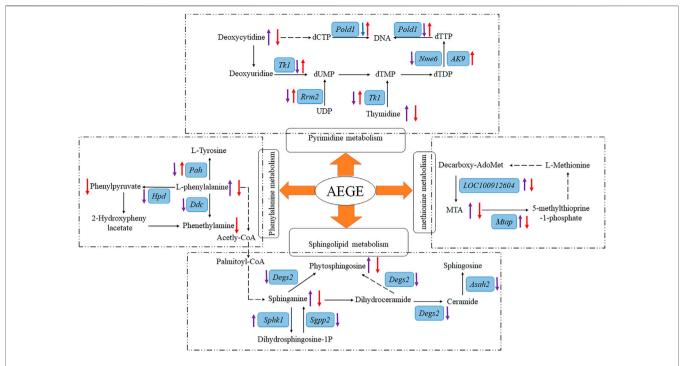


FIGURE 6 | Overview of metabolic pathway analysis. After treatment with AEGE, the concentration or expression of metabolites and genes (blue background and italic) were changed ("↑" means upregulated; "L" means downregulated; purple arrow represents the ratio of IR to sham groups; red arrow represents the ratio of AEGE to IR groups). Dashed arrow indicates multiple steps in the pathway.

injury. This may be owing to the antioxidant and antiinflammatory mechanisms of AEGE.

To further establish the relationship between the results from transcriptomic and metabolomics studies, data of the potential metabolites and the altered genes were integrated. The main metabolic pathways of the following metabolites were identified: phenylalanine, pyrimidine, methionine, and sphingolipids. AEGE could treat CIR injury by affecting these pathways at both transcriptional and metabolic levels. Details of the metabolic pathways are shown in **Figure 6**.

L-phenylalanine is an essential aromatic amino acid that plays a key role in the biosynthesis of other amino acids (Pardridge, 1998). When present in sufficiently high levels, phenylalanine acts as a neurotoxin that disrupts or attacks neural cells and tissues. Plasma L-phenylalanine levels can be increased in rats with traumatic brain injury (Vuille-Dit-Bille et al., 2012). Phenylpyruvic acid is a keto-acid, which is an intermediate or catabolic byproduct of phenylalanine metabolism. Tyrosine is an amino acid synthesized from phenylalanine in the presence of phenylalanine hydroxylase. We found the metabolite levels L-phenylalanine to be significantly higher and the expression levels of Pah, Ddc, and Hpd genes to be significantly lower than those in the IR group. However, the levels of the metabolites, phenylpyruvic acid, and L-tyrosine, were not significantly different compared to those in the sham group. This may have occurred because

of the decrease in L-phenylalanine metabolism due to CIR, which led to the accumulation of L-phenylalanine, causing subsequent damage to the brain cells. After administration of AEGE, the levels of L-phenylalanine, phenylpyruvic acid, and L-tyrosine decreased significantly, and the expression of the Pah gene increased significantly. The expression trend of Pah protein analyzed using western blot was consistent with the results obtained using transcriptomics. Therefore, it could be inferred that AEGE can decrease L-phenylalanine levels. Reduced levels of L-phenylalanine may reduce the oxygen consumption of the brain, energy production, and storage, all of which are beneficial in brain recovery through phenylalanine metabolism.

Phytosphingosine exerted strong cytotoxic effects, modulated the Caenorhabditis elegans muscarinic receptor-mediated acetylcholine signal transduction pathway, and induced cell death (Lee et al., 2001). Sphinganine is a bioactive compound involved in cell proliferation, differentiation, transcription, autophagy, and apoptosis, all of which are relevant to inflammatory disease (Merrill et al., 2009). In this study, we found that sphinganine and phytosphingosine accumulated significantly in rats in the IR group, causing damage to brain cells. Moreover, we found that the expression of Degs2, Sgpp2, and Asah2 was significantly decreased, and that of the Sphk1 gene was increased significantly in the brain tissue of rats with IR. This could likely be a protective mechanism of the body to

defend itself against high concentrations of sphinganine and phytosphingosine, to convert sphinganine to the less toxic dihydrosphingosine-1P, and reduce the conversion of sphinganine to phytosphingosine. After treatment with AEGE, the levels of phytosphingosine and sphinganine decreased significantly compared to that in the IR group. This reduction may be attributed to the regulation of phenylalanine metabolism by AEGE, which led to the decrease in acetyl-CoA levels. Therefore, the therapeutic effects of AEGE may be achieved by regulating the levels of sphingomyelin and sphingosine in sphingolipid metabolism by regulating phenylalanine metabolism.

Deoxycytidine is one of the principal nucleosides of DNA and is composed of cytosine and deoxyribose. Thymine is one of the pyrimidine bases of living matter. Exogenous uridine and cytidine play a role in maintaining brain function in rats with CIR injury (Löffler et al., 2018). In the IR group, the levels of deoxycytidine and thymine increased significantly, and the expression of Tk1, Pold1, Rrm2, and Nme6 genes decreased significantly compared to that in the sham group. The consistent trends of the two metabolites might be closely related to the enzymes controlled by the genes integrated with DNA. Following AEGE treatment, the expression of Tk1, Pold1, Rrm2, and AK9 were found to be significantly upregulated. Therefore, it could be reasonably deduced that AEGE regulates the balance between dCTP and dTTP through genes including Tk1, Pold1, Rrm2, AK9, and Tyms. Moreover, the expression trend of Tk1, POLD1, and Rrm2 proteins, which were verified using western blotting was the same as that obtained using metabonomics analysis. This result explains the decrease of blood deoxycytidine and thymine levels after treatment with AEGE. Collectively, these findings suggested that AEGE could improve the disorder in pyrimidine metabolism caused by CIR injury.

5'-Methylthioadenosine (MTA) yield methylthioprine-1-phosphate and adenine through the metabolism of S-methyl-5'-thioadenosine phosphorylase (Mtap), which is an important step in the methionine- and purine-recovery pathways. MTA affects the regulation of gene expression and plays a role in proliferation, differentiation, and apoptosis (Ansorena et al., 2002). Protein methionine oxidation potentiates the activation of NF-κB and contributes to CIR injury (Gu et al., 2016). In this study, we found that LOC100912604, Mtap, and MTA were significantly upregulated, which may have accelerated the metabolism and oxidation of methionine after CIR. After treatment with AEGE, LOC100912604, Mtap, and MTA were significantly downregulated, which restored methionine metabolism and reduced the damage to brain cells resulting from methionine oxidation. The expression trend of Mtap analyzed using western blotting was consistent with the results of transcriptomics analysis. Thus, intervention may regulate methionine metabolism and likely contribute to its therapeutic effects.

The main limitation of this study concerning the metabolomics component is one which is common to all

metabolomic investigations - identification of metabolites. Because of the unavailability to obtain the reference compounds, identifying them remained an enormous difficulty.

CONCLUSION

In summary, rats pretreated with AEGE suffered less severe CIR injury. Our findings revealed that AEGE significantly reduced the area of cerebral infarction caused by CIR injury. The mechanism of AEGE in alleviating CIR was via the reduction of oxidative stress and inflammation.

Results of transcriptomic and metabonomic studies indicated that six metabolites, namely, sphinganine, thymine, phytosphingosine, L-phenylalanine, deoxycytidine, 5'-methylthioadenosine; and six genes, namely, Tk1, Pold1, Rrm2, Pah, Mtap, and LOC100912604, were significantly altered in the IR group. The representative proteins in the altered pathways were determined using Western blot. These metabolites and genes could be regulated after treatment with AEGE, suggesting that the therapeutic effect of AEGE in CIR may be related to the regulation of phenylalanine and pyrimidine metabolic pathways, sphingolipid metabolism, and methionine metabolism.

Although this new prescription of ASE combined with GEB is seldom used in a clinical setting, it provides useful clues for the further development of this herbal combination.

DATA AVAILABILITY STATEMENT

The datasets generated for this study can be found in the Sequence Read Archive, https://www.ncbi.nlm.nih.gov/gds/?term=GSE160500.

ETHICS STATEMENT

The animal study was reviewed and approved by the Animal Care Committee of the Jiangxi University of Chinese Medicine. All standard biosecurity and institutional safety procedures have been adhered to in all the experiment procedures in this article.

AUTHOR CONTRIBUTIONS

BL, RC, and ZL conceived and designed the experiments; BL wrote manuscript; QW, ZL, SY and YF were involved in data acquisition; BL and RC have made statistical analyses. All authors read and approved the final manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.619076/full#supplementary-material.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Identification, Biological Activities and Biosynthetic Pathway of *Dendrobium* Alkaloids

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Mou Z, Zhao Y, Ye F, Shi Y, Kennelly EJ, Chen S and Zhao D (2021) Identification, Biological Activities and Biosynthetic Pathway of Dendrobium Alkaloids. Front. Pharmacol. 12:605994. doi: 10.3389/fphar.2021.605994 Dendrobium is a genus of flowering plants belonging to the Orchidaceae family with more than 1,400 species. Many Dendrobium species have been used as medicinal plants in several Asian countries for thousands of years. Alkaloids were reported as the major biological markers due to their complex chemical compositions and various types. In this review, we summarized the structural types of alkaloids, their pharmacological activities, as well as the mechanisms of biological activities. More than sixty alkaloids were isolated and identified from the Dendrobium genus. Moreover, the pharmacological effects of Dendrobium alkaloids as hepatic lipid and gluconeogenesis regulation, as neuroprotection, and as anti-tumor, anti-inflammatory, anti-diabetes, and anti-virus factors were described. Besides, the total chemical synthesis of dendrobine is provided, while the biosynthetic pathway of dendrobine has been proposed based on the functions of associated genes. For applications of these invaluable herbs, more researches on the extraction of biological markers from compounds are needed. Further confirmation of the proposed biosynthetic pathways is anticipated as well.

Keywords: alkaloids, orchidaceae, Dendrobium, anti-inflammatory, antitumor, mechanisms, biosynthetic pathway

INTRODUCTION

Apart from Asteraceae, the orchid family is the second-largest flowering family, which has 28,000 species distributed in about 736 genera (Chase et al., 2015), among which Dendrobium is one of the largest genera. It contains more than 1,500 species (www.theplantlist.org), most of which are epiphytic or lithophytic, and it is widespread in South, East, and Southeast Asia, like China, Japan, Philippines, Vietnam, India, and Indonesia. Some species are also found in New Guinea, Australia, and the islands of the Pacific (Zhu et al., 2009). The plants of Dendrobium species have been used as traditional or folk medicine in many Asian countries for thousands of years. For instance, there are $96 \ Dendrobium$ species in China, and about $30 \ species$, known as shí hú (石斛) or shí hú lán (石斛 \cong), have been widely used as ethnic medicine for tonifying the stomach, nourishing Yin (to enhance the production of body fluids, such as blood, saliva, tears, etc.), and clearing heat and toxic matter (Yang et al., 2006; Flora of China, 2020). The earliest written record of the medicinal usage of Dendrobium was found in the ancient text "Shen Nong's Herbal Classic" 2000 years ago, in which it was considered to be a "superior grade" herbal medicine. Hundreds of years later, Dendrobium was

TABLE 1 | The ethnomedicine use of Dendrobium in some countries.

Country	Dendrobium species	Local name	Ethnomedicine use	References
China	Dendrobium nobile Lindl.	shí hú (石斛)	Used as a tonic and antipyretic for treating human disorders	Lam et al. (2015)
	Dendrobium chrysotoxum Lindl.	shí hú lán (石斛兰)	Used for clearing heat and toxic matter, and enhancing immunity	Lin et al. (2018)
	Dendrobium fimbriatum Hook.	huáng c ǎ o (黄草)		Yang et al. (2006)
	Dendrobium officinale Kimura et Migo	xiān c ǎ o (仙草)		Yuan et al. (2018)
	Dendrobium aphyllum (Roxb.) C.E.C.Fisch			Wang et al. (2020
	Dendrobium huoshanense Z. Z. Tang et S. J.			
	Cheng			
	Dendrobium findlayanum C. S. P. Parish et Rchb. f.			
	Dendrobium loddigesii Rolfe			
Japan	Dendrobium moniliforme (L.) Sw.	Fu-ran	Gives long life to men	Cakova et al. (2020)
Indian	Dendrobium macraei Lindl. (jeevanti)	Charaka samhita	Used as an astringent to the bowels, as anaphrodisiac, and in asthma and bronchitis	Lam et al. (2015)
	Dendrobium alpestre royle (jewanti)	Ayurved Jeevanti		
Thailand	Dendrobium draconis Rchb. F.	Unknown	Employed as a blood tonic	Ng et al. (2012)

documented in detail in "Compendium of Materia Medica" in Ming Dynasty (1590 AD). Nowadays, Dendrobium nobile Lindl., Dendrobium chrysotoxum Lindl., Dendrobium fimbriatum Hook., Dendrobium officinale Kimura et Migo, and Dendrobium huoshanense Z. Z. Tang et S. J. Cheng are included in Chinese Pharmacopoeia (2020 edition). Among these five species, Dendrobium nobile Lindl. is one of the 50 fundamental herbs used in traditional Chinese medicine (TCM). Generally, the fibrous stems of Dendrobium are employed as the officinal parts in ethnopharmacology, persevered by dry processing (Chinese Pharmacopoeia Commission, 2020). These stems are usually used either alone or mixed with other tonic Chinese herbs, like xī yáng shēn (American Ginseng) and gǒu qǐ zǐ (Barbary Wolferry Fruit) (Lin et al., 2018). Aside from China, Dendrobium species have also been used as ethnomedicines in Japan, Indian, and Thailand (Table 1). Given their high medicinal value and wide ethno-applications, the Dendrobium genus was recognized as a prized folk medicine (Ng et al., 2012).

Due to the important pharmacological activities and economical value of Dendrobium genus, up to now, many phytochemical and pharmacological researches have been implemented. The active constituents in Dendrobium are polysaccharides, alkaloids, flavonoids, bibenzyls, and several trace elements (He et al., 2020). The polysaccharides Dendrobium from exhibit immunomodulatory and hepatoprotective activities; and the alkaloids are antioxidant, anticancer, and neuroprotective, while other compounds display anti-angiogenesis, anticytotoxicity, and anti-mutagenesis effects (Ng et al., 2012; Xu et al., 2013). Alkaloids are the earliest identified category of compounds in Dendrobium (Chen and Chen, 1935). More importantly, Dendrobium alkaloids are the key constituents that responsible for their pharmacological activities, making them potential candidates for new drugs. Therefore, some important bioactive markers such as dendrobine (20) have attracted many scientists to

investigate their chemical, pharmaceutical, and biological mechanisms, as well as biogenetic pathways (Li Q. et al., 2017).

Dendrobium alkaloids with complex chemical structures consist of pyrrole, indolizidine, terpenoid alkaloids, organic amine alkaloids, indole, quinazoline, and others (Xu et al., 2013). In accordance with other genera of Orchidaceae plants, indolizidine alkaloids and organic amine alkaloids are the major constituents of this genus (Lam et al., 2015). These chemicals are considered as active ingredients for effects like anticytotoxic, antitumor, cytoprotection, inflammatory, gluconeogenesis regulation, and preventing neuronal apoptosis (Ng et al., 2012). For instance, Dendrobium nobile Lindl. is a famous TCM recorded in Chinese Pharmacopoeia (2020 edition). The alkaloids of Dendrobium nobile Lindl. (DNLA) are considered to have beneficial effects on liver metabolism, hepatic lipid homeostasis, neuronal activity, and resistance effects on tumors, cancers, and virus based on previous studies (Table 2). Dendrobine (20), a sesquiterpene alkaloid, makes up 92.6% of the DNLA (Xu et al., 2017). Dendrobine (20) is the first identified active alkaloid of Dendrobium nobile Lindl. (Chen and Chen, 1935), and is regarded as the standard agent for qualitative and quantitative evaluation of Dendrobium nobile Lindl. (Li R. et al., 2017).

In this review, we aim to summarize the structural types, pharmacological activities, and the mechanisms of biological activities of *Dendrobium* alkaloids. Additionally, the proposed biogenetic pathways of dendrobine (20) are also included.

STRUCTURAL IDENTIFICATION OF DENDROBIUM ALKALOIDS

Alkaloids are representatives of the first category of compounds extracted from *Dendrobium* (Xu et al., 2013). *Dendrobium* alkaloids were isolated by the traditional alkaloid extraction method given their basic chemical structure. Dried powders of

TABLE 2 | Summary of the pharmacological of alkaloids isolated from Dendrobium nobile Lindl.

No	Organ	Alkaloids content of crude extract	Constituents of alkaloid extract	Pharmacological activities	References
1	Stem	79.8%	Dendrobine (20), 92.6% Dendrobine-N-oxide (22), 3.3% Nobilonine (45), 2.0% Dendroxine (24), 0.9% 6-Hydroxy-nobilonine (46), 0.32%	Beneficial effects on liver glucose and lipid metabolism gene expressions	Xu et al. (2017) Li et al. (2019)
			13-Hydroxy-14- oxodendrobine (26), 0.07%	Protective effects on CCl ₄ -induced acute liver injury	
2	Stem	79.8%	Dendrobine (20), 92.6%	Protective effects on hepatic lipid homeostasis and acute liver injury	Huang S. et al. (2019); Zhou et al. (2020)
3	Stem	Unkown	Mixed fat-soluble alkaloids	Anti-tumor efficacy in human colorectal cancer	He et al. (2017)
4	Unkown	96.1%	Dendrobine (20), 90.7% Dendramine (23), 2.31% 3-Hydroxy-2-oxodendrobine (26), 1.29% Nobilonine, (45), 4.47%	Protection from OGD/RP-induced neuronal damages	Wang et al. (2010)
5	Stem	96.1%	Dendrobine (20), 90.7% Nobilonine (45), 4.47% Dendramine (23), 2.31% 3-Hydroxy-2-oxodendrobine (26), 1.29%	Protection of brain impairment	Li et al. (2011)
6	Unkown	54.5%	Dendrobine (20), 30.5%	Attenuation of LPS-induced hyperphosphorylation of tau protein and protection against LPS-induced apoptosis	Yang et al. (2014)
7	Unkown	79.8%	Dendrobine (20) Dendrobine-N-oxide (22)	Prevention of neuronal apoptosis and synaptic loss	Nie et al. (2016)
			Nobilonine (45) Dendroxine (24) 6-Hydroxy-nobilonine (46) 13-Hydroxy-14- oxodendrobine (26)	Regulation of a- and β-secretase in hippocampal neurons	Huang J. et al. (2019)
8	Dendrobine standard	>98%	Dendrobine (20), >98%	Anticancer activity toward non-small cell lung cancer cells	Song et al. (2019)
9	Dendrobine standard	98%	Dendrobine (20), 98%	Anti-influenza a virus	Li et al. (2017)

Dendrobium spp. were liquid-liquid extracted with various solvents, such as ethanol, methanol, or chloroform, then fractionated successively with water, petroleum ether, ethyl acetate, n-butyl alcohol, etc. (Yang et al., 2020). Subsequently, these fractions were purified on different silica gel column chromatography systems with various polarity ranges of solvents (Morita et al., 2000). Moreover, high performance liquid chromatography (HPLC) and ultra-performance liquid chromatography (UPLC) coupled with mass spectrometry were developed to discover new compounds of Dendrobium (Xu et al., 2020). Up to now, more than sixty alkaloids (Figures 1-5, 1-63) have been identified from this genus. The chemical structures include pyrrole, indolizidine, terpenoid, amine, and indole alkaloids. These compounds were mainly isolated from the whole plants, stems, or leaves of Dendrobium nobile Lindl., Dendrobium officinale Kimura et Migo, Dendrobium findlayanum C. S. P. Parish et Rchb. f., Dendrobium chrysanthum Wall. ex Lindl., Dendrobium crepidatum Lindl. ex Paxton, Dendrobium anosmum Lindl., Dendrobium devonianum Paxton, Dendrobium

friedericksianum Rchb. f., Dendrobium hildebrandii Rolfe, Dendrobium loddigesii Rolfe, Dendrobium lohohense Tang et F. T. Wang, Dendrobium moniliforme (L.) Sw., Dendrobium pierardii R. Br., Dendrobium primulinum Lindl., and Dendrobium wardianum R. Warner (Inubushi et al., 1964; Lüning et al., 1965; Elander et al., 1969; Ekevag et al., 1973; Begum et al., 2010; Lam et al., 2015; Hu et al., 2016; Hu et al., 2016; Xu et al., 2019).

Pyrrole Alkaloids

Most pyrrole alkaloids from Orchidaceae were found in *Dendrobium*, *Pleione*, and *Liparis* plants. Till now, only five pyrroles were reported in *Dendrobium*, and all of them are simple phthalide-pyrrolidine alkaloids (**Figure 1**). Shihunine (1), a water-soluble phthalide-type alkaloid, was the first pyrrole alkaloid from *Dendrobium lohohense* Tang et F. T. Wang in 1968 (Inubushi et al., 1964). Shihunidine (2) was also isolated from the same species by Li et al. (1991). Cis-trans isomerizations of dendrochrysines (3 and 4) and dendrochrysanines (5 and 6), the other four pyrrole isomers

alkaloids, were isolated from *Dendrobium chrysanthum* Wall. ex Lindl. (Ekevag et al., 1973; Yang et al., 2005), while hygrine (7) was produced in *Dendrobium primulinum* Lindl. (Lüning et al., 1965).

Indolizidine Alkaloids

Indolizidine alkaloids are important constituents of *Dendrobium* (Xu et al., 2019). Twelve indolizidine alkaloids were observed in *Dendrobium*, most of which were from *Dendrobium crepidatum* Lindl. et Paxton (**Figure 2**, 8–19). Dendroprimine (8) is a simple indolizidine alkaloid reported in *Dendrobium primulinum* Lindl. (Lüning et al., 1965). Other indolizidine alkaloids such as crepidine (9), crepidamine (10), isocrepidamine (11), and isodendrocrepine (12) were found in *Dendrobium crepidatum* Lindl. et Paxton (Elander et al., 1973; Hu et al., 2020). The other three alkaloids of this type (±)-homocrepidine A [(±)-13] (±)-dendrocrepidamine A [(±)-14], and homocrepidine B (15) were first identified from the same *Dendrobium* species by Hu et al. (2016; 2020). Then the absolute configurations of the new

pairs enantiomeric octahydroindolizine compounds (±)-homocrepodine A [(±)-13] and (±)- dendrocrepidamine A [(±)-14], were verified by single-crystal X-ray diffraction (Hu et al., 2016; Hu et al., 2020). Recently, four new indolizidine alkaloids, crepidatumines A to D (16–19), were purified from *Dendrobium crepidatum* Lindl. et Paxton by Xu et al. (2019; 2020).

Terpenoid Alkaloids

Terpenoid alkaloids are another important secondary metabolites principally isolated from *Dendrobium* (Xu et al., 2013). The types of alkaloids are various based on their mono-, sesqui-, di-, and triterpenoid skeletons. Dendrobine (20) was the first terpenoid-alkaloid elucidated from *Dendrobium nobile* Lindl. in 1932 (Chen and Chen 1935). Subsequently, a total of 25 dendrobine-type alkaloids were found in *Dendrobium nobile* Lindl., *Dendrobium findlayanum* C. S. P. Parish et Rchb. f., *Dendrobium wardianum* R. Warner, and *Dendrobium moniliforme* (L.) Sw., most of which are sesquiterpenoid alkaloids (**Figure 3**, 20–42, 51–52).

Interestingly, dendrobine-type alkaloids are a class of characteristic picrotoxanes with highly complex structures, which are only distributed in *Dendrobium* genus (Begum et al., 2010; Meng et al., 2017). All of these dendrobine-type alkaloids contain basic skeletons comprising one picrotoxane-type sesquiterpenoid combined with a five-membered C2-C9-lined N-heterocycle and C3-C5-linked lactonic ring (Xu et al., 2013).

Two thirds of terpenoid alkaloids in the genus *Dendrobium* were isolated from the certain species of *Dendrobium nobile* Lindl.. Mubironines A-C (27–29) were identified from the whole plant (Morita et al., 2000), and the absolute components of these three compounds were confirmed by single-crystal X-ray diffraction. Dendroterpene A and B (30–31) were found from the stems recently (Wang P. et al., 2019). Other terpenoid alkaloids from *Dendrobium nobile* Lindl., compounds 20–26 and 32–41 have been reported over eighty years (Chen and Chen, 1935; Shhosuke and Yoshimasa, 1964; Inubushi and Nakano, 1965; Okamoto et al., 1966a; Okamoto et al., 1966b; Granelli et al., 1970;

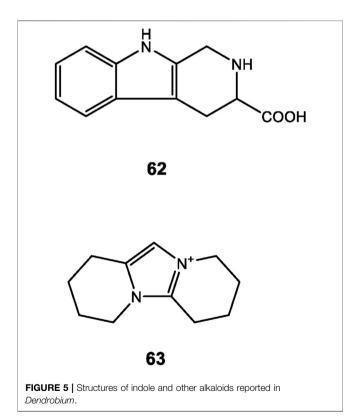
Elander and Leander, 1971; Hedman and Leander, 1972; Okamoto et al., 1972; Glomqvist et al., 1973; Wang et al., 1985; Meng et al., 2017; Wang Q. et al., 2019; Liu et al., 2020; Yang et al., 2020). A total of eleven terpenoid alkaloids were purified from another three Dendrobium Dendrofindline B (42) was isolated from Dendrobium findlayanum C. S. P. Parish et Rchb. f. (Liu et al., 2020). Besides, seven new seco-dendrobines, findlayines A-F (43-48), and dendrofindline A (49) were identified from the same species. (Yang et al., 2018; Liu et al., 2020; Yang et al., 2020). In 2007, Liu et al. (2007) reported the isolation and structural identification of moniline (50) from the stems and leaves of Dendrobium moniliforme (L.) Sw.. Dendrowardine (51) and wardianumine A (52) were purified from *Dendrobium* wardianum R. Warner by Liu and Zhao. (2003) and Zhang et al. 2017, respectively.

Amine Alkaloids

Amine alkaloids are a class of widely spread natural amines with basic nitrogen but cannot form a ring in the skeleton. Most

amines in *Dendrobium* are amides (**Figure 4**, 53–61). For example, *N-cis*-p-coumaroyltyramine (53) and *N-cis*-feruloyltyramine (54) were identified from the stems of

Dendrobium devonianum Paxton (Zhang et al., 2013). Pierardine (61) was isolated from Dendrobium pierardii R. Br. (Elander et al., 1969).



Indole and Other Types of Alkaloids

2,3,4,9-tetrahydro-1 H-pyrido [3,4-b] indole-3-carboxylic acid (62) was the only reported indole alkaloid from *Dendrobium devonianum* Paxton (Zhang et al., 2013) (**Figure 5**). Moreover,

anosmines (63) are another type of alkaloids isolated from two species of *Dendrobium*, whose structures were confirmed by X-ray crystallography (Hemscheidt and Spenser, 1993).

Metabolic Analysis of *Dendrobium*

At present, metabolomics has been widely utilized in the field of medicinal plants, such as bioactive components identification, drug metabolism, toxicology, and investigation on metabolic pathways, etc. (Liang et al., 2009). Alkaloids are regarded as chemical markers in quantitative analysis of Dendrobium. Generally, the metabolic profiling of Dendrobium alkaloid compounds was established by liquid chromatography coupled to single (LC-MS) and tandem (LC-MS/MS) mass spectrometry, in combination with multivariate data analyses, where secondary metabolites can be accurately quantified based on their fingerprint chromatograms. For example, the comparative metabolite analysis of Dendrobium officinale Kimura et Migo and Dendrobium huoshanense Z. Z. Tang et S. J. Cheng showed that the accumulation of alkaloids was species-specific (Song et al., 2020). Ten potential anti-inflammatory alkaloid components were detected from the extraction of Dendrobium aphyllum (Roxb.) C. E. C. Fisch by UPLC-MS (Wang P. et al.,2019), while eight water-soluble metabolites containing rare imidazolium alkaloids and anosmines (4) were identified by the screening of Dendrobium nobile Lindl., Dendrobium officinale Kimura et Migo, and Dendrobium loddigesii Rolfe, using chromatography along with spectroscopic techniques (Chen et al., 2018). Besides, DNLA was reported to improve hepatic lipid homeostasis based on the results of UPLC-MS of 48 kinds of hepatic bile acids in the livers of high fat diet (HFD)-fed mice (Huang S. et al., 2019). Furthermore, the combination of

metabolomic and transcriptomic technologies revealed the possible pathways in alkaloid biosynthesis of *Dendrobium* officinale Kimura et Migo (Guo et al., 2013).

PHARMACOLOGICAL ACTIVITIES

Dendrobium alkaloids are active components with antiinflammatory, antitumor, and anti-viral effects, which can also regulate hepatic lipid and gluconeogenesis, and protect from hyperglycemia. For a better understanding of the bioactivities of *Dendrobium* alkaloids, previous studies on pharmacological efficacy are summarized.

Anti-inflammatory Activity

Inflammation induced by endotoxin such as lipopolysaccharide (LPS), is an immune defense response of organisms to tissue injury and microbial agents (Guha and Mackman, 2001). Most anti-inflammatory activities were tested with the LPS-induced RAW264.7 model by evaluating the indices of nitric oxide (NO) production and the expression of inducible NO synthase (Chen et al., 2018). The anti-inflammatory activities of Dendrobium alkaloids have been reported. For example, anosmines (63) that were presented in four *Dendrobium* species exhibited inhibitory activity against NO production and inflammation in LPSactivated RAW264.7 cells without cytotoxic activity (Chen et al., 2018). Besides (+)-homocrepidine A [(+)-13] isolated from Dendrobium crepidatum Lindl. ex Paxton was evaluated for its anti-inflammatory activity (NO inhibition) with LPSinduced RAW 264.7 macrophages, and the half maximal inhibitory concentration (IC₅₀) value was 3.6 µM. However, the other enantiomeric isomer (-)-homocrepodine A [(-)-13], displayed an IC_{50} value of 22.8 μ M, which was almost 7 times less active than [(+)-13]. Besides, their racemic mixtures (\pm)-homocrepodine A [(\pm)-13], showed a moderate inhibitory effect (IC₅₀ = $5.0 \mu M$). Similar pharmacological activities were observed (\pm)-dendrocrepidamine A [(\pm)-14] (Hu et al., 2020). Compared with the enantiomers of racemic indolizidine and their racemic mixtures, homocrepidine B (15) also displayed moderate anti-inflammatory activity with the IC50 value of 27.6 μM (Hu et al., 2016). Furthermore, the total alkaloids, mainly consisted of six indolizine-type compounds from the same Dendrobium species, showed protective effects against the LPS-induced acute lung injury in mice by the down-regulation of the TLR4-mediated MyD88/MAPK signaling pathway (Hu et al., 2018). Taken together, the pharmacological investigations of Dendrobium alkaloids on anti-inflammatory shed light on scientific guidance for the source of this genus.

Improved Regulation of Hepatic Lipid Homeostasis and Gluconeogenesis

The liver is quite essential to the regulation of lipid and glucose homeostasis. On the other hand, the disruption of homeostasis will result in metabolic disorders of the liver, including fatty liver and diabetes, which are the most common chronic liver disease all over the world (Rinella, 2015). DNLA was found to impact the regulation of liver glucose and the expressions of lipid metabolism genes in mice livers by increasing the expressions of PGC1a, Glut2, Cpt1a, Acox, ATGL/Pnpla2, and FoxO1 genes, and decreasing the mRNA transcription from the Srebp1 gene (Xu et al., 2017). Moreover, excessive accumulation of hepatic lipids is responsible for liver metabolic dysfunction. Modulation of bile acids has been reported as an effective intervention strategy for maintaining hepatic lipid homeostasis (Chiang, 2013). DNLA exerted protective effects on hepatic lipid homeostasis by enhancing taurine-conjugated bile acids and decreasing the cholic acid/chenodeoxycholic acid ratio (Huang S. et al., 2019). To be specific, DNLA decreased four types of bile acids and increased five types of bile acids among 48 kinds of hepatic bile acids in the livers of high-fat diet (HFD)-fed mice (Huang S. et al., 2019). On the other hand, DNLA regulated hepatic gluconeogenesis by mediating the hepatic antioxidant components through hepatic metallothionein and the gene expression of the nuclear factor erythroid 2-related factor 2 antioxidant pathway, which plays critical roles in host defense against abnormal gluconeogenesis (Xu et al., 2017). The mechanisms were further elucidated that DNLA improved mitochondrial function and inhibited mitochondrial apoptotic cell death (Zhou et al., 2020). Overall, considering the beneficial effects of Dendrobium alkaloids on liver metabolism, Dendrobium alkaloids could be used as natural compounds in the development of new treatments for hyperlipidemia and hyperglycaemia.

Anti-tumor Activity

It was reported that Dendrobium alkaloids could inhibit tumor cell growth and mediate apoptosis. (He et al., 2017; Song et al., 2019; Wang et al., 2014). Specifically, the alkaloid extracts of Dendrobium candidum Wall. ex Lindl. were reported to significantly inhibit the growth of transplanted Lewis tumors, meanwhile, the mixed alkaloids could improve the spleen index and regulate the expressions of TNF-α and IL-2 (Wang et al., 2014). Moreover, the fat-soluble alkaloids extracted from Dendrobium nobile Lindl. were found to induce the apoptosis of human colorectal cancer HT-29 cells with an IC50 value of 0.72 mg/ml at 48 h, where the cell cycle was arrested in G2 phase. Besides, the extraction decreased the mitochondrial membrane potential (ΔΨm) and induced ROS accumulation by increasing expression levels of apoptotic proteins, such as Caspase-9, Caspase-3, and intracellular cytochrome C (He et al., 2017), which may be related to the mitochondria-mediated apoptotic pathway. The combined treatment using sesquiterpene alkaloids, dendrobine (20) and cisplatin, was also effective for inhibiting the non-small cell lung cancer cells (NSCLC) in vitro and in vivo, where the cytotoxicity was induced by the simulation of c-jun NH₂-terminal kinase (JNK)/p38 stress signaling pathways, and the expression change of pro-apoptotic proteins Bax and Bim further led to the apoptosis (Figure 6, revised from song et al., 2019, created with BioRender.com). Besides, dendrobine (20) also mediated apoptotic cell death by the mitochondrial-mediated pathway (Song et al., 2019). On the whole, due to the distinct association with cell death signaling pathways, dendrobine (20)

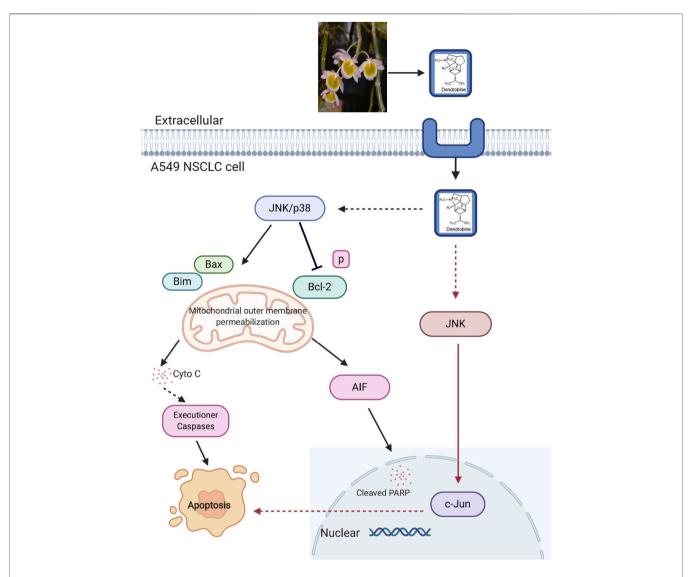


FIGURE 6 | Signaling pathway involved in dendrobine induced apoptosis in cancer cells. JNK, c-Jun N-terminal kinase; p38, p38 mitogenactivated protein kinase; Cyto C, cytochrome C; AIF, apoptosis inducing factor; Blc-2, B-cell lymphoma two; Bim, Bcl-2 interacting mediator of cell death; PARP, poly ADP-ribose polymerase.

can be regarded as a potential agent for the development of novel anti-NSCLS strategies especially when combined with cisplatin. (Song et al., 2019).

Renal Protective and Anti-Diabetic Effects

In China, the dried stems of some *Dendrobium* species including *Dendrobium huoshanense* Z. Z. Tang et S. J. Cheng, *Dendrobium officinale* Kimura et Migo, and *Dendrobium nobile* Lindl. have been used to nourish kidney and improve the symptoms of diabetes (Cakova et al., 2020). For instance, shihunidine (2) and shihunine (1) isolated from *Dendrobium loddigesii* Rolfe displayed inhibitory effects on Na⁺/K⁺-ATPase of the rat kidney (Li et al., 1991). Li et al. (2019) recently reported that DNLA showed vital hypoglycemic effects in diabetic rats. The shihunine (1) extracts from *Dendrobium loddigesii* Rolfe at the dose of 50 mg/kg decreased the triglycerides level by 43.7%, compared

with the non-treated db/db mice, and inhibited the expression of cleaved cysteine aspartic acid-specific protease 3. The result of western blot analysis also verified the agonistic effects of shihunine (1) extracts on the expressions of adenosine monophosphate-activated protein kinase phosphorylation and glucose transporter four in the liver or adipose tissues. Moreover, in clinical application, *Dendrobium* combined with other herbs, such as *Astragalus* spp. and *Schisandra* Michx., was applied for the therapy of diabetes (Cakova et al., 2020).

Neuro-Protective Activity

It was reported that *Dendrobium* alkaloids exerted beneficial effects on neuronal systems (Wang et al., 2010; Li et al., 2011), among which *Dendrobium nobile* Lindl. was most extensively studied on the treatment of central nervous system disorders. DNLA, containing dendrobine (20), dendrobine-N-oxide (22),

nobilonine (45), dendroxine (24), 6-hydroxy-nobilonine (46), and 3-hydroxy-2-oxodendrobine (also referred as 13-hydroxy-14oxoHudendrobine) (26), was known as the active components of Dendrobium nobile Lindl. (Wang et al., 2010; Xu et al., 2017; Nie et al., 2018). Investigation on the mechanisms underlying the neuroprotective effects of DNLA revealed that DNLA prominently improved the neurobehavioral performance and prevented LPS-induced elevation in tumor necrosis factor receptor one via inhibition of phosphorylated p38 mitogenactivated protein kinases and the downstream nuclear factor kappa-B signal pathway (Li et al., 2011; Ng et al., 2012). Moreover, DNLA decreased the level of intracellular amyloid β peptide (Aβ) by improving impaired autolysosomal proteolysis in amyloid precursor protein/presenilin one mice (Nie et al., 2018), and regulating α- and β-secretase in hippocampal neurons of Sprague-Dawley rats (Huang J. et al., 2019). The reduction of Aβ attenuated Aβ₂₅₋₃₅-induced spatial learning and memory impairments by increasing the protein expression of neurotrophic factors, such as brain-derived neurotrophic factor, ciliary neurotrophic factor, and glial cell line-derived neurotrophic factor (Nie et al., 2016; Nie et al., 2018). Furthermore, DNLA lowered the LPS-induced hyperphosphorylation of tau protein and prevented neuronal apoptosis in rat brains (Yang et al., 2014). Given the neuro-protective effect of Dendrobium alkaloids, they could be promising therapeutic agents for the treatment of neurodegenerative disorders, such as Alzheimer's disease (Cakova et al., 2020).

Anti-influenza A Virus Activity

Dendrobine (20) displayed antiviral activity against influenza A viruses, including A/FM-1/1/47 (H1N1), A/Puerto Rico/8/34 H274Y (H1N1), and A/Aichi/2/68 (H3N2) in the antiviral assay, plaque assay, time-of-addition assay, and pseudovirus neutralization assay, with IC $_{50}$ values of 3.39 \pm 0.32, 2.16 \pm 0.91, and 5.32 \pm 1.68 µg/ml, respectively. The low IC $_{50}$ values of dendrobine (20) indicated that this compound could be applied as potential promising agents to treat influenza virus infection (Li R. et al., 2017). More importantly, the anti-virus test using dendrobine (20) provided valuable information for the full application of the TCM named "shí hú" (Li R. et al., 2017).

CHEMICAL SYNTHESIS AND BIOSYNTHETIC PATHWAY OF DENDROBINE

Dendrobine (20) is the first identified sesquiterpene alkaloid from *Dendrobium nobile* Lindl., which is recommended as the exclusive chemical marker for the quality control of this species by Chinese Pharmacopoeia (2015 and 2020 edition). The rule suggested that the mass fraction of dendrobine (20) should be greater than 0.4% in the medicinal *Dendrobium nobile* Lindl..

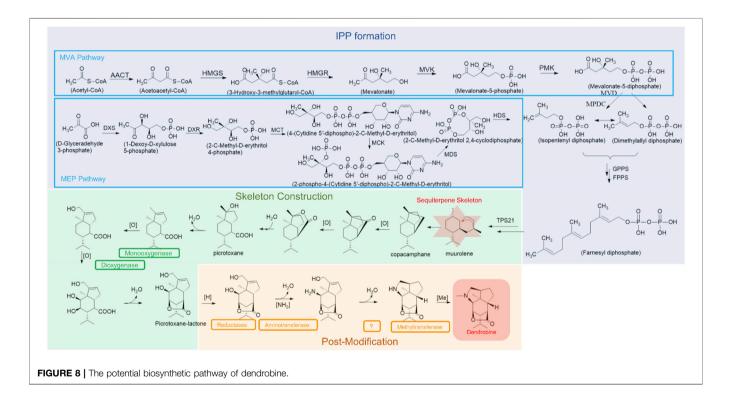
Chemical Synthesis of Dendrobine

Dendrobine (20) with a complicated tetracyclic ring system and seven contiguous stereocenters displayed remarkable bioactivities. Up to now, several cases are available on the total chemical synthesis of dendrobine (20). Connolly and Heathcock (1985) first synthesized dendrobine (20) in 1985. Several decades later, Kreis and Carreira (2012) achieved the total chemical synthesis based on 18 cascaded reactions with a key amine group, and the main synthesis pathway is summarized in Figure 7 (Kreis and Carreira, 2012). Other three dendrobine-alkaloids (–)-dendrobine (20) (–)-mubironine B (27), and (–)-dendroxine (24) were also obtained by total synthesis (Guo et al., 2018). Despite the advances of these total synthesis methods, it remains challenging to overcome the compound yield after a series of reactions (Li Q. et al., 2017).

Biosynthesis of Dendrobine

Dendrobine (20) belongs to the class of terpenoid indole alkaloids (TIAs) (Wang et al., 2020). The biogenetic pathway of TIAs is conservative among alkaloid-producing plants (Li Q. et al., 2017). Based on the results of transcriptome and metabolomic analysis, the putative dendrobine (20) biosynthetic pathway was proposed, and a series of key metabolic genes were labeled in **Figure 8** (Guo et al., 2013; Li Q. et al., 2017; Chen et al., 2019).

Three core stages were involved in the biogenetic pathway, including the formation of isopentenyl diphosphate (IPP), the construction of sesquiterpene skeleton, and the process of post-modification. Firstly, the mevalonate (MVA) and 2-Cmethyl-D-erythritol 4-phosphate (MEP) pathways were considered as the upstream of dendrobine (20) biosynthetic pathway, mainly for the synthesis of IPP (Chen et al., 2019). Three key enzyme-coding genes involved in the MVA pathway, acetyl-CoA C-acetyltransferase (AACT)phosphomevalonate kinase (PMK) gene, and diphosphomevalonate decarboxylase (MVD) gene, were observed to be positively associated with dendrobine (20) accumulation in Dendrobium nobile Lindl. through large-scale transcriptome sequencing, and then validated through qRTanalysis (Li Q. et al., 2017). In contrast, hydroxymethylglutaryl-CoA synthase (HMGS) gene and 3hydroxy-3-methylglutaryl coenzyme A reductase (HMGR) gene were found to be less effective in dendrobine (20) biosynthesis in the same species (Li Q. et al., 2017), though HMGS and HMGR both played significant roles in alkaloid biosynthesis in Dendrobium officinale Kimura et Migo (Chen et al., 2019). The result shows that HMGS and HMGR may differently contribute to the production of dendrobine (20) in Dendrobium spp.. In the MEP pathway, rate-determining genes 1-deoxy-D-xylulose-5-phosphate synthase (DXS) and 1-deoxy-D-xylulose-5-phosphate reductoisomerase (DXR) isolated from protocorms of Dendrobium officinale Kimura et Migo were largely up-regulated by the methyl jasmonate (MeJA) treatment, suggesting their significant roles in the sesquiterpene biosynthesis based on the analysis of KEGG enrichment and relative expression (Fan et al., 2016; Chen et al., 2019). The crucial impacts of DXS and DXR in Dendrobium officinale Kimura et Migo were later confirmed by the high correlations between total alkaloid contents and their transcripts (Chen et al., 2019), furthermore, DXS was a leaf-specific expression gene accounting for high alkaloids content in leaves (Shen et al., 2017).



IPP is an important downstream product of MVA and MEP pathways, which is the precursor for the construction of synthetic terpenes. IPP formed the skeleton of muurolene-type sesquiterpene initially catalyzed by TPS21 enzyme (Li Q. et al., 2017), then this sesquiterpene was further oxidized by monooxygenases and/or dioxygenase to produce picrotoxane-lactone. Cytochromes P450s (CYP450s) is a complex superfamily of monooxygenase, and they are vital for the formation of sesquiterpene alkaloids (dendrobine). At present, some CYP450s have been discovered in a few

Dendrobium species (Coon, 2005; Guo et al., 2013; Li Q. et al., 2017; Yuan et al., 2018; Chen et al., 2019). For instance, 59 full-length CYP450s candidate genes involved in the dendrobine (20) biosynthesis were identified and characterized in *Dendrobium officinale* Kimura et Migo through tissue-specific transcriptomic analysis, phylogenetic analysis, and further gene expression pattern induced by MeJA treatment (Chen et al., 2019). In *Dendrobium huoshanense* Z. Z. Tang et S. J. Cheng, 229 genes were identified as putative CYP450s, 7.8% of which were CYP71 family members

associated with hydroxylation steps of alkaloid biosynthesis (Yuan et al., 2018). However, the family members and expression patterns of CYP450s remain unclear in most *Dendrobium* plants. It is worth mentioning that all other 25 dendrobine-type alkaloids (20–42, 51–52) identified from *Dendrobium* were believed to share similar biosynthesis pathways due to the mutual sesquiterpene backbone of these alkaloids (Guo et al., 2013; Chen et al., 2019).

Following the generation of sesquiterpene skeleton, dendrobine (20) was finally synthesized by the postmodification of picrotoxane-lactone with a series of enzymes, including reductases, aminotransferases, and methyltransferases (Guo et al., 2013; Yuan et al., 2018). In Dendrobium nobile Lindl., the expression level of methyltransferase-like protein 23 (METTL23) gene, histone-lysine N-methyltransferase ATX4 (ATX4) gene, and alanine aminotransferase 2 (AAT2) gene were enhanced after inoculation with MF23 (Mycena sp.), which was positively related with the content of dendrobine (20), implying their important roles in dendrobine (20) biosynthesis (Li Q. et al., 2017). Transcription factors play vital roles in modulating the expression of dendrobine (20) biosynthesis genes, such as C3H, bHLH, bZIP, MYB, and WRKY in Dendrobium officinale Kimura et Migo (Yuan et al., 2018).

Although the common biosynthesis pathway for most TIAs through the construction of strictosidine backbone exists in many plants (Wang et al., 2018), no enzyme involved in strictosidine formation has been verified in dendrobine (20) biosynthesis. However, due to the complex dendrobine (20) metabolism, accurate identification of genetic networks from a large number of candidate genes is needed in the future.

The metabolism of dendrobine (20) was affected by abiotic and biotic stresses. For example, light intensity was reported to influence the content of dendrobine (20) (Li J. L. et al., 2017). MeJA, a signaling molecule in the biosynthesis of alkaloids, could induce the accumulation of *Dendrobium* alkaloids by an active precursor supply (Chen et al., 2019). Besides, symbiosis with mycorrhizal fungus could stimulate the biosynthesis of dendrobine (20) by regulating the expressions of genes

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involved in the MVA pathway (Li Q. et al., 2017). Other relevant factors need to be further elucidated.

CONCLUSION

In this paper, we summarized the structural types, pharmacological activities, and mechanisms of Dendrobium alkaloids, as well as the suggested biogenetic pathway of dendrobine (20), which is an important type of sesquiterpene alkaloids. Despite the advances of the investigation on alkaloids, more emphasis should be laid on the discovery of more novel skeletons in *Dendrobium* genus based on abundant alkaloid metabolites, and the improvement of isolation methods. Moreover, many current studies on Dendrobium were only focused on their crude extracts, or the activity of mixtures, which necessitates the need for figuring out the typical pharmacological activity of pure Dendrobium alkaloids. Additionally, further investigation on novel pharmacological activities of these alkaloids should be implemented. Meanwhile, in-depth researches on the biological mechanisms of these activities are also desired. Finally, although the biosynthetic pathway of dendrobine (20) has been proposed, further confirmation is anticipated.

AUTHOR CONTRIBUTIONS

DZ and SC contributed to the conception of the review. YZ and EK helped collect and perform the chemical analysis of compounds. FY helped to analyze the pharmacological activities of alkaloids. ZM and YS contributed to the mechanisms and biosynthetic pathways of alkaloids and wrote the manuscript.

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Andrographolide Against Lung Cancer-New Pharmacological Insights Based on High-Throughput Metabolomics Analysis Combined with Network Pharmacology

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Andrographolide (Andro) has known to treat various illnesses such as colds, diarrhea, fever and infectious diseases. However, the effect mechanism of Andro is still unclear. Therefore, we used high-throughput metabolomics analysis to discover biomarkers, metabolic profiles and pathways to reveal the pharmacological action and effective mechanism of Andro against lung cancer. The metabolic effects of Andro on lung cancer animal was explored by ultra-performance liquid chromatography-triple-time of flight/mass spectrometry (UPLC-TOF/MS) analysis. Our results showed that Andro exhibited significant protective effects against lung cancer. Compared with control group, a total of 25 metabolites biomarkers was identified in urine of model animals, which 18 of them were regulated toward the normal direction after Andro treatment, and network pharmacology analysis showed that they were related with 570 proteins. Biological pathways analysis showed that the 11 metabolism pathways were regulated by Andro treatment in lung cancer mouse, and amino acid metabolism and arachidonic acid metabolism have great potential as target pathways for Andro against lung cancer. It revealed that high-throughput metabolomics combined with network pharmacology analysis provides deeply insight into the therapeutic mechanisms of natural product for promoting medicine development and disease treatment.

Keywords: target, metabolic pathway, urine biomarker, untargeted metabolomics, lung cancer, liquid chromatography

INTRODUCTION

Lung cancer accounting for 20% of all cancer death has been the major murderer for many years, which mostly because it is asymptomatic in primary stage and typically perceived at advanced stages (de Groot et al., 2018; Barta et al., 2019; Kim et al., 2020). The risk factors of lung cancer were related with cigarette smoking, E-cigarettes, biomass fuels, chronic obstructive pulmonary disease, occupational exposures, ambient air pollution, diet and nutrition as well as genetic factors (Trédaniel et al., 1994; Malhotra et al., 2016; Woodard et al., 2016; Sheng et al., 2018). Lowdose chest tomography chest X-rays and sputum cytology screening have been made in clinical

practice for early diagnosis, which possesses high rates of positive findings and is appropriate for diagnosis of lung cancers with low threats (Woznitza et al., 2017; New and Keith, 2018). Currently, there are three main treatment methods for lung cancer, which are chemotherapy, radiation therapy and surgery (Wibowo et al., 2016; Azar et al., 2017; Saad and Mathew, 2020). However, chemotherapy brings out adverse effects to a certain extent resulting from a long period management (Gridelli et al., 2011). Radiation therapy is only suitable for patients with small cell lung cancer, and it must be combined with some painkillers during the process of treatment (Forde et al., 2014; Postow et al., 2015; Verma and Simone, 2019). There is an imperative demand to find an emerging method with low side effects and intense activity for lung cancer treatment.

Andrographis paniculata (Burm. f.) Nees is a well-known medicinal plant in Southeastern Asian countries, has been widely applied as immunostimulant and anti-inflammatory drugs in clinic practice for many years (Puri et al., 1993). Andrographolide (Andro) is known to possess ability to treat the common cold, myocardial ischemia, respiratory tract infections, diarrhea, inflammation and infectious diseases (Zhu H. L. et al., 2011; Hossain et al., 2014; Wintachai et al., 2015; Ding et al., 2017). Some studies reported that it protected against acute lung injury exerted by reducing expression of myeloperoxidase and neutrophil-derived proteases, increasing in adhesion molecules (Zhu et al., 2013; Yang et al., 2014; Peng et al., 2016a; Gao et al., 2018). It also increases Nrf2 activity to protect against cigarette smoke-induced oxidative lung injury (Guan et al., 2013; Peng et al., 2016b). Andro ameliorates lung inflammation and fibrosis by inhibition of AIM2 inflammasome-mediated pyroptosis, activation of heme oxygenase-1 (Zhu Z. T. et al., 2011; Yang et al., 2013; Gao et al., 2019). The antimicrobial mechanism of Andro is related with up-regulation of human β -defensin-2 in human lung epithelial cells (Shao et al., 2012; Tan et al., 2016). It can down-regulate PI3K/Akt signaling pathway in lung cancer cells during in the process of proliferation, migration and invasion (Lee et al., 2010; Lin et al., 2011; Luo et al., 2013; Luo et al., 2014; Lim et al., 2015). Cisplatin-mediated anticancer effects was enhanced by Andro through blockade of autophagy and activation of the Akt/mTOR pathway (Mi et al., 2016; Yuwen et al., 2017).

Metabolomics method can used to discover the biomarker and pathways related to disease processes and elucidate the mechanism of drugs (Johnson et al., 2016; Zhang et al., 2014; Zhang A. et al., 2017; Qiu et al., 2020). The untargeted metabolomics has ability to undertake simultaneous assessment of metabolites without any sample knowledge for hypothesis generation (Liang et al., 2014; Wang et al., 2014; Wu and Feng, 2016; Varma et al., 2018; Zhang. et al., 2019a; Xie et al., 2019). The major disadvantage of untargeted metabolomics is that sample analysis generate lots of data leading to the majority of biological features are unidentifiable (Ribbenstedt et al., 2018; Zhang Y. et al., 2017; Ren, et al., 2018). At present, the combined analytical platform includes the ultra-performance liquid chromatography (UPLC) or gas chromatography in tandem with mass spectrometry (MS) and nuclear magnetic resonance spectroscopy (NMR) (French et al., 2018; Sun et al., 2018; Zhang

et al., 2018, Zhang et al., 2019b). These techniques allow for characteristic fingerprints of objects, predictive algorithms with pattern recognition statistical approaches to explain biological effect (Xia et al., 2013; Liang et al., 2015; Zhang et al., 2020). In this work, the untargeted metabolomics strategy based on UPLC-TOF/MS was used to explore the potential biomarkers and related metabolic pathways and to reveal the anticancer effect of Andro.

EXPERIMENTAL

Animals and Feeding

Animal care and experimental procedures were performed in accordance with the criteria outlined in the "Guide for the Care and Use of Laboratory Animals" prepared by the National Academy of Sciences. A total of forty-seven male C57BL/6 mice (6–8 weeks old, $20 \pm 2\,\mathrm{g}$ weight) in SPF grade were purchased from Envigo Laboratory Animal Co., Ltd (Suzhou, China, catalog no. SCXK 2019-0002), which were bred and maintained in pathogen-free cages with 12 h light/dark cycles from 9:00–21:00, temperatures of $24^{\circ}\mathrm{C} \pm 2^{\circ}\mathrm{C}$, humidity of $50 \pm 5\%$, and food and water ad libitum.

Reagents

Pentobarbital sodium, sodium chloride solution and neutral buffered formalin were purchased from Xinxiang Sanwei Disinfectant Co., Ltd. (Tianjin, China). Andro (97.5% purity) was provided by Northern Biotechnology Research Institute (Beijing, China) and its chromatographic fingerprint of HPLC is shown in Supplementary Figure S1. Cisplatin was purchased from APIChem Technology (Hangzhou, China) and used as the positive drug. Interleukin-6 (IL-6), interleukin-2 (IL-2) and interleukin-10 (IL-10) were was purchased from Toronto Research Chemicals (Toronto, Canada). Interleukin-1 beta (IL-1β) was obtained from Origene Technologies, Inc (Beijing, China). Tumor necrosis factor-α (TNF-α) and nuclear transcription factor-κB (NF-κB) were bought from Biotechnology BioengineeringCo., Ltd. (Shanghai, China). Immunoglobulin G (IgG), immunoglobulin A (IgA) and immunoglobulin M (IgM) were purchased from Bioworld Technology, Inc (St Louis Park, MN, United States). Vascular endothelial growth factor (VEGF) was purchased from Jackson ImmunoResearch (West Grove, PA, United States). Hypoxia-inducible transcription factor-1a (HIF-1α) and matrixmetallo proteinase-2 (MMP-2) were purchased from BIOSS (Beijing, China). Interferon-γ (TFN-γ), transforming growth factor-\(\beta\) (TGF-\(\beta\)), toll like receptor 4 (TLR4) and myeloid differentiation factor 88 (MYD88) were provided from BioswarmBiotechnology Co., Ltd. (Hangzhou, China). Methanol, acetonitrile and formic acid were of chromatographic grade and purchased from Fisher Chemical Company (Geel, Belgium). Pure water was brought from the A.S. Watson Group Ltd. (Hong Kong, China). Chromatographic grade leucine enkephalin were purchased from Invitrogen Life Technologies (Carlsbad, CA, United States).

Instrument

High-performance ultra-performance liquid chromatography-Triple-time of flight/mass spectrometry (UPLC-Triple-TOF/MS) system used in this research consisted of a ACQUITY H-CLASS UPLC (Waters Corp., Milford, MA, USA) and a Triple TOF™ 5,600 + Mass Spectrometer detector equipped with positive and negative modes of electrospray source (AB SCIEX, Foster City, CA, United States). H3018DR cryogenic high-speed centrifuge (Sigma Laborzentrifugen GmbH, Osterode am Harz, Germany); Normal-temperature centrifuge (Scientific Industries Inc., Bohemia, NY, United States)); WH-861 Vortex Shaker (Tanon Science andTechnology Co. Ltd. China); CS-6400 automatic biochemical analyzer (Vital Scientific, Eppendorf, Germany)); BCD-206TAS Low-temperature refrigerator (Haier Company, China); AE240 mettler electronic balance (Mettler Toledo, Columbus, Ohio, United States).

Grouping, Modelestablishment and Administration

After seven days of adaptive feeding, C57BL/6 mice were divided into four groups in the light of the principle of weight uniformity: normal control group (NC, n = 10), lung cancer model group (LC, n = 13), cisplatin-treated group (LC + Cis, n = 12) and Androtreated group (LC + Andro, n = 12). Lewis lung carcinoma cells were obtained from the Cancer Center of West China Medical University (Sichuan, China), then were cultured and generated in Dulbecco's modified Eagle's medium (Thermo Fisher Scientific, Inc., Waltham, MA, United States) containing 10% fetal bovine serum (Thermo Fisher Scientific, Inc.). Under 37°C and 5% CO₂ saturated humidity, the medium was changed every other day. Cells were every digested by trypsin, and the logarithmic phase cells were collected for experiment. A single dose 1×10^7 /ml Lewis lung cancer cells 0.2 ml were inoculated subcutaneously into the light axillary of C57BL mice. Tumors with a diameter of approximately 1-1.5 cm were formed in the right armpit of the modeled mice (10 days following injection), which the mice were considered as successfully established in xenografts manner (Li et al., 2016; Zhang Y. et al., 2019; Zhao et al., 2019). From the first day of modeling, mouse in NC and LC group were received dosage of 0.2 ml/10 g physiological saline via intragastric administration, mouse in LC + Cis group and LC + Andro group were respectively received dosage of 4.0 mg/kg/day cisplatin and 10.0 µMol/molar/kg/day Andro in intragastric administration way for twenty-eight days.

Sample Collection and PreparationUrine Sample

After the final time of Andro administration, each mice in NC, LC, LC + Cis and LC + Andro group was individually fed in metabolic cages to gather urine for 24 h. The urine samples were centrifuged at 10,000 g for 15 min at 4°C, and then the supernatant liquid were delivered into a new eppendorf tube stored in -80°C refrigerator until metabolomics study. Prior to analysis, urine samples were thawed at 4°C until no ice was visible in the sample. Subsequently, 100 μL of aliquots of the urine samples were added 400 μL methanol in order to precipitate the proteins. The solution mixture was vibrated for 60 s and centrifuged at 12,000 g for 15 min, which gained supernatant was evaporated to dryness at 60°C under a stream of nitrogen. The

residue was dissolved again in 150 μL of methanol followed by vibrated for 30 s and centrifuging at 12,000 rpm for 10 min. 10 μL clear supernatant from each mice were mixed into a new eppendorf tube as quality control (QC) sample and the remained samples were passed through a 0.22 μm PTFE filter for UPLC-Triple-TOF/MS analysis.

Serum Sample

At 24 h after the final time of Andro treatment, mouse in NC, LC, LC + Cis and LC + Andro group were mildly anesthetized with sodium pentobarbital (50 mg/kg, i.p.). The blood samples of the animals were respectively collected from the abdominal aorta by a syringe, which were placed 10 min for coagulation and centrifuged at 3500 g for 15 min at 4°C. The obtained supernatant serum was delivered into a clean plastic tube and stored under -80°C until blood biochemical analysis.

Tumors Tissue Sample

Mice in each group were sacrificed by cervical spine removal, and the axillary subcutaneous tumor tissue was quickly and completely peeled off on ice. After weighting, the tumor samples were placed in liquid nitrogen and stored in a refrigerator at -80° C for tissue biochemical analysis.

Biochemical Indexes Detection

Prior to analysis, serum and tumor samples were thawed at 4° C until no ice was visible in the sample. According to the manufacturer's instructions, serum biochemical parameters level of IL-6, IL-1 β , TNF- α , VEGF, HIF-1 α , MMP-2, IgG, IgA, IgM, IL-2 and TFN- γ were evaluated using ELISA kits. Tumor tissue samples were homogenized and dissolved by corresponding solution based on the manufacturer's instructions of kits, then the IL-10, TGF- β , TLR4, MYD88 and NF- κ B level were measured by automatic biochemical analyzer.

Metabolomics Analyses

Chromatography and Mass Spectrometry Conditions

All urine samples were analyzed using the UPLC-Triple-TOF/MS system following the manufacturer's instructions. An Acquity UPLC HSS C18 column (1.7 μ m, 2.1 \times 100 mm²) from Waters Corporation (Massachusetts, United States) was used for chromatographic separation. The column oven was kept at 33°C, and the temperature of the sample manager was maintained at 15°C. The flow rate was set 0.3 ml/min and the injection volume was 3 µL. 10 and 90% acetonitrile aqueous solutions were applied as weak and strong wash solvents respectively in the analyzed process. The mobile phase consisted of A (0.1% formic acid-water) and B (0.1% formic acid-acetonitrile). UPLC elution conditions were run as following: 0-1.5 min, 8% B; 1.5-4 min, 8-35% B; 4-8 min, 35-70% B; 8-9 min, 70-90% B; 9-11 min 90-8% B; 11-13 min 8% B. QC samples were sampled six times before analysis, and then was injected once every eight experimental samples. Using the Triple-TOF/MS model, the electrospray ionization (ESI) source was operated in both positive and negative modes. 50 to 1200 Da mass spectrum data were collected in MSE centroid mode. Accurate mass determination using leucineenkephalin (m/z 556.2771 in ESI+and 554.2615 in ESI-) was considered as external reference for Lock SprayTM injected at a

flow of 10 μ L/min in order to ensure the mass reproducibility and accuracy. The optimized MS parameters in the positive-ion detection mode are as follows: source temperature, 140°C; desolvation temperature, 460°C; desolvation gas flow 800 L/h; capillary voltage, 2.6 kV; cone voltage, 45 V, cone gas flow, 55 L/h, collision energy, 15–55 eV. The negative ion mode parameters was the same as the positive-ion detection mode, except for being negative in the capillary voltage 2.0 kV and cone gas flow 45 L/h. In addition, the air curtain gas was set 40 psi; 55 psi of atomizing gas and 55 psi of auxiliary atomizing gas.

Metabolome Data Interpretation

MarkerLynx XS Version 4.1 software (Waters Co., Milford, MA, United States) was used to command the instrument system, perform the sample list and obtain raw data in m/zXML format, and then XCMS (www.bioconductor.org/) was applied to extract the peak data, peak matching, peak alignment, and export before multivariate statistical analysis of variables. Three-dimensional data matrix including sample identity (ID), molecular mass (MS), peak area, and standardized ion strength was saved after data preprocessing by unit variance scaling and the mean-centered method. The exported data were imported to SIMCA-P software (Version 14.1, Umetric, Umea, Sweden) for multivariate analysis such as principal component analysis (PCA) and orthogonal projections to latent structures discriminant analysis (OPLS-DA). PCA is an unsupervized method of pattern recognition approach that have ability to gain the overview and classification showing maximum variation and pattern recognition between. A score plot of the OPLS-DA model as supervised method was employed to visualize the metabolic difference between two different groups. S-plots generated from the OPLS-DA predictive results probe into the potential biomarkers that made a remarkable contribution to the metabolic distinction, which ion with the variable importance in the projection (VIP) value above 1.0 were considered significant. Meanwhile, data between two different groups were dissected by two-way analysis of variance to test the significance of differences, which significant differences meet p values less than 0.05 in test were considered significant. Afterward, the potential ions were verified by the raw MS data in chromatogram and accurate masses of quasimolecular ions were exported into biochemical databases online including METLIN (http://metlin.scripps.edu/), SMPD (http://www.smpdb. ca/), HMDB (http://www.hmdb.ca/) and KEGG (http://www.kegg. com/) (5 ppm as the accepted mass error) to confirm the structure of biomarkers. Next, the biomarkers were further identified by comparing the retention time and the tandem mass spectrometry (MS/MS) fragments of metabolites with those of the chemical standards. Adducts were obtained with the mass tolerance at 10 ppm. MetaboAnalyst 5.0 (http://www.metaboanalyst.ca/) was used to seek out vital potential metabolic pathways enrichment and topological analysis and network establishment. The metabolic correlation protein analysis of Andro efficacy was performed by Cytoscape 3.7.1 and Gene Cards (https://www.genecards.org/).

Statistical Analysis

During the experiments, all the tests were carried out at least three times using independent samples. All data are presented as mean \pm standard deviation, which statistical analysis was

conducted using SPSS software, version 12.0 software (SPSS, Inc., Chicago, IL, United States). The Student's t-test was applied to compare the difference between two individual groups, then P-values ≤ 0.05 were considered to indicate a statistically significant and P-values ≤ 0.01 were considered to indicate statistical significant. All statistical analyses were conducted on GraphPad Prism 6.05 software.

RESULTS

Effect of Andro on Biochemical Index

The mouse in NC group with smooth and shiny hair present normal feeding, drinking, excretion and weight gain in active state. In LC group, mouse with dirty and messy fur have a decreasing drinking, feeding and increasing excretion, moist cage, and weight reduction. Compared with LC group, the general states of the mouse in LC + Andro and LC + Cis is being made better.

As shown in Figure 1, compared with the NC group, the serum content of IL-6, IL-1β, TNF-α, VEGF, HIF-1α and MMP-2 from the LC group were increased, and IgG, IgA, IgM, IL-2 and TFN-y level were decreased. Meanwhile, IL-10, TGF-β, TLR4, MYD88 and NF-κB in tumor tissue were increased, indicating that the LC model of mouse was successfully developed. After therapeutic period, Andro could remarkably reduce IL-6, IL-1β, TNF-α, VEGF, MMP-2 level in blood and IL-10, TGF-β, NF-κB level of tumor tissue with significantly statistical implications (p < 0.01). The content of serum MMP-2, tumor tissue TLR4, MYD88 were also reduced by Andro treatment with statistical implications (p < 0.05). In addition, the level of IgG, IgA, IgM, IL-2 and TFN-γ in LC + Andro groups was significantly higher than those in the model group. Among them, the blood IgG, IL-2 and TFN- γ possess significantly statistical implications (p < 0.01) compared with LC group. Mouse in LC + Cis and LC + Andro group showed similar trends in biochemical indicators, indicating that Andro has a certain therapeutic effect on lung cancer, mainly by blocking the body's inflammatory response, promoting the regulation of the immune system, inhibiting the generation of cardiovascular disease, and preventing the proliferation, differentiation and metastasis of cancer cells.

Metabolic Profiling Analysis

Under the abovementioned condition, urinary sample from different groups could present in excellent peak shape, temperate intensity and clearly separation. In the initial stage, nine chromatographic peak were selected in overlaid chromatograms of the QC, which the relative standard deviation (RSD) of the peak area and retention time are respectively less than 5% indicating that the detection method possesses well repeatability. Due to spectra complication, the discrimination between each group were not clearly highlighted. Multivariate statistical analysis was applied to discern the discrepancy of metabolic components among the four groups. In Figures 2A,B, the positive and negative mode plots of urinary samples are shown that four group exhibit the obvious separation and did not exceed the limit indicating metabolic differences among the different four groups is significant and anomalous

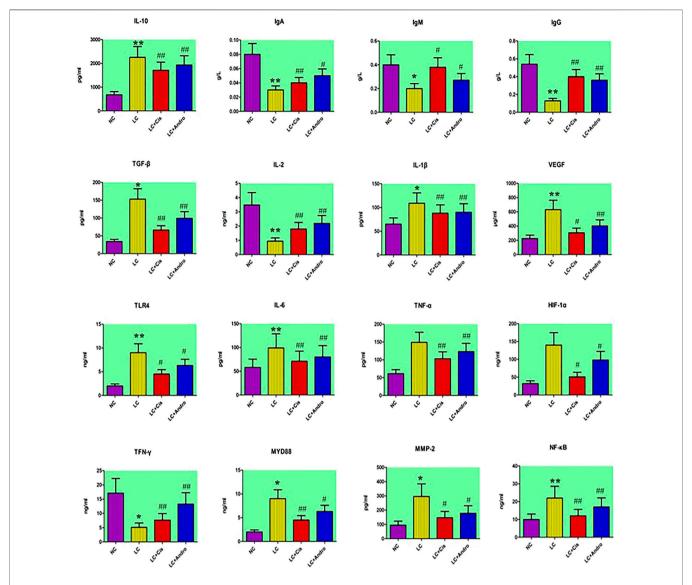


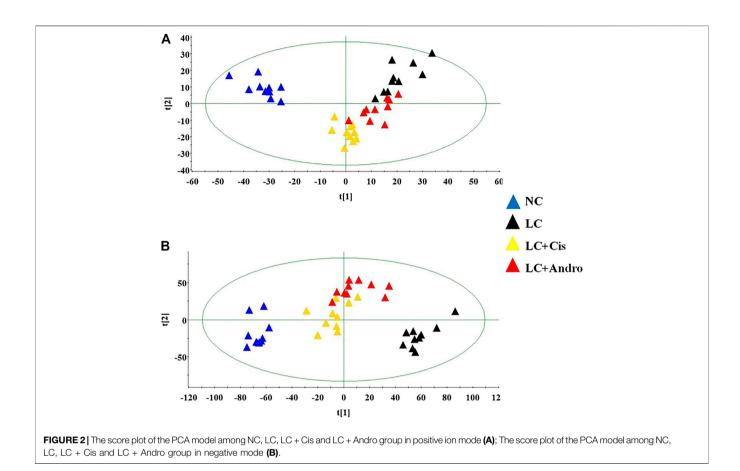
FIGURE 1 The changes of chemical indexes content in different groups after Andro administration. "*" LC group vs NC group, p < 0.05; "**" LC group vs NC group, p < 0.01; "#" LC + Cis or LC + Andro group vs LC group, p < 0.05; "##" LC + Cis or LC + Andro group vs LC group, p < 0.01.

sample was not existed in the clustering of data. The samples from the NC group clustered together and remained relatively far from those from the LC groups. In addition, the clustering of LC + Cis group and LC + Andro group remained relatively far from LC group and close to NC group. Compared with LC + Andro group, the clustering of LC + Cis group is more close to NC group. The results suggested that metabolic state of LC mouse could be regulated by Andro treatment and the further multivariate analysis was necessary to explore potential relationships.

Biomarkers Screening, Discovery and Identification

Firstly, the data of NC and LC group were separately compared in both ion mode as shown in **Figures 3A,B**, which there are evident

separation between the clustering of NC group and LC groups, and the dispersion within the group is relatively clear. Secondly, a cross validation test that was performed the calculation of the R2 and Q2 values to evaluate the goodness of fit of the OPLS models, which R2 close to 1 is the requisite condition for a good model, and Q2 more than 0.5 represent good predictability of the model. In **Figures 4A,B** goodness of fit test was carried out to assess the predictability of the model indicating that the model have a well goodness. The clustering of LC group can be obviously separated from NC group (R2Y (cum) = 0.970 and Q2 (cum) = 0.791 in the ESI + model, and R2Y (cum) = 0.982 and Q2 (cum) = 0.738 in the ESI- model) as shown **Figures 4B,C**. The mass-to-charge ratio with large dispersion in the statistical analysis of the loading plot acts a vital role in the separation between groups, the loading plot generated from OPLS-DA model as shown in **Figures 5A,B** bring



out the ions with major differences in abundance between NC group and LC group. From the **Figures 5C,D** of volcano plot, the VIP value was larger, the contribution was greater. Potential metabolite marker selection need to simultaneously satisfy the strength of both contribution and variable reliability from the same OPLS-DA model, which the value of the VIP score is more than 1.0 and p value is less than 0.05 in Student's t-test.

Combined with the retention time, exact mass-to-charge ratio of the variables and online databases, 25 urine meatbolites including valine, inositol phosphate, alanine, thymine, proline, L-glutamine, pyridoxic acid, 3-hydroxybutyric acid, arginine, arachidonic acid, xanthurenic acid, glucose, isoleucine, p-cresol sulfate, kynurenic acid, tyrosine, chenodeoxycholic acid, creatinine, phenylpyruvic acid, coproporphyrin III, 12,13-EpOME, glycyl-threonine, 9 (S)-HPODE, 3-oxohexadecanoic acid, lactic acid were identified as biomarkers associated with the metabolic disturbances in animals with the lung cancer. The basic information such as molecular formula, compound name, corresponding m/z, VIP value was listed in Supplementary Table S1. Among them, specific content changes of 18 metabolites were determined to be changed trend back to NC group level after treatment with Andro, which eight metabolites including 12,13-EpOME, creatinine, inositol phosphate, lactic acid, thymine, arginine, coproporphyrin III and arachidonic acid were downregulated in the urine, and ten metabolites including alanine, L-glutamine, isoleucine, 3-hydroxybutyric acid, proline, valine, tyrosine, xanthurenic acid, kynurenic acid and p-cresol sulfate were up-regulated as shown in heatmap of **Supplementary Figure S2A**. Detailed the comparisons of metabolite relative peak area in NC, LC, LC + Andro and LC + C is group are shown in **Supplementary Figure S2B**, which Andro treatment has a greater influence on the content of isoleucine, 3-hydroxybutyric acid, arginine, coproporphyrin III, alanine, L-glutamine, lactic acid, arachidonic acid with significantly statistical implications (p < 0.01).

Metabolic Pathways Regulated by Andro

The changes in the levels of potential biomarkers suggested that the metabolic disturbances in mouse with lung cancer were relieved by Andro referring to phenylalanine, tyrosine and tryptophan biosynthesis, arachidonic acid metabolism, tyrosine metabolism, arginine and proline metabolism, alanine, aspartate and glutamate metabolism, porphyrin and chlorophyll metabolism, pyruvate metabolism, arginine biosynthesis, pyrimidine metabolism, phosphatidylinositol signaling system and inositol phosphate metabolism after Pareto method to standardize the data. As shown in **Figure 6A**, the impacts on the pathways phenylalanine, tyrosine and tryptophan biosynthesis and arachidonic acid metabolism were stronger, where the metabolic pathway with the influence value greater than or equal to 0.30 can be selected as the potential key metabolic pathway of drugs. From KEGG global metabolic network of

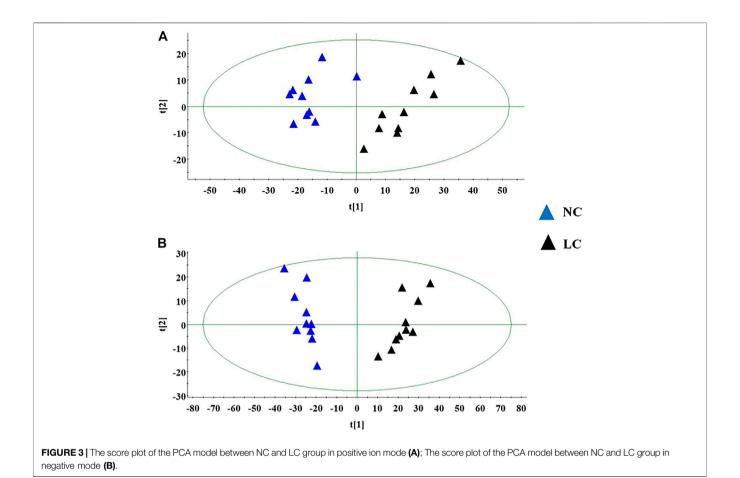


Figure 6B, potential metabolites regulated after Andro administration were closed with valine, leucine and isoleucine biosynthesis, alanine, aspartate and glutamate metabolism, phenylalanine, tyrosine and tryptophan biosynthesis, etc.

The Target Prediction

A total of 570 proteins were predicted and closely related with metabolites regulated by Andro, which mainly involves amino acid metabolism and arachidonic acid metabolism. ASS1, TAT, ALDH4A1, PTPN11 and JAK2in **Figure 7** has higher correlation degree considered as potentially important markers for further study.

DISCUSSION

In this study, the biochemical analysis and pathological studies have shown that Andro treatment can enhance the immune system function of lung cancer model animals, inhibit inflammation reaction, tumor cell growth and metastasis. TNF- α is an inflammatory factor with multiple types of biological effects, which is secreted by activated macrophages, monocytes and T cells to mediate the process of inflammation and directly participate in the process of lung tissue injury and apoptosis (Inui et al., 2018). IL-6 secreted by monocytes and

macrophages is an inflammatory mediator involved in the immune regulation of infection and tumors (Zhao et al., 2018). IgM with a large molecular weight cannot pass through blood vessel walls, and can be used for early diagnosis of body infections (Macpherson et al., 2008; Liu and May 2016; Hansen et al., 2019; Zhou et al., 2019). TLR4 is a member of the Toll-like receptor superfamily that plays a biological role in the form of binding to ligands (Zhang J. et al., 2019). Tumor cells can release a large number of cytokines in the process of immune remodeling, such as IL-10 and TGF- β , the latter can weaken the killing activity of cytotoxic T lymphocytes and natural killer cells, evading immune surveillance and promote tumor metastasis (Solinas et al., 2010; Wei et al., 2010; Bellomo et al., 2016; Anguiano-Hernandez et al., 2019; Dong et al., 2019).

A flow chart for the experiments was shown in Figure 8. According to urine metabolomics analysis, Andro can regulate 18 of 25 biomarkers associated with the pathogenesis of lung cancer, including alanine, L-glutamine, isoleucine, 3-hydroxybutyric arginine, proline, valine, tyrosine, acid, 12,13-EpOME, creatinine. inositol phosphate, lactic acid, thymine, xanthurenic acid, kynurenic acid, p-cresol coproporphyrin III, arachidonic acid, which is mainly related to phenylalanine, tyrosine and tryptophan biosynthesis, arachidonic acid metabolism, arachidonic acid metabolism, arginine and proline metabolism, alanine, aspartate and

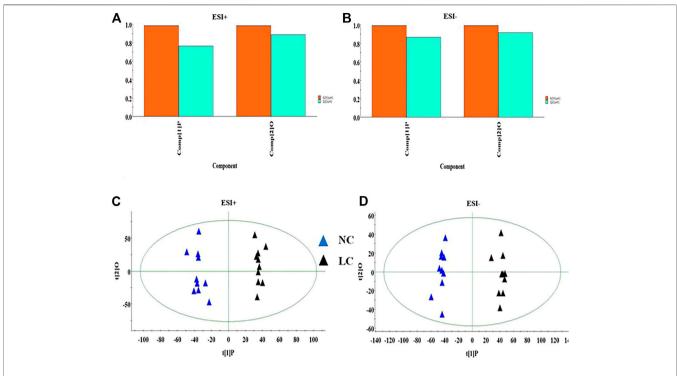


FIGURE 4 | The goodness of fit test for OPLS model in ESI+ and ESI- mode (A,B). OPLS-DA analysis of the data derived from the ESI+ and ESI- mode between NC and LC group (C,D).

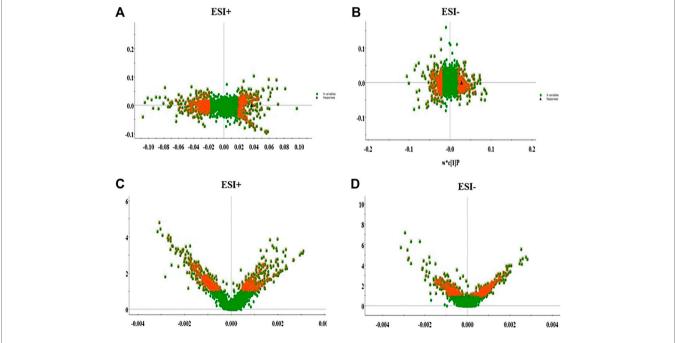
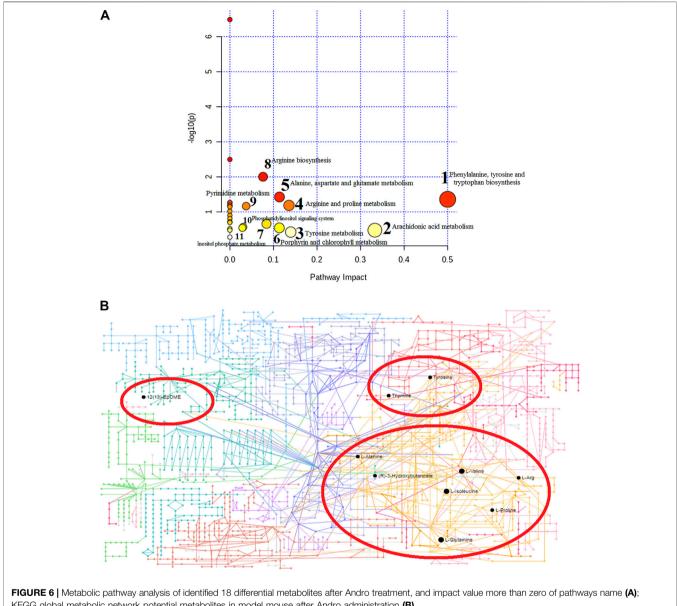


FIGURE 5 | The loading plot for OPLS model between NC and LC group in ESI+ and ESI- mode (A,B). VIP plot for OPLS model between NC and LC group in ESI+ and ESI- mode (C,D).

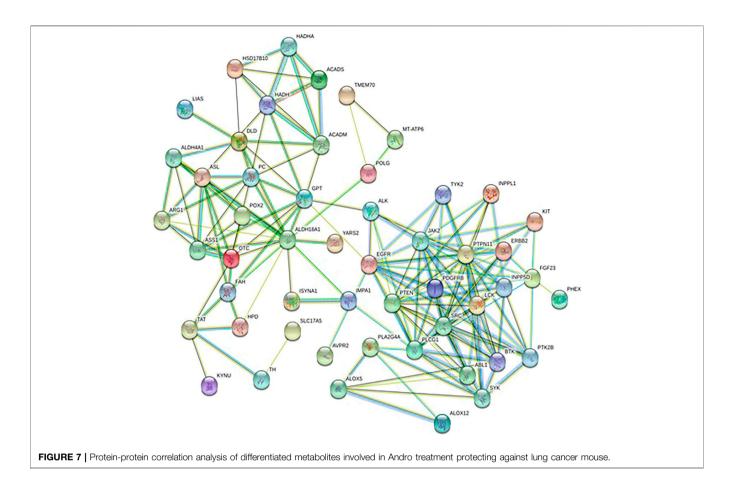


KEGG global metabolic network potential metabolites in model mouse after Andro administration (B)

glutamate metabolism, porphyrin and chlorophyll metabolism, pyruvate metabolism, arginine biosynthesis, pyrimidine metabolism, phosphatidylinositol signaling system and inositol phosphate metabolism. In the light of the impact value of the metabolic pathway, the pharmacological action and effective mechanism of Andro mainly acts on the amino acid metabolism pathway and arachidonic acid metabolic pathway to protect against lung cancer.

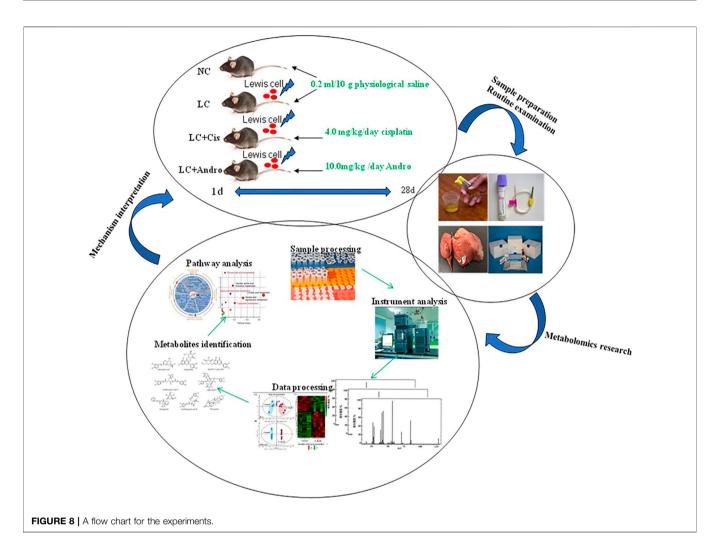
Amino acid metabolism not only plays an important role in the body's anabolism, but also plays an important role in the proliferation, apoptosis and invasion of tumor cells. Some amino acids are considered as tumor markers and present abnormal expression in patients with different tumors of lung cancer, skin cancer, prostate cancer, colon and breast cancer (Zhang et al., 2013; Liang et al., 2016; Nan et al., 2016; Lukey et al., 2017).

However, the abnormal state is not much different from normal people in chronic wasting diseases. During the process of tumors growth in the lung, it not only affects the human respiratory and circulatory system, but also causes changes in the body's energy metabolism even the overall metabolic state leading to some amino acid metabolism-related enzymes alteration in the body. The abnormal expression of amino acids metabolism provides energy for tumor tissues, constructs related proteins required for their growth and development, then it can also escape the tumor cell killing effect and immune surveillance of the host immune system (Vettore et al., 2020). Amino acids can also be used as signal molecules to participate in various signal pathways of tumor cells, which regulate themselves to take part in the formation of cellular energy-related metabolic regulation signal pathways, and control cell proliferation, growth and Invasion



ability as downstream proteins of proto-oncogenes (Liang et al., 2017; Sivanand and Vavder Heiden, 2020). Alanine is a nonessential amino acid produced by glycogen in the human body, which is produced by the conversion of carbohydrate pyruvate or the decomposition of DNA, dipeptide carnosine and goose serotonin. It can be converted into pyruvate and tricarboxylic acid cycle intermediates, and then converted into glucose through gluconeogenesis, as an energy source to meet the huge energy demand consumed by various metabolic activities of tumor cells. When branched chain amino acid is insufficient, alanine level is usually decreased, which may be related to muscle metabolism. Alanine can promote energy synthesis in cells and provide sufficient energy for cell growth (Deberardinis et al., 2008). It is an inhibitory neurotransmitter in the brain as the same as GABA, taurine and glycine. In addition, tumor cells also use glutamine as another source of energy. As the main substrate of aerobic metabolism of tumor cells in mitochondria, the proliferating tumor cells need to consume a large amount of glutamine (Bathe et al., 2011). Some clinical trials have demonstrated that patients receiving glutamine higher supplementation have nitrogen balance, polymorphonuclear neutrophil granulocytes producing cysteylleukotrienes, lymphocyte recovery and intestinal permeability have been improved. Glutamine is converted to glutamate by the reaction of glutaminase and amidase. The glutamate product can be directly incorporated into GSH, or enter the Krebs cycle as

2-oxoglutarate through transamination or oxidative deamination reactions. Subsequently, the OAA formed in the Krebs cycle is transamination to aspartic acid, which is removed from the Krebs cycle for pyrimidine biosynthesis (Deberardinis et al., 2008; Bathe et al., 2011). This study revealed that the levels of alanine and glutamine in the model group were reduced, and Andro could restore the level of alanine and glutamine content to the control group trend by regulating alanine, aspartate and glutamate metabolism, and pyrimidine metabolism. Arginine, as an essential amino acid, is synthesized in the urea cycle of adults. It helps to process ammonia and can be converted into glucose and glycogen when needed. Arginine can activate AMP kinase, and then stimulate skeletal muscle fatty acid oxidation and muscle glucose uptake leading to the increasing level of the insulin secreted by pancreatic β cells. It also is involved in the metabolism of nitric oxide that is a vasodilator and free radical used by nitro-oxidative stress, apoptosis, cell cycle, angiogenesis, invasion and metastasis. Therefore, arginine deprivation may provide a potential treatment for lung cancer (Yang et al., 2009; Grimm et al., 2013). In our study, it was found that the arginine content in the urine of lung cancer mice reduced after Andro treatment, which was related to the regulation of arginine and proline metabolism as well as arginine biosynthesis. Proline is a non-essential amino acid synthesized from glutamic acid. It is an important part of collagen and has potential endogenous excitotoxin/neurotoxin activity, which can act as a neurotoxin



and metabolic toxin to damage nerve cells and nerve tissue causing adverse health effects when it keeps at a high level for a long time. According to reports, the plasma concentration of proline in the model group was significantly reduced compared with the control group, and the rapid increase of proline dehydrogenase transcription by the tumor suppressor p53 triggered the degradation of this amino acid in cancer (Zhao et al., 2014; Phang et al., 2015). After Andro treatment, the proline content in the urine of lung cancer mice was increased medicated by regulating arginine and proline metabolism. Tyrosine, like other amino acids, is a component of protein and an alternative energy source for cell function. The liver is the main organ where tyrosine degradation occurs, producing intermediates or precursors for gluconeogenesis and ketone production. The degradation of tyrosine is catalyzed by a series of enzymatic reactions, which tyrosine metabolism disorders are related to many diseases, such as Huntington's disease and esophageal cancer. In the catalytic reaction of phenylalanine hydroxylase, tyrosine can be metabolized to phenylalanine. The lack of polycyclic aromatic hydrocarbons or the decrease of liver activity can cause phenylalanine metabolism disorder and acute liver damage. The decreasing level of tyrosine in urine of the model group can infer that the liver function in the lung cancer body is abnormal (Wiggins et al., 2015; Herman et al., 2019). Andro can adjust phenylalanine, tyrosine and tryptophan biosynthesis, and tyrosine metabolism to promote tyrosine level close to normal state.

Tumor cell membrane phospholipids can release arachidonic acid (AA) through the action of phospholipase A2 (PLA2), then it was catalyzed to produce eicosanoids such as prostaglandins (PGE), leukotrienes and hydroxyeicosatetraenoic acid (HETEs) through the key enzymes from arachidonic acid metabolism network such as cyclooxygenase (COX), lipoxygenase (LOX) and cytochrome P450 monooxygenase, and further activates downstream signaling pathways such as PI3K/Akt. Thus, arachidonic acid plays an important role in the regulation of tumor cell proliferation and apoptosis. COX-2 is often overexpressed in tumor cells, which results in the accumulation of a large amount of PGE2 in tumor tissues (Łuczaj et al., 2015). PGE2 can inhibit tumor cell apoptosis, promote cell division, angiogenesis, tumor invasion and metastasis by binding to special receptors on the cell membrane. In addition, cPLA2 catalyzes membrane phospholipids to produce AA and lysophospholipids, which directly or indirectly participate in

tumorigenesis and development (Clay et al., 1999; Sabino et al., 2002). This study found that the content of AA in the model group mice was increased, indicating that lung cancer caused severe inflammation in the body and may exist cancer cell division, angiogenesis, tumor invasion and metastasis. Andro can reduce AA levels by regulating arachidonic acid metabolism. Metabolite products such as lactic acid level is significantly increased in cancer patients, while glucose level is significantly decreased due to the continuous existence of the Warburg effect, which is the result of abnormal metabolization in tumor cells, that is, the strong Glucose metabolism. Cancer cell metabolism mainly involves the final conversion of glucose to lactate through enzyme-catalyzed anaerobic fermentation (Fan et al., 2009; Rocha et al., 2010; Rocha et al., 2011). Lactic acid is also the cyclic carbon source of tricarboxylic acid (TCA) for non-small cell lung cancer to maintain tumor metabolism in the body. Therefore, the elevated lactate levels found in the serum of patients with non-small cell lung cancer can be attributed to the large number of cell proliferations. Our research has found that the lactic acid content in the urine of lung cancer mice was increased, which showed that the tumor metabolism in cancer animals was accelerated. After Andro treatment, the abnormal lactic acid content was reduced mainly achieved by regulating pyruvate metabolism. In the human body, thymine participates in numerous enzymatic reactions, which thymine and deoxyribose 1-phosphate biosynthesized from thymidine through interaction with thymidine phosphorylase. In addition, it can be also converted to dihydrothymine (Jordan et al., 2010; Faubert et al., 2017).

Thymine is a potentially toxic compound that is associated with numerous diseases, such as thymidine treatment, periodontal detection depth, colorectal cancer temporomandibular joint disease in human. It is also associated with innate metabolic disease of β-uropropionase deficiency (Xu et al., 2016). Pathway analysis results have shown that Andro can reduce abnormally elevated levels of thymine in urine by regulating pyrimidine metabolism. As a kind of porphyrin, coporphyrin III enters mitochondria, where it is oxidized and decarboxylated to form protoporphyrin IX. It is catalyzed by iron chelatase, which combines Fe²⁺ with protoporphyrin-IX to form heme. Drug toxicity can cause liver damage and hemoglobin synthesis dysfunction resulting to the increasing level of the synergistic porphyrin III in the urine, which in turn causes abnormal bilirubin metabolism and increases the level of DBIL (Bröer, 2008; Deja et al., 2014). The level of coproporphyrin III in the urine of lung cancer mice is elevated, which shows that lung cancer may cause liver damage and hemoglobin synthesis dysfunction. After Andro treatment, the abnormal content of coproporphyrin III was changed to the horizontal direction of the control group. Inositol, as a reactant of tumor cell energy metabolism and lipid metabolism, is significantly increased when the body's immune function is low and tumor cell proliferation. Tumor energy, carbohydrates, and lipid metabolism in patients are more active, and their immune function protecting against tumor cells proliferation is faster.

Some studies have added two other characteristics of cancer, namely reprogramming energy metabolism and evading immune destruction. In tumors from animal model, various energy metabolism pathways such as such as inositol phosphate metabolism, oxidative phosphorylation and purine metabolism and citrate cycle have changed. Inositol phosphate metabolism is altered in cancers body, and then they regulate chromatin remodeling (Steger et al., 2003; Hanahan and Weinberg, 2011). Andro can reduce inositol phosphate content in the urine of model mice by phosphatidylinositol signaling system and phosphate metabolism indicating that Andro can inhibit the energy, carbohydrate and lipid metabolism of tumor cells. Branched-chain amino acids (BCAA) such as valine, isoleucine and leucine possess similar structures with different metabolic pathways. Valine deficiency is marked by impaired brain nerve function, and isoleucine deficiency is marked by muscle tremors. Studies have reported that glycine, valine and methionine in the serum of lung cancer patients are significantly lower than those in healthy controls, which are considered to be essential in the development of primary tumor types (Khunger et al., 2018). 3-Hydroxybutyric acid, also known as β-hydroxybutyric acid, is a typical partial degradation product of branched-chain amino acids released from muscles for liver and kidney gluconeogenesis (Hashim et al., 2019). 12,13-EpOME is a very hydrophobic long-chain fatty acid. During the occurrence and development of tumors, a large amount of energy and raw materials are needed to meet the needs of their own growth due to the rapid metabolism of tumor cells, which will lead to an increase in fatty acid oxidation products in the body and a decrease in fatty acid content. This study found that the level of 12,13-EpOME in urine was increased, indicating that there may be serious abnormalities in lipid metabolism in cancer bodies. Xanthine acid as a metabolite of tryptophan catabolism is the substrate of methyltransferase in the tryptophan metabolism pathway. Xanthine is a product of the purine degradation pathway and will be converted to uric acid under the action of xanthine oxidase. p-Cresol sulfate that causes nephrotoxicity and vascular toxicity by activating the renal renin-angiotensin-aldosterone system (RAAS), and leads to renal tubular cell stress response cells and renal fibrosis is a uremic toxin (Battelli et al., 2018; Battelli et al., 2019). Creatinine is a breakdown product of creatine phosphate in muscles. The loss of water molecules in creatine leads to the formation of creatinine. Creatinine is transferred to the kidneys through plasma, and then cleared from the body through glomerular filtration and partial renal tubular excretion (Evans et al., 2019). ALK rearrangements result from inversions or translocations on chromosome 2 that fuse variable regions of a partner gene with exon 20 of the ALK gene (Shaw et al., 2009; Gainor et al., 2013; Tsao et al., 2016).

As an integral part of systems biology, metabolomics has developed rapidly in recent years. At this stage, metabolomics research in lung cancer is mainly focused on metabolic pathways of blood, urine, tissue cells, and breathing gas,

while sputum and pleural effusion are rarely reported in the literature, and further research is needed (Crutchfield et al., 2016; Dakappagari et al., 2017; Li et al., 2018). Since the existing analytical instruments, analytical techniques, and data processing methods are not perfect, and specimen preparation lacks uniform standards, metabolomics technology still needs further development. With the continuous insight into metabolomics research, HMDB improvement, the successful docking of various omics data and the verification of multiple biological models, panoramic information on the transcription, protein and metabolic levels of various tumors such as lung cancer could be obtained, and more molecular markers for early diagnosis, efficacy and prognosis evaluation will be discovered providing a theoretical basis for improving the clinical diagnosis and treatment of lung cancer.

CONCLUSION

This study discovers biomarkers, metabolic profiles and pathways as potential targets for insight into the pharmacological action and effective mechanism of Andro against lung cancer by highthroughput metabolomics analysis combined with network pharmacology. Andro can regulate 18 of 25 biomarkers associated with the pathogenesis of lung cancer, such as alanine, L-glutamine, isoleucine and 3-hydroxybutyric acid. Andro embodies the characteristics of enhancing the immune system function, inhibiting inflammation reaction, tumor cell growth and metastasis as well as balancing visceral metabolism, which was involved in amino acid metabolism, arachidonic acid metabolism, porphyrin and chlorophyll metabolism, pyruvate metabolism, pyrimidine metabolism, phosphatidylinositol signaling system and inositol phosphate metabolism. Andro were shown to address multiple relevant targets and signaling pathways in the Lewis lung cancer model. Due to generating the majority of biological data. Further, it could expand the number

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of biological samples and perform clinical biological verification in the research process of lung cancer.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding authors.

ETHICS STATEMENT

The animal study was reviewed and approved by the Ethics Committee of Harbin Medical University.

AUTHOR CONTRIBUTIONS

WL and WZ designed the experiments; WL, LJ, J-WZ, D-JW, QR, WZ performed the experiment and analyzed the data; WL wrote the paper and WZ revised it. All the authors approved the final manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.596652/full#supplementary-material.

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Huanglong Antitussive Granule Relieves Acute Asthma Through Regulating Pulmonary Lipid Homeostasis

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Yan H, Qian G, Yang R, Luo Z, Wang X, Xie T, Zhao X and Shan J (2021) Huanglong Antitussive Granule Relieves Acute Asthma Through Regulating Pulmonary Lipid Homeostasis. Front. Pharmacol. 12:656756. doi: 10.3389/fphar.2021.656756 **Background:** Asthma is a respiratory disease with chronic airway inflammatory, and individuals with asthma exacerbations is one of the most frequent causes of hospitalization. Huanglong antitussive granule (HL Granule), a Chinese proprietary herbal medicine, has been proved to be effective in the clinical treatment of pulmonary disease. This study is devoted to the pharmacodynamics of HL Granule in acute asthma and the possible mechanism from the perspective of lipidomics.

Methods: Mice were divided into four groups, control group, acute asthma model group, HL Granule treatment and montelukast sodium treatment group. Acute asthma was induced by ovalbumin (OVA). Histopathology, pulmonary function and enzyme linked immunosorbent assay (ELISA) were used to validated model and effect of HL Granule. Lipids were detected by ultra-high-performance liquid chromatography coupled to hybrid Quadrupole-Exactive Orbitrap mass spectrometry (UHPLC-Q-Exactive Orbitrap MS) and identified by MS-DAIL and built-in Lipidblast database. Differentially expressed lipids recalled in HL Granule treatment group were extracted for heatmap, enrichment analysis and correlation analysis.

Results: HL Granule was effective in decreasing airway hyperresponsiveness (AHR), airway inflammatory and the levels of IL-4 and IL-5. A total of 304 and 167 lipids were identified in positive and negative ion mode, respectively. Among these, 104 and 73 lipids were reserved in HL Granule group (*FDR* < 0.05), including acylcarnitine (ACar), fatty acid (FA), lysophosphatidylcholine (LPC), phosphatidylcholine (PC), lysophosphatidylethanolamine

Abbreviations: ACar, acylcarnitine; ACar, acylcarnitine; AHR, airway hyperresponsiveness; BALF, bronchoalveolar lavage fluid; Cer, ceramide; DG, diglyceride; ELISA, Enzyme linked immunosorbent assay; FA, fatty acid; HL Granule, Huanglong antitussive granule; LC-MS, liquid chromatography-mass spectrometry; LPC, lysophosphatidylcholine; LPE, lysophosphatidylcholine; PC, phosphatidylcholine; PE, phosphatidylcholine; PE, phosphatidylcholine; PE, phosphatidylcholine; Penh, enhance pause; PG, phosphatidylglycerol; PI, phosphatidylinositol; PS, phosphatidylserine; SM, sphingomyelin; TG, triglyceride; TIC, total ion chromatograms; UHPLC-Q-Exactive Orbitrap MS, ultra-high-performance liquid chromatography coupled to hybrid Quadrupole-Exactive Orbitrap mass spectrometry

(LPE), phosphatidylethanolamine (PE), phosphatidylglycerol (PG), phosphatidylinositol (PI), phosphatidylserine (PS), diglyceride (DG), triglyceride (TG), sphingomyelin (SM) and ceramide (Cer). Furthermore, 118 and 273 correlations among 47 and 96 lipids in the positive and negative were observed, with ether-linked phosphatidylethanolamine (PEe) and phosphatidylcholine (PCe) (FDR < 0.001, Spearman correlation coefficient $r^2 > 0.75$).

Conclusion: HL Granule might improve pulmonary lipid homeostasis and could be used as an alternative or supplementary therapy in clinical for the treatment of asthma.

Keywords: acute asthma, treatment, huanglong antitussive granule, lipidomics, pulmonary lipids

INTRODUCTION

Asthma is a common chronic respiratory disease, characterized by respiratory symptoms and airflow limitation that vary over time, with different degrees of chronic airway inflammation and remodeling (Papi et al., 2018). In patients with asthma, acute exacerbation is defined as the changes of previous state, including symptoms, such as wheezing, shortness of breath, chest tightness and cough that recurrence or aggravation with decreasing respiratory function (Kostakou et al., 2019). Environmental determinants, such as allergen, polluted air, smoking, respiratory tract infection, etc, are known to induce asthma (Khreis et al., 2017; Neophytou et al., 2018; Mikhail and Grayson, 2019). Among them, infection is the main cause of acute asthma in children of any age, followed by allergy in schoolage children (Dondi et al., 2017). Epidemiological studies show that the global prevalence of asthma is increasing (Lundbäck et al., 2016). The prevalence continues in low-and middle-income countries with lower incidence before, such as China, while may have reached a stable period in high-income countries with high incidence, such as Europe (Lundbäck et al., 2016; Huang et al., 2019; Rodriguez et al., 2019). Acute asthma is mainly a disease occurring in early childhood and the most common cause of hospitalization in children. There were 640,000 children visiting the pediatric emergency department every year, causing serious social and economic burden (Pardue Jones et al., 2016; Saglani et al., 2019). Moreover, acute asthma not only affects the quality of life in children, but also may develop into respiratory failure, even life-threatening if seriously. In Europe, about 15,000 people die a year due to asthma (Fergeson et al., 2017).

Currently, the interventions available for acute asthma remain relatively limited. The commonly used drugs for asthma are β 2-adrenergic agonists, corticosteroids (ICSs) and leukotriene modifiers, usually montelukast sodium (Ramsahai et al., 2019). Montelukast sodium, a highly selective leukotriene receptor antagonist, has significantly contributed to asthma control, e.g., reducing asthma severity, especially early wheezing and disease control, over the past 20 years, and was demonstrated decreased peripheral blood eosinophil and induced inhibition of both early and late phase bronchoconstriction in asthma patients. In clinical practice, many doctors prefer montelukast sodium over ICSs (Valentovic, 2007; Lee and Kim, 2020). However, the United States Food and Drug Administration (FDA) recently reminded a black box warning of montelukast sodium, which is severe neuropsychiatric adverse reactions and has been added to

the latest Global Initiative of Asthma (GINA) (Glockler-Lauf et al., 2019; Global Strategy for Asthma Management and Prevention Global Initiative for Asthma (GINA), 2020). At present, traditional Chinese medicine (TCM), whether used alone or in combination with conventional asthma medication, has been widely applied to asthma treatment in China. Furthermore, TCM may propose possible explanations to explain asthma heterogeneity. TCM emphasizes the holistic concept and dialectical treatment that the human body is an organic whole, and a disease may have different treatments with different syndrome differentiations. In present study, HL Granule, a Chinese proprietary herbal medicine, has been widely used in various respiratory diseases, such as asthmatic bronchitis, cough variant asthma and other diseases with cough and wheeze (Naiming, 2004; Wenjin, 2018; Yin, 2019). According to the theory of TCM, the reason that asthma recurrent episodes is the phlegm in vivo all the time, which induces asthma on the premise of deficiency of healthy qi. HL Granule has the effect of tonifying kidney Qi, cleaning lung, relieving cough, calming panting, as well as ameliorating expectoration of phlegm., which is composed with Astragalus atropilosulus (Huangqi), Epimedium brevicornu (Yinyanghuo), Platycodon grandiflorum (Jiegeng), Pheretima (Dilong), Belamcanda chinensis (Shegan), Houttuynia cordata (Yuxingcao), Ephedra sinica (Mahuang), Crataegus pinnatifida (Shanzha) and Lepidium apetalum (Tinglizi) (Supplementary Table S1), However, no study has explored the efficacy and mechanism of HL Granule in the treatment of asthma. Therefore, in the study, we focused on the pharmacodynamics and possible mechanism of HL Granule while treating acute asthma, and explored the possibility of HL Granule as a supplementary or alternative therapy for montelukast sodium.

Lipidomics is a branch of metabolomics and the separate discipline that studies lipids systematically. Lipids are one of the most important components of living organisms, which can be divided into eight categories, including fatty acids, glycerides, phospholipids, sphingolipids, glycolipids, polyketide, sterols and isoamylenol ester (Fahy et al., 2011; Zhang et al., 2018). Changes in various biological processes will cause changes in lipids. Meanwhile, lipid changes are involved in various biological processes, including energy metabolism, cell membrane-related functions, signal molecules, inflammatory reactions, biomacromolecule-recognition signals, etc. (Barrera et al., 2013). Most of the intracellular life activities occur at the metabolic level, which reflect the environment of cells, and the

of metabolites complete fluctuation represent the pathophysiological characteristics including the interaction between heredity and environment (Kelly et al., 2017), while asthma is a complex disease that involves the interplay of genes and environmental factors. Studies have shown that lipid metabolism of asthmatic patients in bronchoalveolar lavage fluid (BALF) is disturbed (Kang et al., 2014). Lipids with significant changes, on the one hand, may be used as biomarkers (Ackerman et al., 2016; Trinh et al., 2016); on the other hand, play an important role in innate immunity and inflammation (MacEyka and Spiegel, 2014; O'Donnell et al., 2018). Therefore, the pharmacodynamic mechanism of HL Granule in an acute model of asthma was studied on the basis of lipidomics.

In present study, firstly, we detected pulmonary function, histopathology and inflammatory factors to evaluate the model and the curative effect of HL Granule. Afterward, on the basis of established stable and effective lipid analysis method (Yang et al., 2019), we used liquid chromatography-mass spectrometry (LC-MS) technology to research the changes of lipids in the lung tissue. Lastly, we constructed a lipid map of acute asthma and analyzed the regulatory effect of HL Granule on disordered lipids to explore the possible pharmacodynamic mechanism of HL Granule in the treatment of acute asthma.

METHODS AND MATERIALS

Chemicals and Regents

HL Granule (Lot No, 190107121) was purchased from Shanxi Dongke Pharmaceutical (Shanxi, China). Montelukast Sodium Oral Granule (Lot No, 829966) was purchased from Mercksharp and DohmeCorp (Inc. Kenilworth, NJ, United States). Standards of astragaloside IV (Lot No, 140321), icariin (Lot No, 18012906), irisflorentin (Lot No, 20041001), citric acid (Lot No, 19061002), quercetin 3-O-β-D-glucose-7-O-β-D-gentiobioside (Lot No, 19112806), deapio-platycodin D (Lot No, 19070307), platycodin D2 (Lot No, 19070306), deapio-platycodin D2 (Lot No, 19070308) and polygalacin D (Lot No, 170623) were from Chengdu Pufei De Biotech (Chengdu, China). Standards of astragalosid I (Lot No, 120525), astragaloside II (Lot No, 120528), calycosin (Lot No, 120615), calycosin-7-O-beta-Dglucoside (Lot No, 120819) and platycodin D (Lot No, 120826) were from Chengdu Herbpurify (Chengdu, China). Standards of ephedrine hydrochloride (Lot No, 171241-200506) and pseudoephedrine hydrochloride (Lot No, 171237-200806) were from National Institutes for Food and Drug control (Beijing, China). Standards of 3-O-β-D-glucopyranosyl platycodigenin (Lot No, P27A9S60106), platycodin D3 (Lot P28M8F32837) platycoside E (Lot No, and No. P06M10S81977) were from Shanghai Yuanye Biotech (Shanghai, China). The standard of deapio-platycoside E/platycoside g1 (Lot No, FY37239B0234) was purchased from Nantong Feiyu Biotech (Nantong, China). Ovalbumin (OVA) was obtained from Sigma-Aldrich (St. Louis, MO, United States).

High performance liquid chromatography (HPLC) grade acetonitrile, methanol, formic acid, ammonium formate and

ammonium acetate were purchased from Merck (LiChrosolv, Merck, Darmstadt, Germany). MS grade isopropanol was from ROE Scientific (United States). Standards of lysoPE (17:1) (Lot No, LM171LPE-11), SM (17:0) (Lot No, 170SM-13), TG (17:0/17: 1/17:0 D5) (Lot No, 170/171/170TG(DG)-10) and PE (17:0/17:0) (Lot No, LM170PE-19) were obtained from Avanti Polar Lipids (AL, United States).

Components' Detection of HL Granule

HL Granule was dissolved in double distilled water, and ultrasound extracted for 30 min by methanol. The extraction was centrifuged by 12,000 rpm/min at 4°C for 10 min, and supernatant was injected into the instrument for components' detection. Chromatographic separation was performed on Waters ACQUITY UPLC H-CLASS system (Waters, Milford, MA, United States) with a AQUITY UPLC HSS T3 column (2.1 × 100 mm, 1.8 μ m, United States). The column compartment was maintained at 35°C. The mobile phase was consisted of solvent A (0.1% formic acid in water) and solvent B (0.1% formic acid in acetonitrile). Gradient conditions were as follows: 0 min, 10% B, 0–23 min, 10%-90% B, 23–24 min, 90% B, 24–26 min, 90%-10% B, 26–30 min, 10% B, at a flow rate of 0.2 ml/min.

Mass spectrometry data was acquired by LTQ ORBITRAP XL mass spectrometer system (Thermo Scientific, United States) both in the positive and negative ionization mode. The temperature of the heated capillary was 270°C and that of the ESI probe was 300°C. The flows of sheath gas and auxiliary gas were set to 40 and 10 units, respectively. The scan range of the Orbitrap analyzer was m/z 500–1800 and MS¹ data were acquired by LTQ in data dependent acquisition mode. Both of the positive and negative adopted the same MS parameters.

Experimental Animals

Female C57BL/6J mice (6 weeks old) were purchased from Nanjing Qinglongshan animal farm (Certificate number 201909516, Jiangsu, China). All the animal experiments were approved by the Animal Care and Use Committee of Nanjing University of Chinese medicine (Permit number: 201903A018). Before experiments, mice were housed in a facility free of specific pathogens and had one-week adjustment period.

Mice were divided into four groups, ten mice per group: control group, acute asthma model group, HL Granule treatment group and montelukast sodium treatment group. Acute asthma model was induced by ovalbumin (OVA). In detail, on the first and 14th day, mice were sensitized by intraperitoneal (IP) injection with 0.2 ml sensitizing solutions, containing 20 μg OVA and 1 mg aluminum hydroxide. From day 20, mice inhaled 3% (wt/vol) atomized OVA for 30 min by using an ultrasonic nebulizer (Yuwell, Nanjing, China) for four consecutive days. On the 19th day, model mice were divided into three groups according to different treatments, i.e., model group, HL Granule group and montelukast sodium group, and individually oral gavaged with double distilled water (0.1 ml/10 g) (model group), HL Granule (9.1 g/kg/d) (HL Granule group), and montelukast sodium (1.52 mg/kg/d) (montelukast sodium group)

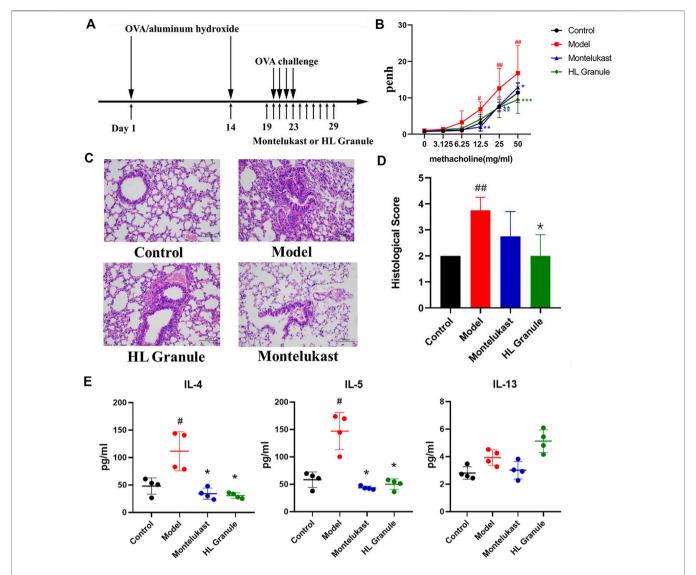


FIGURE 1 The protective effect of HL Granule on acute asthma in mice. **(A)** The flowchart of induced and treatment in the model of acute asthma. The model of acute asthma was established and sensitized by intraperitoneal injection of 0.2 ml OVA, followed by atomization of 3% OVA. **(B)** Pehn in each group. The data was collected in response to gradient concentration (0, 3.125, 6.25, 12.5, 25, and 50 mg/ml) of inhaled MCh. **(C, D)** Representative HE staining pictures (x200, C) and histological scores, n = 4. **(E)** The expressions of IL-4, IL-5 and IL-13 in BALF by Elisa. Results are presented as mean \pm SD, statistics in **(B)** was using two-way ANOVA, n = 3; statistics in D and E were using Kruskal-Wallis test, n = 4; #p < 0.05, #p < 0.05 compared to control group; #p < 0.05 compared to model group.

at 24 h intervals for seven consecutive days. Throughout the experiment, control group was given IP injections and inhalation of saline following the same procedure as acute asthma model, and was administered by gavage with double distilled water (0.1 ml/kg) from day 19–25. The procedure has been summarized in **Figure 1A**.

Histopathology and Biochemical Analysis

Histopathology. Lung tissue sections were stained with hematoxylin and eosin (HE) to investigate the pathological changes. Histological scores were graded from 0 (normal) to 4 (severe) based on Inflammatory cell infiltrated in peribronchiolar and alveolar wall, degeneration, necrosis or exfoliation of

bronchial epithelium, the integrity of alveolar wall, mucus secretion and goblet cell proliferation.

Pulmonary function analysis. Pulmonary function was evaluated by Whole Body Plethysmography (Emka Technologies, France) after the last administration. The airway was stimulated with increasing concentrations of erosolized methacholine (MCh) (0, 3.125, 6.25, 12.5, 25, 50 mg/ml). Then, enhanced pause (Penh) was determined to evaluate the bronchoconstriction function.

Enzyme linked immunosorbent assay (ELISA). ELISA kits were used to detect the expression of Interleukin-4 (IL-4), Interleukin-5 (IL-5) (Biolegend, San Diego, CA) and Interleukin-13 (IL-13) (Yi Fei Xue Biotechnology, China) in BALF.

Statistical Analysis

Data are expressed as mean \pm standard deviation (SD) in scatter plots and column bar graphs. Box-whisker Plot shows median, lower, and upper quartiles, as well as minimum and maximum values. GraphPad Prism 8.0.2 (GraphPad Software, United States) was used to analyze data by Mann-Whitney non parametric test for two unmatched groups and one-way ANOVA or two-way ANOVA for multiple comparisons. Enrichment p-values are given by the Kolmogorov-Smirnov-test. p < 0.05 is considered significant.

Untargeted Lipidomics Analysis With UHPLC-Q-Exactive Orbitrap MS

Lipid Extraction for Detection. A total of 20 mg lung tissue was used to extract lipids by the MTBE/MeOH/H2O system. First, tissue homogenate was extracted by 225 μl ice methanol solution containing internal standards (LPE (17:1), SM (17:0), TG (17:0/17:1/17:0) and PE (17:0/17:0), 5 $\mu g/m l$). After vortexing for 10 s, 750 μl MTBE was added, and the mixture was vortex for 10 min. Subsequently, 188 μl of deionized water was added and the mixture was vortexed for 20 s. After centrifuging 2 min by 14,000 rpm at 4 C, the upper phase was dried in a vacuum concentrator. Finally, the upper phase lipid was reconstituted in the mixed solvent of methanol: toluene (9:1, v/v) for lipidomic analysis.

Quality Control Samples. The preparation was carried out by mixing equal aliquots of 5 µl from each sample, and their pretreatment was carried out in the same manner as the samples. Five QCs were injected before samples, while one QC injection was inserted regularly after every 10 samples.

Chromatographic separation conditions. Untargeted lipidomics analysis of lung tissue was performed on an Ultrahigh-performance liquid chromatography (Thermo Fisher Scientific, United States) coupled to hybrid Quadrupole-Exactive Orbitrap mass spectrometry (Thermo Fisher Scientific, United States). A reversed phase Waters Acquity UPLC CSH C18 (100 mm × 2.1 mm, 1.7 μm) maintained at 60°C was used for the chromatographic separation of lipids. The flow rate was set at 0.3 ml/min. Mobile phase A were ACN/H2O (6:4, v/v), and B IPA/ACN (9:1, v/v), both containing 10 mM ammonium formate and 0.1% formic acid for positive ionization mode. For the negative ionization mode, 10 mM ammonium acetate was used as buffer system. The elution gradient started with 15% B for 4 min, and then increased from 15 to 48% B in 1 min, from 48 to 82% B in 17 min, and from 82 to 99% B in 1 min, and maintained for 1 min, back to 15% B at 24.2 min and maintained for 5.8 min to equilibrate column.

Mass Spectrometer Conditions. The mass spectrometer was operated with the following parameters: spray voltage 3.5 kV (positive) and 3.0 kV (negative). For both ionization modes, the sheath gas and aux gas were separately maintained at 35 and 15 arbitrary units, while the capillary temperature and the heater temperature were 325 and 300°C, respectively. The MS/MS data was acquired by data dependent method and top 10 abundant ions were used for fragmentation. The normalized collision energy (NCE) was set 25, 35, and 45 eV, respectively.

Data processing of lipidomics. Data deconvolution, lipid identification and alignment were analyzed by MS-DIAL 3.3 (MS-DIAL software, Japan). The output data matrix was exported for further statistical analysis. MetaboAnalyst 4.0 (metaboanalyst.ca/faces/ModuleView.xhtml) was used for multivariate analysis. Principal component analysis and heatmap were performed for cluster and visulation. Furthermore, lipid metabolites enrichment analysis was based on ChemRICH (http://chemrich.fiehnlab.ucdavis.edu/) (Barupal and Fiehn, 2017). The differentially expressed lipids were screened using the Kruskal-Wallis test and Mann-Whitney test by R 3.6.3. Correlation analysis was conducted using Spearman correlation and visualized with Cytoscape 3.8.2 (Cytoscape software, United States).

RESULTS

Quality Control of HL Granule by UHPLC-ESI/LTQ-Orbitrap-MS

The chemical profile of HL Granule was firstly analyzed by UPLC-ESI/LTQ-Orbitrap-MS. Both of the positive and negative ionizations were used. A total of 20 components belonging to seven crude materials were qualitative identified based on the standard compounds (**Figure 2**). Flavones and saponins in *Astragalus atropilosulus*, saponins in *Platycodon grandiflorum*, and alkaloids in *Ephedra sinica* were considered as the effective components. The typical total ion chromatograms (TICs) are shown in **Figure 2**. The results laid a foundation for the effectiveness and safety of HL Granule used in this study for asthma treatment.

Curative Effect of HL Granule in The Treatment of Acute Asthma in Mice

To develop an acute asthma like symptoms, OVA was used for sensitization and challenge (Figure 1A). At the end of the challenge period, airway hyperresponsiveness (AHR) was evaluated by calculating the enhance pause (Penh). The results showed that Penh increased significantly in model group (p < 0.05, 12.5 mg/ml methacholine; p < 0.01, 25 mg/ ml, 50 mg/ml methacholine), and HL Granule could reverse AHR (p < 0.01, 25 mg/ml, 50 mg/ml methacholine, **Figure 1B**). The results suggested that HL Granule inhibited the bronchoconstriction and improved AHR. inflammatory cell infiltration and airway remodeling were observed by histopathological examination. The results demonstrated that the inflammatory cell infiltration around the trachea and alveolar wall were more serious in the model group without airway remodeling, while HL Granule and montelukast sodium could relieve the inflammatory cell infiltration (Figure 1C). The HE staining was scored semiquantitatively based on inflammatory cell infiltrated, mucus secretion and goblet cell proliferation mainly in airway and alveoli. Histopathological scores confirmed that HL Granule ameliorated OVA induced inflammatory changes and significantly reduced total leukocyte counts (Figure 1D).

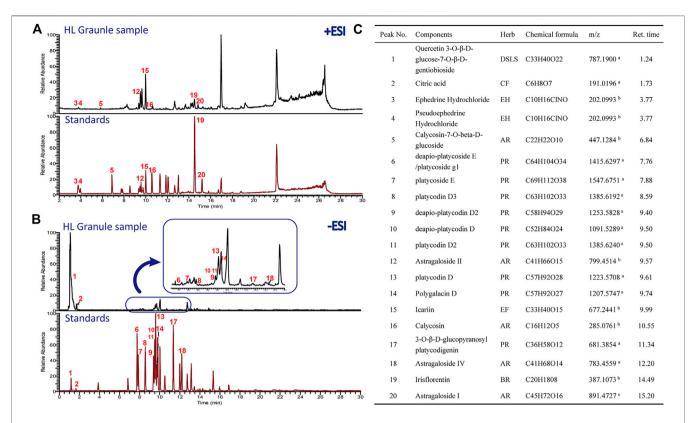


FIGURE 2 | Chromatogram of HPLC analysis of HL Granule extract. (A, B) TICs detected in positive (A) and negative ion mode (B). (C) Major chemical and effective components identified from HL Granule extract. In A and B, the upper of each picture is the chromatograms of the HL Granule sample, while the lower is the mixed standard reference compounds. Numbers in red corresponds to the chemical components in (C). AR: Astragali Radix (Astragalus atropilosulus); BR: Belamcandae Rhizoma (Belamcanda chinensis); CF: Crataegi Fructus (Crataegus pinnatifida.); DSLS: Descurainiae Semen Lepidii Semen (Lepidium apetalum); EF: Epimedii Folium (Epimedium brevicornu); EH: Ephedrae Herba (Ephedra sinica); PR: Platycodonis Radix (Platycodon grandiflorum). a [M - H]-; b [M + H]+; c [M + Na]+.

Moreover, the curative effect of HL Granule was slightly better than montelukast sodium in alleviating lung pathology (Figure 1D).

T helper 2 (Th2) cell-mediated immunity is considered as an important role in the pathogenesis of asthma. Eosinophils and CD4⁺ cells producing interleukin-5 (IL-5) are frequently found in the blood and lung lavage fluid. To observe the Th2 cell mediated immunity, the levels of IL-4, IL-5, and IL-13 in BALF were analyzed in acute asthma model and the curative effect of HL Granule. The results showed that the levels of IL-4 and IL-5 increased significantly in asthmatic mice (p < 0.05). Administration of HL Granule significantly reduced IL-4 and IL-5 in BALF by 65.9 and 72.5% compared with those of the OVA groups (p < 0.05) (**Figure 1E**). In summary, the results suggested that HL Granule could be used in acute asthma treatment, and might be considered for replacing montelukast sodium as an adjuvant treatment of asthma. However, there was no significant change to IL-13.

Lipidomic Profiling of HL Granule Treatment of Acute Asthma

Lipids play a central role in lung physiology and pathology. The role of lipids in lung and respiratory disease has attracted more attention in recent years, including cystic fibrosis, asthma and COPD, which are all associated with abnormal metabolism. To examine the lipid changes of OVA induced asthmatic mice, the lipid profile of lung tissue was analyzed. A total of 304 and 167 lipid molecular species sorted into five lipid categories and 22 lipid subclasses were confidently annotated based on the database matching in the positive and negative ion mode (Figure 3A). The most commonly identified lipid species in the developing method belonged to glycerophospholipids, which were dominant with 57.89% in total. Glycerophospholipids were found in the highest amounts in the membranes of all cells. Glycerolipids were account for 18.00%, which are considered as the quantities in fat stores. Additionally, sphingolipids were minor components, and only account for 5.98%. In summary, glycerophospholipids, sphingolipids, fatty acyls and glycerolipids were all important lipids in lung tissue of acute asthma.

Then, pooled QC samples were used to monitor the analytical performance. In order to evaluate and remove the systematic error, different normalization methods were applied after peak picking up and lipid annotation. The results showed the QC samples were clustered together by the random forest (SERRF) method, indicating that a robust data matrix can be obtained by the SERRF method (**Figures 3B,C**). Then, PCA models were applied to the

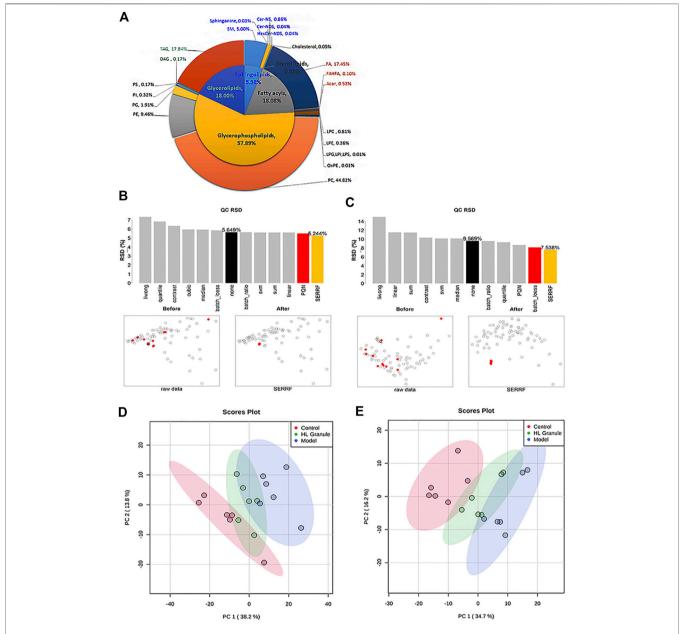


FIGURE 3 | lipids related to HL Granule treatment of acute asthma. **(A)** Double pie chart of lipids detected in lung tissue of acute asthma mice in positive and negative ion mode. **(B, C)** RSD and scatter plots of lipids in samples and QCs after normalization in positive **(B)** and negative ion mode **(C)**. **(D, E)** PCA of lipids in lung of mice in positive (D) and negative ion mode **(E)**, n = 6.

positive and negative lipidomic data respectively. For the positive lipidomic data, the first two components explained about 50% variables (PC1 = 38.2%, PC2 = 13.8%). For the negative lipidomic data, the first two components explained about 50.9% variables (PC1 = 34.7%, PC2 = 16.2%). The PCA score plots indicated that the component one can distinguish the observations of control and acute asthma obversions (**Figures 3D,E**). Remarkably, all the observations of HL Granule treatment appeared to cluster from the model group to the control group, suggesting that HL Granule could regulate lipids disorder in lung tissue of OVA

induced asthmatic mice. The score plot from negative data showed the same cluster profiles.

Characterization of Differentially Expressed Lipids

To compare the inter groups, the Kruskal Wallis test was used. Correspondingly, to verify the hypothesis about the irrelevance of differences between two groups, the Mann-Whitney test was used. A total of 162 lipids in the positive and 109 lipids in the negative were significantly changed after the OVA induced asthma,

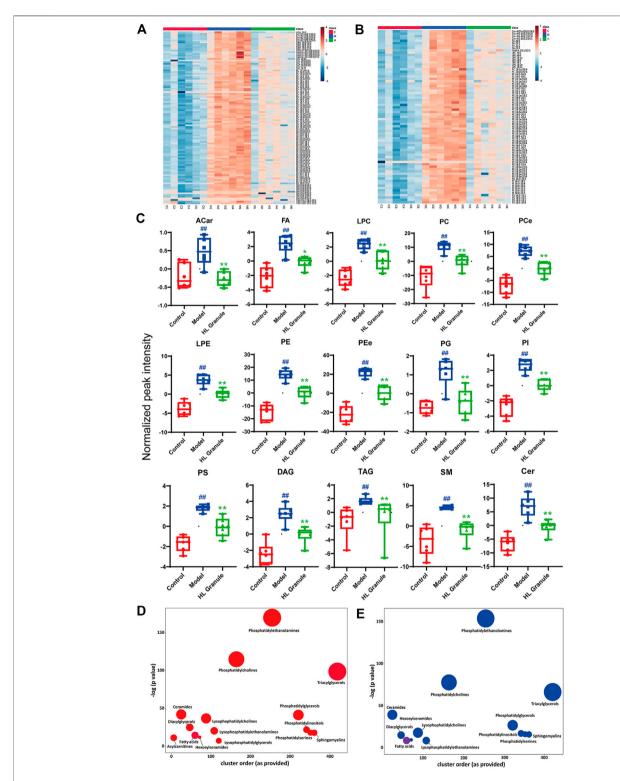


FIGURE 4 | Summary of differentially expressed lipids. (**A**, **B**) Heatmaps of differentially expressed lipids in positive (**A**) and negative (**B**) ion mode, n = 6. Each column represents a sample, each row represents a differential lipid, and each block represents the corresponding intensity value, red to blue of the corresponding lipid in each sample, representing the value from large to small. Differentially expressed lipids were reversed in HL Granule group compared to model group (FDR < 0.05). (**C**) Box-whisker Plot of differentially expressed lipid subclasses, in positive and negative ion mode, n = 6 (**D**, **E**) Enrichment statistics plot of significantly regulated lipids between model and control groups (**D**) as well as HL Granule and model groups (**E**), n = 6. Each node reflects a significantly altered cluster of lipids. Enrichment p-values are given by the Kolmogorov-Smirnov-test. Node sizes represent the total number of lipids in each cluster set. The node color scale shows the proportion of increased (red) or decreased (blue) compounds. Purple-color nodes have both increased and decreased lipids. Results in (C) extends from 25th to 75th percentile and the line represents the median, the Mann-Whitney test was used between two groups, n = 6; ##p < 0.01 compared to control group; **p < 0.01, compared to model group.

acylcarnitine (ACar), fatty acid (FA), including lysophosphatidylcholine (LPC), phosphatidylcholine (PC), lysophosphatidylethanolamine (LPE), phosphatidylethanolamine (PE), phosphatidylglycerol (PG), phosphatidylinositol (PI), Phosphatidylserine (PS), diglyceride (DAG), triglyceride (TAG), sphingomyelin (SM) and ceramide (Cer). The lipids were considered upregulated if fold change (FC) > 2 and FDR < 0.05, and downregulated if FC < 0.5. The results from nonparametric tests showed that the lipid levels of OVA groups were significantly increased compared to control groups. Whereas, treatment of HL Granule significantly reduced the lipid levels. The differentially expressed lipids were illustrated by heatmaps (Figures 4A,B, Supplementary Tables S2, S3). Each square represents the intensity value of a specific lipid in a sample. The transition in color from red to blue represents the intensity value becoming smaller. The darker the red is, the larger the value is, and vice versa. As shown in heatmaps, under the condition of FDR < 0.05, a total of 104 lipids upregulated in the model group were reversed, including ACar, LPC, PC, LPE, PE, PG, DG, TG, SM and Cer, in positive ion mode (Figure 4A, Supplementary Table S2). In negative ion mode, a total of 73 lipids were found downregulated (FDR < 0.05), including FA, LPC, PC, LPE, PE, PI, PS, and Cer (Figure 4B, Supplementary Table S3). Box-whisker Plots of 15 major subclasses of differentially expressed lipids were shown, which confirmed the significant altered in lipids among control, model and HL Granule groups in lung tissue (Figure 4C). HL Granule could significantly downregulate the up-regulated lipids in model group by regulating the disorder of ACar, FA, LPC, PC, LPE, PE, PG, PI, PS, DG, TG, SM, Cer, as well as ether-linked phosphatidylethanolamine (PEe) and phosphatidylcholine (PCe) in acute asthma.

Enrichment analysis helps to gain mechanistic insight into metabolite lists. As shown in **Figures 4D,E**, each node represents a significantly changed lipid group (p < 0.05) and the node size reflects the total number of lipids contained in each lipid group. The results showed that phospholipids, sphingolipids, fatty acids and glycolipids changed significantly. Among them, phospholipids, including PE, PC, and TG, contained the higher number of lipids and changed more significantly, suggesting that lipids were important in acute asthma, especially phospholipids. More specifically, compared with the control group, 15 lipid classes in the model group changed significantly (**Figure 4D**). Apart from fatty acids and triglycerides with partial downregulation, the other lipid classes showed an overall upward trend. After HL Granule treatment, 13 of them were recalled (p < 0.05) with overall downregulation and partial upregulation in fatty acids (**Figure 4E**).

Combined with the results of lipid molecular species and lipid subclasses., we speculated that HL Granule might regulate phospholipids, sphingolipids, fatty acids and glycolipids, especially phospholipids in lung tissue to relieve acute asthma. Therefore, we speculated that HL Granule may improve acute asthma by regulating lipids homeostasis in lung tissue.

Correlation of the Differentially Expressed Lipids

Spearman correlation was conducted for all differentially expressed lipids. On the basis of FDR < 0.001 and Spearman

correlation coefficient $r^2 > 0.75$, 118 and 273 notable correlations among 47 and 96 lipids in the positive and negative were observed, with PEe and PCe. As shown in Figure 5A, of the 118 edges, PE (16:0e/20:3), PC (18:0/20:5), PE (18:1e/20:4), PC (14:0e/22:5) and PC (16:0e/22:6) showed significant correlation (edges \geq 12). PC and PE are the most abundant phospholipids in all mammalian cell membranes, which can contain ether-bonds at the sn-1 position and are thus sub-classified into alkylacyl phospholipids. Furthermore, as shown in Figure 5B, Cer-NS (d18:1/16:0), Cer-NS (d18:1/22:0), Cer-NS (d18:1/24:1), FA (22: 5), PG (16:0-16:1), PS (18:0-20:3) exhibited suggestive correlation (edges \geq 14). Indubitable, correlation between different classes of phospholipids existed. Additionally, polyunsaturated fatty acids showed more correlation with ceramide non hydroxyfatty acidsphingosine (Cer-NS). Although the relationship between FA and Cer remains unclear in pulmonary disease, C16:0 ceramide has been identified as the principal mediator of obesity-derived insulin resistance and impaired fatty acid oxidation (Raichur et al., 2014). The high level of correlation between the lipids implied that HL Granule may regulate lipid homeostasis by interaction between lipids.

DISCUSSION

HL Granule is composed of nine traditional Chinese medicines, and it has been shown that several herbs functions well in the treatment of acute asthma. Theoretically, Ephedra sinica is considered to be effective, which may have the effects of dispersing external wind and calming latent wind. It was found that Mahuang-Tang, Mahuang-Xixin-Fuzi decoction and Shegan-Mahuang Decoction, which are consisted of Ephedra sinica and Belamcanda chinensis, mitigated airway inflammation and asthmatic airway hyperresponsiveness (He et al., 2018; Gan et al., 2020; Lin et al., 2020). Lepidium apetalum, Platycodon grandiflorum and Pheretima were also found effective in asthma by alleviating airway inflammation (Huang et al., 2016; Kim et al., 2019a; Lee et al., 2020). Recent evidence suggested that formononetin and calycosin, two flavonoids predominantly representing in Astragalus atropilosulus, could alleviate allergic asthma by protecting epithelial integrity via regulating and activating G protein coupled estrogen receptor (Yuan et al., 2020). For supplementary therapy, the coadministration of budesonide and the extracts of Epimedium brevicornu in asthma were better than budesonide individual treatment (Ma et al., 2020). Thus, it is considerable to treat asthma with a combination consisting of HL Granule, which was confirmed by our

Th2 cell-mediated immunity has dominated in the past 30 years of research on the pathogenesis of asthma. IL-4, IL-5 and IL-13 are signature cytokines in Th2 cell mediated immunity. Clinically, serum IL-4, IL-5 and IL-13 levels increased significantly in patients with acute asthma (Lee et al., 2001). Thus, we combined pulmonary function, histopathology, IL-4, IL-5, and IL-13 to observe the therapeutic effect of HL Granule. The results suggested that HL Granule could improve lung

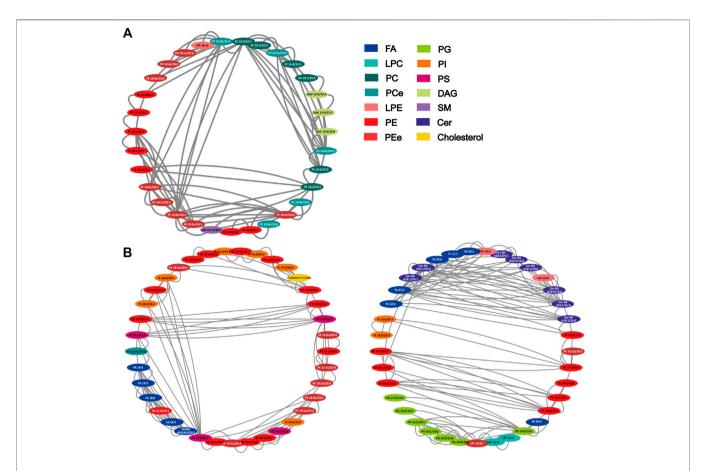


FIGURE 5 | Correlation network of differentially expressed lipids. **(A)** positive ion mode (47 nodes, 118 edges); **(B)** negative ion mode (96 nodes, 273 edges). The network was generated by Cytoscape 3.8.2 with attribute circle layout. Nodes were screened by FDR value <0.001 and Spearman correlation coefficient $r^2 > 0.75$. Edges represent the value of r^2 between two nodes.

function, reduce the inflammatory infiltration of lung tissue, especially around the airway, and decrease IL-4 and IL-5 expressions to relieve acute asthma, although airway remodeling was not obvious. However, some studies have shown that the thickness of airway smooth muscle, which is an important change in airway remodeling, is related to the severity of asthma, not to asthma progression (Hirota and Martin, 2013). Moreover, IL-13 induces excessive mucus production and goblet cell metaplasia (Kuperman et al., 2002). In our model, few mucus and goblet cells were observed by pathological results, which may be one of the reasons for no significant changes to IL-13.

Lipidomics is considered to be an indispensable tool for the researches of many diseases and physiological processes, and has been used to study inflammation-related diseases (Zhang et al., 2018). Clinical findings elucidated that lipid metabolism disorders are frequently observed in asthma patients (Kang et al., 2014; Gai et al., 2019). Therefore, regulating lipid homeostasis for asthma treatment is crux. Presently, there are few studies on the mechanism of regulating lipids on therapeutic drugs for asthma. In our study, we have studied the mechanism of HL Granule regulating lipid homeostasis.

Several studies show a significant treatment of asthma by components from traditional Chinese Medicine according to the regulation of lipid homeostasis. Metabolomics combined with network pharmacology clarified that Astragalus atropilosulus regulated arachidonic acid metabolism and ether lipid metabolism (Wang et al., 2019). Platycodon grandiflorum and Crataegus pinnatifida ethanol extracts, as well as Ephedra sinica methanol extracts may also improve lipid metabolism (Lee et al., 2017; Kim et al., 2019b; Lee et al., 2019). Remarkably, ephedrine, astragaloside IV, calycosin and icariin, which were detected and identified in present study, may be linked to lipids alterations. The chronic-effect study of ephedrine determined that brown adipose tissue (BAT) activity was significantly reduced after a 28 days ephedrine treatment (Carey et al., 2013; Carey et al., 2015). Studies in liver found that astragaloside IV attenuated lipid accumulation in an AMPK-dependent manner (Zhou et al., 2017), while hairy calycosin could effectively control the lipid peroxidation, reduce the levels of serum free fatty acid, and improve the steatosis (Liu et al., 2019). In addition, many studies have shown that the metabolites of icariin have a lipidlowering effect, which has attracted widespread attention in recent years (Wang et al., 2020). Thus, HL Granule has

advantages in regulating lipid homeostasis. However, further studies are needed to explore the detailed mechanism among them.

To explore the mechanism of HL Granule in regulating lipid homeostasis, we used high-resolution lipidomics analysis based on UHPLC-Q-Exactive Orbitrap MS to recognize potential disease-related lipid changes in lung tissue. The method allows to detect a total of 304 and 167 lipids in positive and negative ion mode, of which 162 and 109 lipids in the model group were upregulated (FDR < 0.05, Fold change >2 or Fold change <0.5). Among them, HL Granule could reverse 104 and 73 lipids with statistical difference (FDR < 0.05). In the lung lipidomics, we identified at least thirteen types of lipids are regulated by HL Granule, including ACar, FA, LPC, PC, LPE, PE, PG, PI, PS, DG, TG, SM, and Cer. The observation suggested that HL Granule improved lipid homeostasis of acute asthmatic. The study enables us to understand the new pathway and pharmacological mechanism of HL Granule in the pathogenesis of asthma mediated by pulmonary lipid disorders.

Lung tissue contains 3-4% lipids in wet weight, and about 60% of the lipids are phospholipids (Rouser et al., 1969; Toshima and Akino, 1972). Phospholipids are important parts of cell membrane structure, and some pulmonary phospholipids are the main components of pulmonary surfactant in alveoli. In present study, phospholipids were disordered with the largest number in the lung tissue of acute asthma. The comprehensive analysis of heredity and metabolites suggests that PC increased in patients with asthma (Ried et al., 2013), which is consistent with our results, and HL Granule could downregulate the levels of PC. PE synthesis is critical for mitochondrial and endoplasmic reticulum function. The increased PE levels observed in the groups might be reflective of an increased mitochondrial energy production. This assumption would be further supported by the increased levels of acylcarnitine levels. Additionally, our work reveals the levels of ether phospholipids are increased significantly in the model groups. Ether phospholipids in the plasma membrane act as the substrates for the lipid peroxidation and resulting in the further cell death (Zou et al., 2020). The downregulation of PEe levels suggested the protective effects of HL Granule. It has long been known that ether-linked phospholipids are abundantly present in neutrophils (Nagan and Zoeller, 2001), which could be rapidly recruited and are largely present in the airways of allergic eosinophilic asthmatic patients (Radermecker et al., 2018). A recent data suggested PEe and PCe were associated with ferroptosis sensitivity, which was involved in various pulmonary diseases (Zou et al., 2020).

PG predominantly observed in the lung tissue. The increased levels of PGs might inhibit Toll-like receptor (TLR)-mediated inflammation, and improved mitochondrial activity and inflammation (Chen et al., 2018; Choudhary et al., 2019). In present study, HL Granule downregulated partial PG and PE levels, suggesting a protective of the OVA induced asthma. PIs are the ubiquitous component of eukaryotic cells that participate in signal processes. Especially, glycerophosphoinositol 4-phosphate controls actin dynamics in cell systems (Corda et al., 2002). The literature reported that the PI antagonized the activation of

homologous ligands of TLR 2 and TLR 4, influencing innate immunity and the transcription of many pro-inflammatory genes (Voelker and Numata, 2019). PS is also one of the most abundant lipids in plasma membrane, and recent literatures reported that the exposed PS on the outer leaflet of the plasma membrane is the functional ligand for the signal pathway (Gong et al., 2017). Proteins interacting with PS are involved in almost all aspects of cellular regulation by activating protein kinases and transcription. Phagocytes recognized PS on apoptotic cells which were then cleared through CD36 and oxLPL receptors (Zhang et al., 2018). In the experimental model of allergic airway inflammation, apoptotic cells and inflammatory dendritic cells that express PS inhibitory immune receptor CD300a increased significantly after intraperitoneal injection of alum combined with OVA (Miki et al., 2015). It could be the reason for the increase of PS in the model group, and HL Granule might affect PS related proteins or cells.

Lysophospholipids (LPs) are produced by hydrolysis of phospholipids according to phospholipase A2 (PLA2). LPs exist in all types of cells, as a second messenger molecule to regulate intracellular signaling pathways. LPs also participate in many biological functions, including inflammation (Arifin and Falasca, 2016). In present study, we mainly changed LPC and LPE. Although some studies showed that some LPCs decreased in fasting serum (Ried et al., 2013). However, increasing level of LPC usually played a pathogenic role in the inflammatory injury of asthma (Bansal et al., 2016). LPC also induced migration of lymphocytes and macrophages, inhibited activation and migration of eosinophils, increased production of proinflammatory cytokines, aggravated oxidative stress and promotes apoptosis, thus accumulating inflammation and promoting the development of diseases (Knuplez et al., 2020; Liu et al., 2020). In the study, the upregulated LPCs were recalled by HL Granule which may be one of the reasons for its improvement of inflammation in acute asthma.

Sphingolipid serve as receptors for multiple pathogens and play key roles in immune signaling. Several studies reported that the asthma associated ORMDL3 (ORMDL Sphingolipid Biosynthesis Regulator 3) gene regulated the sphingolipid biosynthesis, and the altered sphingolipids modulate the T cells' metabolism. Our data revealed significant correlation between the ceramide non-hydroxyfatty acid sphingosine (Cer-NS) and long chain fatty acids, suggested the sphingolipid metabolism was involved in the therapeutic action of HL Granule. The accumulation of ceramides is reported to be associated with apoptosis (Hannun and Obeid, 2018). The decreased ceramides of HL Granule suggested the possible anti-apoptosis effect. Moreover, the produced SMs from ceramides on the plasma are supposed to be an acute response to extracellular stimuli. Additionally, plasma ultra-long-chain SM (d18:1/24:0) might work for regulating the activation of macrophages and inflammatory response (Sakamoto et al., 2017).

A research showed that long-chain polyunsaturated fatty acids could be converted into lipid mediators during inflammation to modulate bronchoconstriction and airway inflammation (Fussbroich et al., 2019). The key enzymes of fatty acid oxidation are involved in the OVA induced asthma, which

could significantly reduce allergen-induced AHR, the number of inflammatory cells, and the production of asthma-related cytokines and chemokines (Al-Khami et al., 2017). HL Granule could downregulate the levels of long-chain fatty acids, and further studies are required to identify the specific mechanisms. Correlation analysis revealed that the alteration of long chain fatty acids is highly correlated with that of ceramide levels. The results suggested the biosynthesis of ceramide from the fatty acids was involved in the protection of asthma by HL Granule. In addition, a specific ceramide species, C16:0 ceramide was recently identified regulating FAO and impairing fatty acid oxidation in obesity (Raichur et al., 2014). Our results show that HL Granule downregulated the level of acyl carnitine, which has the potential to activate inflammation. We also identified that DG and TG increased uniformly in the lung tissue, and HL Granule could regulate these upregulated lipids.

In summary, our research confirmed that HL Granule could be used in acute asthma treatment, but one deserved attention, is that different doses of HL Granule in the treatment, including variable treatment dose, optimal treatment dose, toxicities underwent dose, and so on, should be focused on in next studies. Additionally, there are few studies on lung lipids and asthma at present, and our exploration of the effect of HL Granule on acute asthma by regulating pulmonary lipid homeostasis is also preliminary. Further researches are needed to verify and reveal the role and interaction of lipids in asthma and drug intervention.

CONCLUSION

In conclusion, we established an acute model of asthma with AHR, airway inflammation, and increasing levels of IL-4 and IL-5, which could be effectively reduced by the treatment of HL Granule. A total of 304 and 167 lipids were detected and identified in positive and negative ion mode in lung tissue, of which 162 and 109 lipids were significantly upregulated in model group (FDR < 0.05, FC > 2or FC < 0.5). 104 and 73 lipids could be reversed by HL Granule, with statistical difference (FDR < 0.05), including ACar, FA, LPC, PC, LPE, PE, PG, PI, PS, DG, TG, SM, and Cer. Notably, 118 and 273 correlations among 47 and 96 lipids in the positive and negative were observed, with PEe and PCe (FDR < 0.001, Spearman correlation coefficient $r^2 > 0.75$). Therefore, we found that lipid disorders play an important role in asthma. HL Granule may regulate pulmonary lipid homeostasis for the treatment of acute asthma. Furthermore, our study has significance for clinical guides. In view of the side effects of drugs used in the treatment of asthma such as montelukast sodium, HL Granule could be used as an alternative or supplementary therapy in clinic.

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DATA AVAILABILITY STATEMENT

The raw data supporting the conclusion of this article will be made available by the authors, without undue reservation, to any qualified researcher.

ETHICS STATEMENT

The animal study was reviewed and approved by the Animal Care and Use Committee of Nanjing University of Chinese Medicine (Permit number: 201903A018).

AUTHOR CONTRIBUTIONS

HY and GQ were responsible for acquisition, analysis, and interpretation of data and had written the first draft of the manuscript, JS provided information for research design. RY, ZL, and XW participated in the analysis and provided experimental support. TX and XZ designed this study and edited the final manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.656756/full#supplementary-material.

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Pharmacokinetic Profile and Oral Bioavailability of Diosgenin, Charantin, and Hydroxychalcone From a Polyherbal Formulation

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Background: Diosgenin, charantin, and hydroxychalcone are utilized for standardization of popular antidiabetic herbal drugs *Trigonella foenum-graecum* L belonging to family Fabaceae, *Momordica charantia* L. belonging to family Cucurbitaceae, and *Cinnamomum verum* J. Presl belonging to family Lauraceae. However, no reports on the bioavailability of these markers were available. The present study was undertaken to determine the bioavailability and pharmacokinetic profile of the markers and formulations containing the herbs.

Methods: The pharmacokinetic profile and absolute bioavailability of the pure active markers were determined in male Wistar rats by administrating individually the doses of 1.5 mg/kg i.v. and 15 mg/kg p.o., followed by estimation of serum levels of the markers at 0, 10, 30, 60, 120, and 240 mins till 24 h time points by a validated bioanalytical HPTLC method. Two standardized antidiabetic capsule formulations containing spray dried hydroalcoholic extracts of seeds of *Trigonella foenum-graecum* L. (42.8 mg equivalent to 0.95%w/w of diosgenin), fresh fruits of *Momordica charantia* L. (21.4 mg equivalent to 0.4% w/w of charantin), and bark of *Cinnamomum verum* J. Presl (10.71 mg equivalent to 0.079 %w/w hydroxychalcone) were prepared. In one formulation, piperine 1.5 mg was added along with the other herbal extracts mentioned. Bioavailability and pharmacokinetic profile of these two formulations were determined in male Wistar rats through estimating serum levels of active markers diosgenin, charantin, and hydroxychalcone at 0, 10, 30, 60, 120, and 240 mins till 24 h later oral administration of the formulations (Formulation without piperine F1 and formulation with Piperine F2).

Results: Plasma concentrations were found to decline mono-exponentially following intravenous administration, and the mean elimination half-life ($t_{1/2}$) was observed to be 7.93, 8.21, and 4.66 h, respectively. The absolute oral bioavailability of pure markers was observed to be 9.0 \pm 0.2%, 8.18 \pm 0.36%, and 10.54 \pm 0.52% by the dose normalization method. The oral bioavailabilities of the formulations with respect to diosgenin, charantin, and hydroxychalcone were found to be 9.78, 10.743, and 8.07%, respectively. The formulation containing piperine indicated a significant (ρ < 0.01) increase in the bioavailabilities of all the marker compounds.

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Salunkhe R, Gadgoli C, Naik A and Patil N (2021) Pharmacokinetic Profile and Oral Bioavailability of Diosgenin, Charantin, and Hydroxychalcone From a Polyherbal Formulation. Front. Pharmacol. 12:629272. doi: 10.3389/fphar.2021.629272 **Conclusion:** In conclusion, diosgenin and charantin have low bioavailabilities as compared to hydroxychalcone. The bioavailabilities of all the three marker compounds can be increased exponentially with the addition of piperine.

Keywords: diosgenin, charantin, hydroxychalcone, bioavailability, pharmacokinetics, antidiabetic, herbal formulations

INTRODUCTION

The seeds of Trigonella foenum-graecum L, fruits of Momordica charantia L, and the bark of Cinnamomum verum J. Presl have been reported to possess antidiabetic activity (Rajesh et al., 2016; Mahmoud et al., 2017; Geberemeskel et al., 2019). Around 75% of herbal formulations available in Indian market for treatment of diabetes contain these herbs. Diosgenin from seeds of T. foenumgraecum is reported to have antidiabetic activity in the long-term use by restoration of pancreatic β -cells, downregulation of enzymes involved in hepatic gluconeogenesis and glucose export, upregulation of hepatic glucokinase, and increase in the amounts of hepatoprotective and antioxidant enzymes (Jesus et al., 2016). Charantin from fruits of M. charantia acts through stimulating peripheral and skeletal muscle glucose utilization, inhibition of adipocyte differentiation, suppression of key gluconeogenic enzymes, stimulation of key enzyme of the HMP pathway, and preservation of islet β cells and their functions (Nagappan et al., 2018). Hydroxychalcone from the bark of C. verum acts by mimicking the effect of insulin through enhancing glucose uptake and phosphorylation of insulin receptor in adipocytes; moreover, hydroxychalcone was also reported as a potential dietary PPARy ligand (Eissa et al., 2017).

The pharmacological actions of any drug are dependent on the serum levels of the same. The appropriate serum levels of a drug are dependent on its absorption and distribution metabolism of the drug. The bioavailability of a drug is defined as measurement of the rate and extent to which a drug reaches at the site of action (Kumar and Sanjita, 2013). In case of extracts of herbs or herbal drugs, it is challenging to determine bioavailability due to presence of many constituents. There is very little or no data available revealing pharmacokinetics and bioavailability of phytoconstituents and the formulations containing herbal extracts thereof. Such studies not only help in understanding the efficacy of formulations but also helpful in improving efficacy of formulation through adapting various ways of increasing bioavailability of phytoconstituents.

Herbal drugs are prone to content variations in each harvest and geographical source and hence need serious efforts to be put in standardizing with respect to that of bioavailability and pharmacokinetic study of the herbal formulations. In the present study, three active phytoconstituents viz diosgenin, charantin, hydroxychalcone were studied for their bioavailabilities and pharmacokinetic parameters in albino rats, as the scientific data regarding their bioavailabilities and pharmacokinetic parameters could not be traced (Figure 1).

MATERIALS AND METHODS

Chemicals and Reagents

The seeds of Trigonella foenum-graecum L. and the bark of Cinnamomum verum J. Presl were purchased from the commercial supplier, batch number; 204480093, Sanjeevani Ayurvedic Stores, Angel park, shop number 4, Kalamboli, Navi Mumbai, Maharashtra, India. The fruits of Momordica charantia L. were purchased from the local market Kalamboli, Navi Mumbai, Maharashtra, India. Seeds of T. foenum-graecum, fresh fruits of M. charantia, bark of C. verum were authenticated by Dr. Harshad Pandit from Guru Nanak Khalsa College Matunga, Mumbai. The voucher specimen numbers rbs p 014060319 (Trigonella foenum graecum L.), rbs p 013960219 (Momordica charantia L.), rbs p 013980219 (Cinnamomum verum J. Presl), and rbs p 014040319 (Piper nigrum L.) are deposited, respectively. The active marker compounds diosgenin, charantin, and hydroxychalcone were isolated in the laboratory of Saraswathi Vidya Bhavan's College of Pharmacy, Mumbai, India and were characterized using chromatographic and spectral techniques by SAIF (Sophisticated Analytical Instrumentation Facilities), IIT Bombay. Solvents viz. chloroform, glacial acetic acid, and methanol were of analytical reagent (AR) grade. All other reagents used were of laboratory reagent (LR) grade and were used without further purification. For chromatographic analysis the HPLC grade solvents were utilized.

Isolation of Marker Compounds Isolation of Steroidal Sapogenins (Diosgenin and Charantin)

Diosgenin and charantin are aglycone parts of the steroidal saponin obtained from methanolic extracts of seeds of *T. foenum-graecum* L. and fruits of *M charantia* L., respectively by suitably modifying the reported methods (Sonal and Pratima, 2015; Chen et al., 2017). In brief, the plant materials (50 gm) were defatted with petroleum ether 100 ml (60–80°C), followed by extraction of the marc with polar solvent like methanol (200 ml), to get the glycoside enriched extract. Aglycones of these glycosides were obtained by refluxing the methanolic extracts with 2 M HCl. The aglycones released in this process were then partitioned into the organic phase consisting of diethyl ether (100 ml). The organic phases were then saponified with 10 ml of 10% alcoholic potassium hydroxide to get the aglycone in almost pure form. The aglycones were then purified by recrystallization.

Isolation of Hydroxychalcone

The bark powder of *C. verum* J. Presl (100 gm) was extracted in acetone (150 ml) at 50°C for 1.5 h. The extract was concentrated

at the reduced pressure and the precipitate formed in resulting solution was dissolved using small amount of methanol. The methanolic extract was then fractionated using Sephadex LH-20 column. The yield obtained from polyphenol hydroxychalcone was 0.32 gm % w/w, and as it was not adequate for the experiments, simulated reaction was carried out using cinnamaldehyde (2 gm) and catechin (1 gm) in 50 ml acetone. The reactants were heated at 100°C for 50 mins to get the product having structurally similar polyphenolic present in the cinnamon bark (Tanaka et al., 2008). The synthesized product and the isolated marker compound were confirmed for their identity using spectral studies.

Characterization of the isolated marker compounds was done using TLC, UV-visible spectroscopy, NMR, HRLMS, and elemental analysis and comparing the data with the respective reference standards.

Formulation of Capsules

Two capsule formulations F1 and F2 (**Table 1**) were prepared by incorporating the spray dried hydroalcoholic extracts of seeds of *T. foenum-graecum*, fresh fruits of *M. charantia*, and the bark of *C. zeylanicum*. The F2 formulation contained 1.5 mg of piperine. The extracts utilized for formulations were standardized for the content of diosgenin, charantin, and hydroxychalcone using the HPTLC method (**Table 2**).

The dose for each extract was selected based upon the content of these extracts in the marketed formulation quanto diab-forte (*T foenum-graecum* extract 400 mg, *M charantia* extract 200 mg, and *C zeylanicum* extract 100 mg, respectively), which is utilized for the treatment of diabetes. The piperine content of 1.5 mg is added owing to the amount of the piperine utilized in the herbal formulations (Wadhwa et al., 2014; Mhaske et al., 2018).

The preparation of extracts for formulation of the capsules is described below.

Preparation of Extracts

In case of *T. foenum-graecum* L, the dried seeds were powdered and defatted using petroleum ether (100 ml) for 1 h, followed by extraction of the marc (50 gm), by refluxing it using 70% v/v hydroalcoholic solution. The extract (100 ml) was concentrated to 10 ml and then spray dried (Yield 4 gm).

For preparation of extract of fruits of M. charantia L, 50 gm of fresh fruits were grinded in the mixer and then it was extracted using 70% v/v hydroalcoholic solution (100 ml) for 3 h. The

extract (150 ml) was concentrated to 10 ml, followed by spray drying (Yield 3 gm).

Extraction of cinnamon bark (50 gm) was carried out by refluxing the powder using 70% v/v hydroalcoholic solution, followed by reducing the extract (100 ml) to 10 ml followed by spray drying (Yield 7 gm).

Determination of Content of Marker Compounds

The contents of diosgenin, charantin, and hydroxychalcone were determined from spray dried extracts of *T. foenum graecum* L, *M. charantia* L, and *C. verum J. Presl*, respectively using the HPTLC method. The optimized chromatographic conditions are given in (**Table 2**).

The calibration curves were prepared for individual marker compounds in the range of 0.4 to $1.4 \,\mu g/ml$.

The samples for analysis were prepared by dissolving 10 mg of individual spray dried extract in 10 ml of methanol to give the stock solution of 1 mg/ml (Solution A). 1 ml of Solution A was diluted to 10 ml with methanol to get a solution of $100\,\mu\text{g/ml}$ (Solution B). Further dilutions were made in methanol. The samples were loaded on HPTLC plates and developed the chromatograms using the conditions described in (**Table 2**). The contents of the marker compounds were determined by extrapolating from respective calibration curves (**Table 3**).

Preparation and Evaluation of Formulations

The standardized spray dried extracts were mixed in the proportions indicated in **Table 1** and granules of the same were prepared using the wet granulation method. The dough was formed using microcrystalline cellulose (Avicel) and 60% v/v, followed by addition of required quantity of talc, and then powder blend was passed through sieve number 10 to produce the granules. The granules were gently spread and dried at 45°C in oven for 3 hrs followed by sieving through sieve number 20 supported on 40 and added 10% w/w fines. The granules were then filled in hard gelatin capsules, followed by evaluation of capsules for the content uniformity through determination of content of the marker compounds using the HPTLC method.

Sample Preparation

Granules from 10 capsules were mixed, and a weight of the powder equivalent to 75 mg and was transferred to 100 ml volumetric flask. About 20 ml of methanol (HPLC grade) was added and sonicated for 15 mins or till dissolution of

TABLE 1 | Composition of the herbal formulations developed in laboratory.

Sr no	Ingredients	Composition per capsule		
		Formulation 1	Formulation 2 (mg)	
1	Trigonella foenum-graecum extract	42.8 mg	42.8	
2	Momordica charantia extract	21.4 mg	21.4	
3	Cinnamomum zeylanicum extract	10.71 mg	10.71	
4	70% v/v aqueous ethanol solution	0.11 ml	0.11	
5	Microcrystalline cellulose	51 mg	51	
6	Piperine	_	1.5	

TABLE 2 | HPTLC conditions.

Application mode	Camag Linomat V using 100 μl Hamilton syringe		
Development mode	CAMAG twin trough chamber		
Plate material	Silica gel 60F254 pre-coated HPTLC plates		
Application bandwidth	6 mm		
Developing solvent	Chloroform: glacial acetic acid: methanol: water (4:3:2:1) v/v		
Chamber saturation time	10 min		
Developing distance	90 min		
Development time	20 min		
Detecting wave length	342 nm		
Lamp	UV		
Scanner	CAMAG TLC scanner II		
Integrator	WIN CATS V 1.2.2		

extracts. The volume was then made to the mark using methanol (HPLC grade) (Stock A). The stock solution A was filtered and 1 ml aliquot of the filtrate was further diluted to 100 ml using methanol (HPLC grade). The solutions were further filtered through 0.45 μ syringe membrane and loaded on HPTLC plate for development of chromatogram and analyzed for the content of respective markers.

Bioanalytical Method Development and Validation

The bioanalytical method was developed for the study of the bioavailabilities and the pharmacokinetic parameters of the marker compounds viz. diosgenin, charantin, and hydroxychalcone.

Animals

All animal experiments were approved by the Institutional Animal Ethics Committee (IAEC) and were in accordance with the Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA registration number: SVBCP/IAEC/M ph/18-19/65). Healthy Wistar male rats weighing 180–220 gm were procured from registered breeder Bharat Serum Pvt. Ltd.; Mumbai, India. Experimental animals were maintained on standard pelleted laboratory animal feed and water ad libitum. Animals were maintained at 22 \pm 2°C and 55 \pm 5% relative humidity in the light controlled (12 h light/12 h dark) room.

Analysis of the Marker Compounds in Plasma

Plasma concentrations of active marker compounds were determined using validated high-performance thin layer chromatography (HPTLC) with the UV detection method.

Preparation of Plasma Sample

The plasma samples (150 μ l) were deproteinized by adding mixture of methanol: dichloromethane (1:1), followed by vortex mixing at 3000 rpm for 5 min. The supernatant was separated and further extracted with about 1.5 ml of ethyl acetate by mixing on vortex mixer at 3000 rpm for 10 min. The ethyl acetate layer was then collected and evaporated to dryness, followed by reconstitution with mobile phase (200 μ l) containing chloroform: glacial acetic acid: methanol: water ((4.0: 3.0:2.0:1.0) v/v and 100 μ l was applied on a HPTLC plate. The optimized HPTLC conditions for development and quantification of the constituents is given in **Table 2**.

Preparation of Standard Solutions

Stock solutions of diosgenin, charantin, and hydroxychalcone were prepared by weighing 10 mg of each reference standard and dissolving in methanol (50 ml), followed by making up the volume to 100 ml with methanol to get the concentration of each marker as 100 ppm. The solution was then suitably diluted and 100 μ l of the solution of the marker compounds was spiked in 100 μ l plasma to get the concentration and prepared the solutions with concentrations in the range of 0.4–1.4 μ g/ml of each marker compound. These were then utilized for preparation of calibration curve. The HPTLC analysis of samples and the

TABLE 3 Content of diosgenin, charantin, and hydroxychalcone in the 70% v/v ethanolic extracts of T foenum-graecum, M charantia, and C zeylanicum, respectively.

Names of marker compounds in 70% v/v hydroalcoholic extracts	Mean retention time ±SD (mins)	Mean content of markers per 10 mg of extract ±SD (mean percent w/w)	
Diosgenin from <i>T foenum-graecum</i>	1.742 ± 0.04	0.11 ± 0.005	
Charantin from <i>M charantia</i>	3.942 ± 0.02	0.045 ± 0.02	
Hydroxychalcone from C zeylanicum	7.717 ± 0.06	0.024 ± 0.03	

Results are presented as mean \pm SD (n = 3).

standard solutions were carried out using the parameter described (Table 2).

The retarding factors (Rf) values for diosgenin, charantin, and hydroxychalcone were found to be 0.72, 0.61, 0.30, respectively. The lower limit of quantification of the method was 0.33, 0.090,

 $0.0072~\mu g/ml$, respectively and linearity in the calibration curve were demonstrated up to an upper limit of 1.11, 1.13, 1.12 $\mu g/ml$, respectively. Intra- and inter-day precision and accuracy were determined as per ICH guidelines.

Method Validation

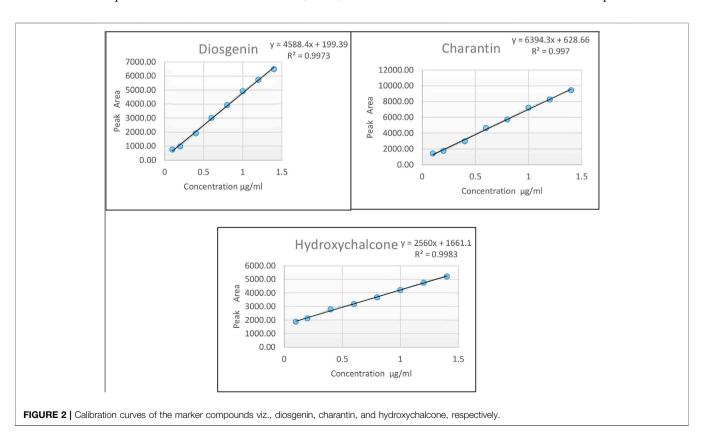
The validation of the analytical method was executed as per "Guidance for industry: Bioanalytical Method Validation" from the United States Food and Drug Administration (Guidance for Industry, Bioanalytical Method Validation, 2001).

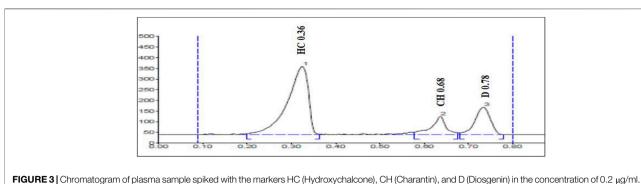
Calibration Curve

For calibration curve, the stock solution containing all the three markers in the concentration of 100 ppm of each was diluted suitably and spiked in blank plasma to get different concentrations in the range of 0.4–1.4 µg/ml, followed by extraction as described in Section Analysis of the marker compounds in Plasma. The standard solution after extraction were applied on HPLTLC plates and developed using the conditions described in **Table 2**. The calibration curves were constructed individually by plotting peak area of diosgenin, charantin, and hydroxychalcone against the concentrations of the marker compounds using linear regression. The experiment was carried out in triplicate (**Figure 2**).

Selectivity

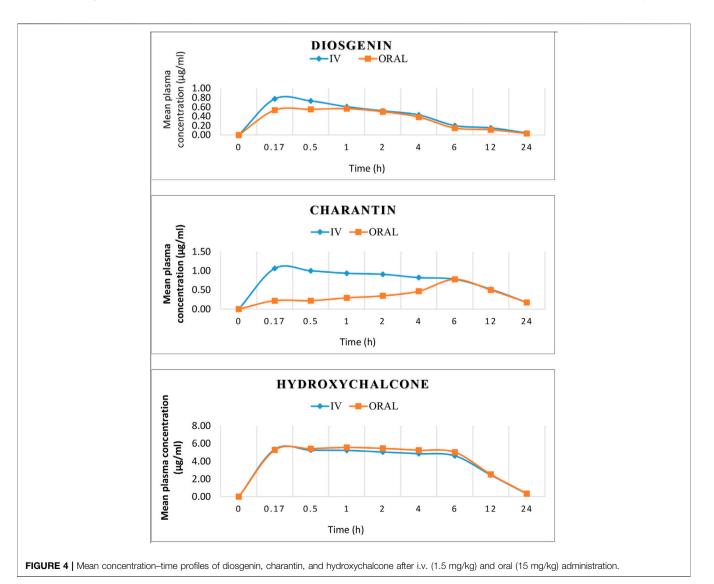
Selectivity of the analytical method was determined by recording the retardation factors of the marker compounds through HPTLC as described in **Table 2**. The blank plasma was also

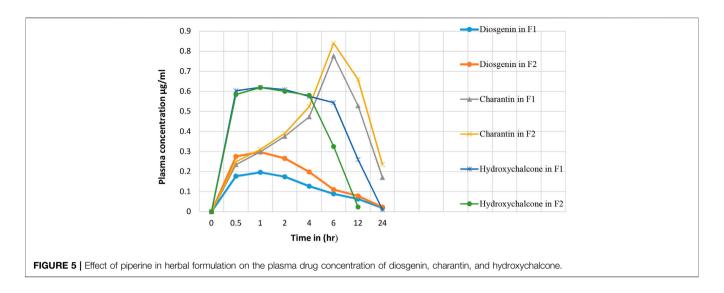




subjected to chromatographic analysis as described in **Table 2**. The third chromatogram was run by spiking the plasma with LLOQ (0.2 μ g/ml) of marker solutions. The interference at the Rf values was determined by comparing the area response in the blank matrix against the mean response of the extracted LLOQ

(0.2 μ g/ml) samples. Also, interference at the Rf was evaluated by comparing the area response in the blank matrix against the mean response of extracted LLOQ (0.2 μ g/ml) samples. The % interference was calculated by taking the ratio of "Area at the Rf of analyte to the Mean area (n = 5) at the Rf of analyte in the





LLOQ." The selectivity of the method was calculated using the following formula

% interference =
$$\frac{\text{area at Rf of analyte}}{\text{mean Area at Rf of analyte}} \times 100.$$

Accuracy and Precision

Accuracy studies were performed in terms of recoveries of hydroxychalcone, charantin, and diosgenin from spiked plasma. For this quality control samples, LQC-lowerconcentration quality control sample (0.4 ppm)quality MQC-medium concentration control samples (0.8 ppm) of all reference standard drugs were analyzed (n = 3), and % accuracy was calculated by comparing the average measured concentrations using the calibration curves to known concentrations.

The inter- and intra-day precision for the analytical method was determined by analyzing the quality control samples of all the marker compounds at LQC (0.4 PPM), MQC (0.8 PPM), and HQC (1.2 ppm) using the HPTLC method described above. For intra-day precision, RSD (Relative Standard Deviation) was calculated for analysis of the quality control samples in six replicates. In case of inter-day precision, RSD for analysis of the quality control samples carried out for three consecutive days was calculated. The analysis was carried out in six replicates.

Recovery and Stability

The extraction recoveries (ER) of diosgenin, charantin, and hydroxychalcone from plasma were determined at three different concentrations low-, middle-, and high-concentration range. Also unextracted dilution was prepared at concentration representing a 100% were applied/spotted and analyzed. The mean absolute % recovery was calculated by taking the ratio of "Mean peak area response of extracted samples at LQC/MQC/HQC" to the "Mean peak area response of unextracted samples at LQC/MQC/HQC."

The mean absolute % recovery was calculated by taking the ratio of "Mean peak area response of extracted samples at MQC (0.8 μ g/ml) level" to the "Mean peak area response of unextracted samples". Overall recovery for analyte was calculated by taking the average of mean of absolute % recovery at LQC (0.4 μ g/ml), MQC (0.8 μ g/ml), and HQC (1.2 μ g/ml) with SD and % CV for analyte are also reported.

Sample stability was determined by analyzing samples for quality control for analyte's stock stability in solvent, refrigerator stock solution stability, freeze and thaw stability, and bench top stability.

Pharmacokinetic Studies

The pharmacokinetic studies were carried out in male Wistar rats. Initially the absolute bioavailabilities of individual marker compounds were determined, followed by determination of bioavailability of the formulations F1 and F2 with respect to the marker compounds.

Determination of Absolute Bioavailability of Marker Compounds

Absolute bioavailabilities of marker compounds viz. diosgenin, charantin, and hydroxychalcone were determined in male Wistar rats. The animals weighing 300-350 gm were fasted overnight before the dosing with free access to drinking water throughout the experimental period. For the purpose of dosing all the three marker compounds viz, diosgenin, charantin, hydroxychalcone were suspended in water to make the dose of 15 mg/kg per oral to be administrated to the groups of three rats. The animals were divided into two groups with six animals in each group. The first group received the marker compounds in the dose of 1.5 mg/kg i.v. via lateral tail vein, while the second group received the marker compounds in the dose of 15 mg/kg p.o. The rats were anesthetized using ether and blood samples were collected through puncturing the retro-orbital plexus at 0, 0.17, 0.5, 1, 2, 4, 6, 12, and 24 h time points. Blood samples were centrifuged to separate plasma and stored at -20°C until bioanalysis.

Determination of Bioavailability of Formulations

Bioavailabilities of the two formulations viz. F1 containing the standardized spray dried extracts of seeds of T. foenum-graecum, fresh fruits of M. charantia, and the bark of C. verum. The F2 containing the spray dried extracts as mentioned in F1 along with the piperine (1.5 mg) were determined by administrating the formulations in the dose of 75 mg/kg b.w. p.o. to the two groups (each group n=6) of male Wistar rats weighing 300-350 gm, fasted overnight. For administration of the formulations, these were suspended in water with 2% w/v and Tween 80, and administrated through oral gavage. The blood samples were collected through puncturing the retro-orbital plexus at 0, 0.17, 0.5, 1, 2, 4, 6, 12, and 24 h time points. Blood samples were centrifuged to separate plasma and stored at -20°C until bioanalysis.

Pharmacokinetic Parameters (Jagannath et al., 2004; Michal et al., 2017)

The pharmacokinetic parameters were calculated for both the individual marker compounds as well as the formulations (F1 and F2).

Non-compartmental analysis of data was performed using statistical moment theory. The peak plasma concentration ($C_{\rm max}$) and the corresponding time ($T_{\rm max}$) were directly obtained from the raw data.

The area under the plasma concentration vs. time curve upto the last quantifiable point, $AUC_{(0-t)}$, was calculated by the linear and log-linear trapezoidal rule summation:

$$AUC_{(0-t)} \ = \sum \frac{C_0 + C_t}{2} \times \ T_t - \ T_0.$$

C = Plasma drug concentration at time t.

T = Time required to attain C.

The $AUC_{(0\text{-}t)}$ was extrapolated to infinity (i.e., AUC $_{(0\text{-}1)})$ by adding the quotient of $C_{last}/K_{el},$

$$AUC_{(t-\infty)} = \frac{C_{last}}{K_{el}},$$

Where C_{last} represents the last measurable time concentration and K_{el} represents the elimination rate constant.

 $K_{\rm el}$ was calculated by the linear regression of the log-transformed concentrations of the last three data points in the terminal phase.

$$K_{el} = -slope \times 2.303.$$

Slope was obtained from log-transformed concentrations of the last three data points in the terminal phase.

The half-life of the elimination phase was obtained from using the relationship,

$$t_{1/2} = \frac{0.693}{K_{el}}.$$

Clearance was calculated using the relationship $Cl = Vd \times K_{el}$

Vd = Apparent volume of distribution

 K_{el} = Elimination rate constant

Apparent volume of distribution was calculated using relationship

$$Vd = \frac{Dose Administered}{Plasma concentration}$$

Absolute oral bioavailability (F) was calculated using relationship F = {[AUC $_{(oral)}$ /AUC $_{(iv)}$] × [Dose $_{(iv)}$ /Dose $_{(oral)}$]} × 100.

Statistical Analysis

The results are expressed as mean \pm standard deviation (SD). Data were statistically analyzed using Student's t test. A p value of less than 0.05 was considered as statistically significant.

RESULTS AND DISCUSSION

Isolation and Characterization of Marker Compounds

Isolation of marker compounds viz, diosgenin, charantin, and hydroxychalcone were done as per the procedure given in Section *Isolation of Marker compounds*. Identity of the isolated marker compounds was determined using chromatographic and spectral studies. The spectroscopic data of the marker compounds were compared with the standard marker compounds for the confirmation of the structures.

Formulation of Capsule

For formulation of capsules, the content of diosgenin, charantin, and hydroxychalcone were determined in the spray dried extracts of *T foenum graecum* L, *M charantia* L, and *C verum* J. Presl, respectively using the HPTLC method.

Standardization of Extracts

The extracted samples were loaded on HPTLC plates and developed the chromatograms using the conditions described in (**Table 2**). The contents of the marker compounds were determined by extrapolating from respective calibration curves.

These standardized extracts were then utilized for preparation of polyherbal formulation.

Evaluation of Polyherbal Formulation

The evaluation of capsules was done for the content uniformity through determination of content of the marker compounds using the HPTLC method; results are represented in **Table 4**.

Validation of Bioanalytical Method

The validation was executed as per "Guidance for industry: Bioanalytical Method Validation" from the United States Food and Drug Administration (Guidance for Industry, Bioanalytical Method Validation, 2001). The results of validation parameters are given as follows.

Selectivity

The selectivity of the method was evaluated by analyzing blank plasma samples prior to spiking. The representative chromatograms

TABLE 4 | Contents of diosgenin, charantin, and hydroxychalcone in polyherbal formulation determined using the optimized HPTLC method.

Name of the hydroalcoholic extracts present in formulation	Mean. Wt. of each capsule (n = 3)	Mean retention time (n = 3)	Mean content of markers (mg) in the formulation 75 mg (n = 3)	Mean % w/w content (n = 3)
T foenum-graecum, (D)	197.52 ± 0.07	1.742 ± 0.04	1.0280 ± 0.02	0.95 ± 0.01
M charantia, (CH)		3.942 ± 0.02	0.5240 ± 0.01	0.4 ± 0.01
C zeylanicum, (HC)		7.717 ± 0.06	0.0822 ± 0.005	0.079 ± 0.002

Results are expressed as mean ± SD (n = 3). D: Diosgenin, CH: Charantin HC: Hydroxychalcone.

of the plasma sample spiked at $0.2 \,\mu g/ml$ of all the three marker compounds and compared with the blank plasma sample. The results presented in **Figure 3** indicate that the chromatogram of the marker compounds was free of interfering peaks at the Rf values of diosgenin (D), charantin (CH), and hydroxychalcone (HC). Thus, it indicated the method selectivity **Table 5**.

Linearity of Calibration Curves

Linearity for the calibration curve of each marker compound was observed in the range of $0.4-1.4 \,\mu\text{g/ml}$ with the regression equations for the marker compounds as given below: the regression equation for diosgenin was Y = 1527.8 X + 65.653 ($R^2 = 0.9955$); the regression equation for charantin was Y = 2139.3 X + 203.2 ($R^2 = 0.9953$); the regression equation for hydroxychalcone was Y = 811.26 X + 599.29 ($R^2 = 0.9952$),

Where X was the concentrations of analytes in rat plasma and Y was the peak areas.

Precision

Precision studies were performed for inter-day and intra-day variation in developed method by applying quality control samples through HPTLC analysis using optimized chromatographic conditions, as given in **Table 2**. The % RSD values of the results of determination of concentrations at LQC, MQC, andHQC levels for hydroxychalcone, charantin, and diosgenin are found within the limit that is lower than 10% as shown in the **Table 6**, and the accuracy was within 85–120% for samples for quality control. The results demonstrated that the method qualifies the precision and accuracy criteria.

Extraction Recovery and Stability

The mean % recoveries for diosgenin, charantin, and hydroxychalcone were found to be 94.25, 88.02, and 93.70%, respectively, at all three levels of quality control samples.

The percent recovery of diosgenin, charantin, and hydroxychalcone are observed within the acceptance criteria of 85–120%, indicates the accuracy of the HPTLC method utilized (ICH Guideline M10 On Bioanalytical Method Validation, 2019).

The stability experiments were carried out to evaluate the degradations of the marker compounds under different experimental conditions. The results presented in **Table 7** indicate that there is no significant degradation of diosgenin, charantin, and hydroxychalcone in plasma under different experimental conditions.

As per the acceptance criteria, % ratio (Stability/comparison) should be within 85–115%; from the above results, it was

concluded that all the marker compounds were within the acceptance criteria for stability study **Table 7**.

Pharmacokinetic Study

Determination of Absolute Bioavailability of Marker Compounds

The above validated bioanalytical HPTLC method was successfully and completely applied evaluate Initially the pharmacokinetics in male Wistar rats. bioavailability of marker compounds was determined by administrating the pure marker compounds individually to Wistar rats by oral (dose 15 mg/kg b.w per oral) and parenteral (dose 1.5 mg/kg b.w i.v.) routes, followed by determination of content of the same in plasma at different time points by the HPTLC method. The results of the absolute bioavailability studies of the individual marker compounds are presented in Table 8.

The nature of the plasma curves following intravenous administration suggested a mono-exponential decline in the plasma concentration vs. time curves of the active marker compounds **Figure 4**.

Results presented in **Table 8** reveal that the highest absolute bioavailability is obtained for hydroxychalcone (10.54%), when calculated by the dose normalization method probably due to polar nature, while the other two markers being steroidal, the bioavailability was between 8–9%.

Elimination rate constant (K_{el}) indicates the rate at which a drug is removed from the body, which is found to be 0.09 and 0.08 h⁻¹, 0.08 and 0.084 h⁻¹, and 0.14 and 0.148 h⁻¹ for i.v. and oral routes of administration for diosgenin, charantin, and hydroxychalcone, respectively. The similar K_{el} values for i.v. and oral routes of administration for marker compounds over the concentration range encountered in clinical settings indicate the first order elimination.

Plasma half-life $(t_{1/2})$ indicates the time required for reducing the concentration of drug to the half of its concentration; it also

TABLE 5 | Selectivity study of diosgenin, charantin, and hydroxychalcone spiked at $0.2~\mu g/ml$ in rat plasma.

Marker compounds		ters	
	Area	SD	% Interference
Diosgenin (0.2 μg/ml)	2035.38	29.25	1.43
Charantin (0.2 µg/ml)	1157.03	20.58	1.77
Hydroxychalcone (0.2 µg/ml)	2465.03	40.78	1.65

TABLE 6 | Precision of diosgenin, charantin, and hydroxychalcone in rat plasma.

Marker compounds	Concentration (µg/ml)	Intra-day assay	Inter-day assay	
		%RSD	%RSD	
Diosgenin	0.4	0.91	0.90	
	0.8	1.42	1.39	
	1.2	0.44	1.00	
Charantin	0.4	1.50	0.77	
	0.8	0.51	1.50	
	1.2	0.21	1.15	
Hydroxychalcone	0.4	0.91	1.06	
	0.8	0.49	0.33	
	1.2	1.25	0.73	

(n = 3).

indicates whether the accumulation of the drug occurs under a multiple dosage regimen and it is essential to decide on the appropriate dosing intervals. $t_{1/2}$ was found to be 7.5638 and 7.9300 h i.v. and oral, respectively for diosgenin, 8.33 and 8.2 h for charantin, and 4.68 and 4.65 h for hydroxychalcone i.v. and oral, respectively, indicating there was no statistically significant difference in the values for intravenous as well as oral routes of administration due to first order elimination.

Volume of distribution (Vd) is theoretical volume that would contain the total amount of administrated drug at the same concentration in plasma. It represents the degree at which drug is distributed in the body tissue rather than plasma. Higher Vd indicates greater amount of tissue distribution and low protein binding. The highest volume of distribution was observed for diosgenin (2.5 ml/kg) followed by charantin (1.4 ml/kg) and least was observed for hydroxychalcone (0.27 ml/kg),indicating high binding protein hydroxychalcone and ultimately low t_{1/2} and lower clearance of drug from the body. In case of diosgenin and charantin, as those are steroidal sapogenin, they have higher lipid solubility and have lower molecular weight compared to that of hydroxychalcone which is water soluble and having higher molecular weight; hence diosgenin and charantin have high volume of distribution and ultimately have high $t_{1/2}$ values.

Drug clearance (Cl) is concerned with the rate at which a drug is removed from the body. It refers to the amount of the drug eliminated per unit time from the body. Clearance is related to the total drug concentration in the plasma (free + protein-bound) and not the free concentration. As per the results obtained, clearance for the hydroxychalcone was found to be 0.0417 ml/h/kg which is the least, followed by diosgenin (0.22 ml/h/kg) and charantin (0.11 ml/h/kg), indicating higher AUC for hydroxychalcone and the highest residence time of the drug in the systematic circulation and that slower will be the decline in plasma concentration of hydroxychalcone.

AUC represents the total drug exposure with respect to the time. Assuming the linear kinetics with elimination rate constant, one can show that AUC is equivalent to the total amount of drug observed in the body. AUC for the diosgenin was found to be 4.47 and 4.95 μ g h/ml for i.v. and oral administration, respectively. AUC for charantin and hydroxychalcone was found to be 12.48 and 15.26 μ g h/ml and 72.99 and 69.25 μ g h/ml with i.v. and p.o. administrations, respectively. Higher AUC value of hydroxychalcone indicates more time hydroxychalcone will remain in the systematic circulation giving higher bioavailability.

 $T_{\rm max}$ represents the time taken by a substance to reach the maximum concentration ($C_{\rm max}$) in the blood. Hydroxychalcone, being a weakly acidic compound due to presence of the phenolic groups, remains unionized at gastric pH and hence indicated very fast absorption after oral administration with short $T_{\rm max}$ of 1h. Charantin being nonpolar steroidal compound takes long time for its absorption which is revealed from the highest $T_{\rm max}$ value of

TABLE 7 | Stability data for diosgenin, charantin, and hydroxychalcone in rat plasma.

Marker compounds	Concentration (µg/ml)	Room temperature standard stock	Refrigerator standard stock solution	Freeze thaw stability (%)	Short-term room temperature stability
		solution stability (%)	stability (%)		(%)
Diosgenin	0.4	85.18 ± 0.45	91.73 ± 0.46	87.06	98.64
	0.8	84.86 ± 1.23	90.24 ± 1.13	94.52	97.90
	1.2	85.03 ± 2.16	89.56 ± 2.21	97.86	98.25
Charantin	0.4	86.79 ± 2.99	85.79 ± 2.43	74.01	95.25
	0.8	86.02 ± 3.49	88.13 ± 2.13	88.12	90.25
	1.2	88.39 ± 1.52	90.14 ± 2.02	97.85	96.54
Hydroxychalcone	0.4	87.59 ± 2.33	90.03 ± 1.56	63.73	63.76
	0.8	85.15 ± 1.67	94.16 ± 1.32	70.63	79.32
	1.2	87.00 ± 1.23	91.23 ± 1.84	79.32	79.02

Results are presented as mean \pm SD (n = 3).

6 h. Although diosgenin is the nonpolar steroidal compound, it takes 1 h to reach the $T_{\rm max}$ due to higher number of OH groups in compound making it more polar as compared to the charantin. The results of pharmacokinetic parameters presented in **Table 9**, indicate that almost same $C_{\rm max}$ values of diosgenin, charantin, and hydroxychalcone, 0.57 and 0.61 µg/ml, 0.71 and 1.06 µg/ml, and 5.42 and 5.35 µg/ml, respectively, for i.v. and oral routes of administration were found.

Mean residence time (MRT) is the average time the drug stays at the site of action. MRT for the marker compounds viz, diosgenin, charantin, and hydroxychalcone was found to be 8.20 and 9.94 h, 14.75 and 11.98 h, and 7.87 and 7.90 h for i.v. and oral routes of administration, respectively. MRT is inversely proportional to the AUC of the drug.

Rate of absorption (K_a) determines the time required for the administrated drug to the reach an effective plasma concentration and may, thus, affect the onset of drug effect. K_a influences both the peak plasma concentration (C_{max}) and time it takes to reach the peak (T_{max}). Highest K_a value of 1.5 h $^{-1}$ was obtained in hydroxychalcone followed by diosgenin (1.1 h $^{-1}$) and the least of case of charantin, 0.46 h $^{-1}$. As the rate of absorption is 0.46 h $^{-1}$, which is less compared to that of diosgenin and hydroxychalcone, it has higher T_{max} value of 6 h.

Bioavailability is the measurement of the rate and the extent to which drug reaches at the site of action. Absolute bioavailability compares the bioavailability of active drug in systemic circulation following non-intravenous administration, with the bioavailability of the same drug following intravenous administration. The absolute bioavailability of the drug, when administrated by extra vascular route is usually less than one (i.e., F <100%). In the present study, absolute bioavailability of diosgenin, charantin, and hydroxychalcone was found to be 9, 8.18, and 10.54%, respectively. Various physiological factors reduce the availability of the drugs prior to their entry into the systemic circulation. Higher absolute bioavailability for

hydroxychalcone may be due to its higher tissue binding, high molecular weight, higher water solubility, and higher volume of distribution. On the other hand, diosgenin and charantin are the steroidal sapogenins having higher lipid solubility, hence have least volume of distribution, which affects their bioavailability.

Determination of Bioavailability of Formulations

The polyherbal formulations were prepared using the alcoholic extracts. The extracts contain several constituents that can influence the bioavailability and pharmacokinetic parameters of the marker compounds. Piperine is used in the current study as it is known for the enhancement of bioavailability of drug component from ancient time and in the traditional system of medicine Ayurveda (Chen et al., 2017; Mhaske et al., 2018).

Results presented in Table 10 indicate the values of pharmacokinetic parameters obtained due administration of the formulations F1 and F2 calculated with respect to the marker compounds viz. diosgenin, charantin, and hydroxychalcone. The elimination rate constants Kel values of the individual marker compounds in all the formulations were found to be similar when compared with the pure molecules diosgenin, charantin, and hydroxychalcone, respectively. Significant reduction (p < 0.01) in the clearance rate of all the three marker compounds is observed in formulation F2 as compared to the formulation F1, indicating availability of the marker compounds for activity due to inhibition of CYP enzymes by piperine Figure 5 (Volak et al., 2008).

There is a significant increase (p < 0.01) in the $\mathrm{AUC_0}^\infty$ values of individual marker compounds in case of administration of the formulations F2 as compared to F1, indicating availability of significantly higher concentrations of the phytoconstituents for action. This is due to the bioenhancing effect of piperine through inhibition of CYP2D6 and CYP3A4 (ICH Guideline M10 on Bioanalytical Method Validation, 2019)

TABLE 8 | Mean (±SD) pharmacokinetic parameters and absolute bioavailabilities for diosgenin, charantin, and hydroxychalcone in rats after a single dose administration.

Parameters	Dio	sgenin	Charantin		Hydroxychalcone	
	Oral single dose administration (15 mg/kg per oral) (µg/ml)	IV single-dose administration (1.5 mg/kg i.v.) (μg/ml)	Oral single-dose administration (15 mg/kg per oral) (µg/ml)	IV single-dose administration (1.5 mg/kg i.v.) (μg/ml)	Oral single-dose administration (15 mg/kg per oral) (µg/ml)	IV single-dose administration (1.5 mg/kg i.v.) (µg/ml)
K _{el} (h ⁻¹)	0.0917 ± 0.003	0.0875 ± 0.004	0.0832 ± 0.0005	0.0844 ± 0.001	0.1481 ± 0.001	0.1488 ± 0.001
t _{1/2} (h)	7.5638 ± 0.21	7.9300 ± 0.37	8.3328 ± 0.05	8.2090 ± 0.13	4.6806 ± 0.04	4.6565 ± 0.04
Vd (ml/kg)	_	2.5397 ± 0.57	_	1.4108 ± 0.001	_	0.2799 ± 0.0004
CI (ml/h/kg)	2.5143 ± 0.09	0.2221 ± 0.05	5.9268 ± 0.31	0.1191 ± 0.002	0.4199 ± 0.01	0.0417 ± 0.0004
AUC $_{\infty}^{0}$ (µg.h/ml)	4.4753 ± 0.06	4.9575 ± 0.44	12.4872 ± 0.11	15.2678 ± 0.03	72.9944 ± 0.49	69.2514 ± 0.09
C _{max} (µg/ml)	0.5773 ± 0.012	0.6122 ± 0.1	0.7725 ± 0.009	1.0633 ± 0.001	5.4245 ± 0.2	5.3583 ± 0.002
T _{max} (h)	1	-	6	_	1	_
AUMC $_{\infty}^{0}$ (µg.h 2 /ml)	36.700 ± 0.77	17.3937 ± 2.10	176.7245 ± 1.83	182.9438 ± 1.74	574.5756 ± 1.08	547.3199 ± 1.21
MRT (h)	8.2008 ± 0.15	9.9420 ± 0.90	14.1521 ± 0.07	11.9823 ± 0.10	7.8716 ± 0.04	7.9034 ± 0.01
Ka (h ⁻¹)	1.1 ± 0.10	_	0.4617 ± 0.02	_	1.5 ± 0.16	_
Absolute bioavailability (%)	9.0 ± 0.2		8.18 ±	: 0.36	10.54	± 0.52

Results are presented as mean \pm SD (n = 6) ($K_{e\Gamma}$ elimination rate constant, $t_{1/2}$ -plasma half-life, Cl-drug clearance, AUC-area under curve, C_{max} -maximum concentration of the drug, T_{max} -the time taken by a substance to reach the C_{max} AUMC-A under the moment curve, MRT-mean residence time, and Ka-rate of absorption).

TABLE 9 | Relative bioavailabilities of diosgenin, charantin, and hydroxychalcone in the formulation without piperine (F1), formulation with piperine (F2), and oral pure drug administration.

Diosgenin:					
Formulations	AUC ₀ [∞] (μg.h/ml)	Dose (mg/kg p.o)	Relative bioavailability		
			Standard	Sample	Relative bioavailability
F2	1.9838	0.68	F2	F1	0.7346
Oral pure drug administration	4.4753	15	Oral pure drug administration	F1	9.7782
			Oral pure drug administration	F2	13.3113
Charantin:					
Formulations	AUC ₀ [∞] (μg.h/ml)	Dose (mg/kg p.o)	Standard	Sample	Relative bioavailability
F2	1.6009	0.179	F2	F1	0.6836
Oral pure drug administration	12.4872	15	Oral pure drug administration	F1	10.7433
			Oral pure drug administration	F2	15.7160
Hydroxychalcone:					
Formulations	AUC ₀ [∞] (μg.h/ml)	Dose (mg/kg p.o)	Standard	Sample	Relative bioavailability
F2	1.4294	0.0364	F2	F1	0.8523
Oral pure drug administration	72.994	15	Oral pure drug administration	F1	8.0701
			Oral pure drug administration	F2	9.4692

(F1-Formulation without piperine, F2-Formulation containing Piperine).

t $_{1/2}$ represents the time required to reduce the concentration of the drug to be half of C_{max} value due to the elimination process. This value in turn also indicates the time for which the drug remains in the body. There was no significant difference in $t_{1/2}$. The highest MRT values of 13.33 and 14.41 h were observed for charantin in F1 and F2, respectively.

Absorption rate constant Ka values for marker compound was found to be significantly increased (p < 0.05) for diosgenin and charantin in F2 as compared to F1, indicating more availability through improved absorption rate constant. In case of charantin, there was a decrease in the value of Ka of the formulation F2 as compared to the formulation F1, indicating increased rate of permeation due to piperine in F2.

Relative bioavailability measures the bioavailability of a formulation of certain drug when compared with another formulation of the same drug. Relative bioavailability is one of the measures used to assess bioequivalence between two drug products. From the results of bioavailabilities of the markers viz. diosgenin, charantin, and hydroxychalcone from the formulations F1 and F2, the relative bioavailabilities for these were calculated and the results are presented in **Table 9**.

Results presented in **Table 9** indicate that the relative bioavailability of diosgenin in the formulation F1 when calculated with reference to F2 was found to be 0.73. When the relative bioavailability for F1 was compared to that of pure oral drug, it was found to be 9.77. Relative bioavailability for the formulation F2 when compared to the pure drug was found to be 13.31. Hence, it can be concluded that there is a 13-fold increase in the bioavailability of diosgenin due to presence of piperine.

TABLE 10 | Effect of piperine on the pharmacokinetic parameters of the marker compounds viz, diosgenin, charantin, and hydroxychalcone after administration of the herbal formulations.

Parameters	Dios	genin	Char	Charantin		Hydroxychalcone	
	F1 (75 mg/kg per oral) (μg/ml)	F2 (75 mg/kg per oral) μg/ml)	F1 (75 mg/kg per oral) (µg/ml)	F2 (75 mg/kg per oral) (μg/ml)	F1 (75 mg/kg per oral) (µg/ml)	F2 (75 mg/kg per oral) (μg/ml)	
K _{el} (h ⁻¹)	0.0900 ± 0.004	0.0890 ± 0.001	0.0896 ± 0.0003	0.0844 ± 0.003	0.1450 ± 0.002	0.1412 ± 0.005	
t _{1/2} (h)	7.7088 ± 0.32	7.7838 ± 0.117	7.7316 ± 0.025	8.2130 ± 0.25	4.7801 ± 0.08	4.9129 ± 0.169	
Cl (mg/h/kg)	0.3456 ± 0.02	0.2199 ± 0.004	0.5553 ± 0.006	0.4548 ± 0.02	0.0685 ± 0.001	0.0350 ± 0.001	
AUC o [∞] (µg.h/ml)	1.9838 ± 0.02	2.7006 ± 0.006	1.6009 ± 0.034	2.3419 ± 0.05	1.4294 ± 0.01	1.6772 ± 0.003	
C _{max} (µg/ml)	0.1962 ± 0.002	0.2975 ± 0.002	0.1008 ± 0.002	0.1506 ± 0.002	0.0954 ± 0.002	0.1517 ± 0.0001	
T _{max} (h)	1	1	6	6	1	1	
AUMC _∞ ⁰	19.7230 ± 0.25	26.1961 ± 0.40	21.3542 ± 0.54	33.7730 ± 1.58	12.490 ± 0.20	12.7395 ± 0.27	
MRT (h)	9.9420 ± 0.03	9.700 ± 0.15	13.3383 ± 0.05	14.4165 ± 0.38	8.7378 ± 0.08	7.5954 ± 0.15	
Ka (h ⁻¹)	1.0 ± 0.02	1.1 ± 0.03	0.73 ± 0.04	0.41 ± 0.04	1.2 ± 0.09	1.5 ± 0.24	

Results are presented as mean \pm SD (n = 6), (K_{ef} -Elimination rate constant, $t_{1/2}$ - plasma half-life, Cl-drug clearance, AUC- area under curve, C_{max} -maximum concentration of the drug, T_{max} -the time taken by a substance to reach the C_{max} AUMC- A under the moment curve, MRT-mean residence time, and Ka-rate of absorption).

As per the results for charantin, the relative bioavailability of the charantin in F1 when compared to that of F2 was found to be 0.68. Relative bioavailability of F1 when compared to that of the oral pure drug was found to be 10.74. At the same time, when relative bioavailability of F2 was compared to that of pure drug, it was found to be 15.71. Relative bioavailability of the formulation has been increased due to piperine.

The relative bioavailability of the hydroxychalcone in F1 when compared with that of F2 was found to be 0.85. When relative bioavailability of F1 was compared with that of oral pure drug, it was found to be 8.07. When F2 was compared with that of the pure drug, it was found to be 9.46. Hence, it was observed that there was an increase in the relative bioavailability of formulation due to presence of piperine.

Results of the relative bioavailability as presented in **Table 10** clearly indicate that there was an increase in the bioavailability of the formulation due to incorporation of piperine. Piperine was known for the enhancement of bioavailability of the drug components from the ancient times. When relative bioavailability was studied, it was found that there was a 13- to 15-fold increase (p < 0.01) in the bioavailability of the marker compounds in the formulation F2 due to piperine.

CONCLUSION

In conclusion, a bioanalytical HPTLC method has been developed and validated for the first time for evaluation of pharmacokinetics and absolute bioavailabilities of marker compounds diosgenin, charantin, and hydroxychalcone in single oral and intravenous administrated rats. The absolute

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bioavailabilities of marker compounds were found to be in the range of 8 to 10% which is increased by about 15% in formulation due to incorporation of piperine.

Further studies can be carried out at various dose levels and measures can be taken for improving the bioavailability.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**; further inquiries can be directed to the corresponding author.

ETHICS STATEMENT

The animal study was reviewed and approved by the Institutional Animal Ethics Committee (IAEC). CPCSEA registration number: SVBCP/IAEC/M ph/18-19/65.

AUTHOR CONTRIBUTIONS

RS: isolation, characterization, HPTLC method development, bioavailability studies, and pharmacokinetic studies. CG: research guide. AN: research guide. NP: bioanalytical method development and validation.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.629272/full#supplementary-material

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Anti-Myocardial Ischemia Reperfusion Injury Mechanism of Dried Ginger-**Aconite Decoction Based on Network Pharmacology**

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Dried ginger-aconite decoction (DAD) is a traditional Chinese medicine (TCM) formula that has been extensively used in the treatment of myocardial ischemia reperfusion injury (MI/ RI). However, its specific mechanism against MI/RI has not been reported yet. Therefore, this paper studies the potential active components and mechanism of DAD against MI/RI based on network pharmacology and experimental verification. Sixteen active components of DAD were screened according to oral bioavailability and drug similarity indices. Through Cytoscape 3.7.0, a component-target network diagram was drawn, and potential active components of DAD against MI/RI were determined. Protein-protein interaction (PPI) and compound-target-pathway (C-T-P) networks were established through the software to discover the biological processes, core targets and core pathways of DAD against MI/RI. High Performance Liquid Chromatography (HPLC) analysis identified the presence of potentially active core components for network pharmacological prediction in DAD. It was found that DAD might have played a therapeutic role in anti-MI/RI by activating the PI3K/Akt/GSK-3ß signaling pathway in order to reduce mitochondrial hypoxia injury and myocardial cell apoptosis. The network pharmacological prediction was validated by Hypoxia/reoxygenation(H/R) model in vitro and ligation model of the ligation of the left anterior descending branch in vivo. It was verified that DAD had activated PI3K/AKT/GSK-3\$ to reduce myocardial apoptosis and play a therapeutic function in MI/RI.

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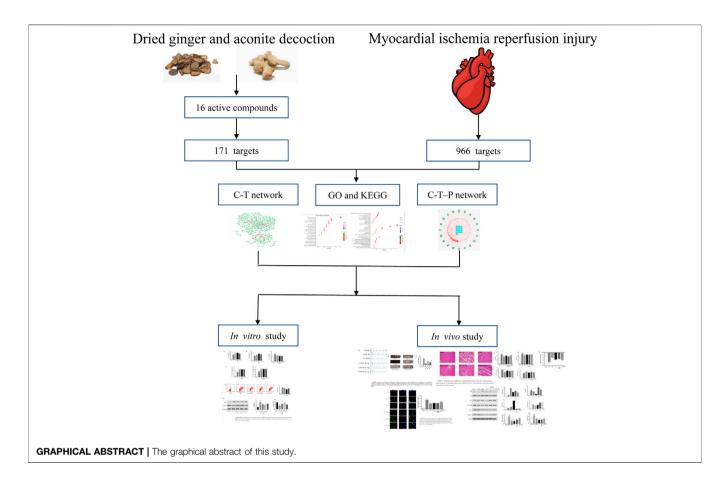
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INTRODUCTION

Myocardial ischemia-reperfusion injury (MI/RI) denotes the further destruction of the cardiac structure, and the further aggravation of metabolic dysfunction or even irreversible damage of the myocardial cell, following the restoration of blood supply of ischemic and anoxic myocardial tissue, which mainly involves re-expansion of myocardial infarction area and life-threatening arrhythmia (Lee et al., 2002; Raedschelders et al., 2012; Inoue, 2016). A common clinical cardiovascular disease, it has since developed into a killer ailment with high morbidity and mortality (Hausenloy and Yellon, 2013; Heusch, 2017). It typically occurs among the middle-aged and elderly population; however, as social competition becomes increasingly fierce, pressure on the youth has also increased, as they are



also prone to develop myocardial ischemic diseases (Ingram et al., 2013; Han et al., 2018). Some studies indicate that 18 million people die of cardiovascular diseases every year globally, of which MI/RI incidence accounts for around 50% (Wei, 2017). MI/RI pathogenesis involves the interaction of multiple mechanisms, including vasoconstrictor release, non-reperfusion, deep inflammatory response, apoptosis and necrosis (Chen et al., 2020; Li et al., 2020a; Samiotis et al., 2021). Albeit not quite effective, the current treatment methods for MI/RI are percutaneous coronary intervention and the use of related thrombolytic drugs; nevertheless, MI/RI still has a high mortality rate worldwide. Therefore, research and attention on the mechanism of MI/RI have a considerable significance for its prevention and treatment.

Traditional Chinese medicine (TCM) plays indispensable role in the prevention and treatment of MI/ RI. It spans a long history, including Yi Qi Huoxue decoction, Gualou Xiebai Baijiu decoction and Si Ni decoction (Deng et al., 2017; Zheng and Bao, 2017; Gao et al., 2019). It has been extensively used in MI/RI treatment, and dried ginger-aconite decoction (DAD), which comprises two kinds of Chinese herbal medicines, is one such medicine. Composed of aconite and dried ginger, DAD is recorded in the Treatize on Febrile and Miscellaneous Disease. Considering the efficacy of Yang for resuscitation, DAD is used to clinically treat ischemic heart diseases (Xu, 1986). Previous studies have indicated that DAD has a protective effect on the hearts of rats with MI/RI, and such effect is closely associated with its antioxidant and apoptosis effect (Shi et al., 2014). However, its bioactive compounds and their pharmacological mechanisms are still relatively unclear.

Network pharmacology integrates biological systems and multi-directional pharmacological approaches, incorporates biological networks and drug action networks, transcends the constraints of single-target beliefs, and begins from multi-target research strategies in order to achieve a comprehensive network analysis of drug effects (Xu et al., 2014; Chen et al., 2017; Zhang et al., 2018a). It is a significant approach to study the mechanisms of the multi-components, multi-targets and multi-pathways of TCM (Hopkins, 2008; Li and Zhang, 2013). The varied components of DAD are complex. Previous studies have determined that DAD can treat MI/RI by reducing the apoptosis of cardiomyocytes; however, the exact mechanism remains vague. Therefore, a comprehensive method is applied in this study to illustrate the molecular mechanisms of DAD. Network pharmacology is used to predict the active components and mechanisms of DAD in MI/RI treatment. HPLC is applied to determine whether DAD contains certain components for network pharmacological prediction. Afterward, in vivo and in vitro experiments are conducted to validate its mechanism on network pharmacological prediction. A graphical abstract of this study is presented in Graphical Abstract.

MATERIALS AND METHODS

Materials

Aconitum abietetorum W.T.Wang and L.Q.Li (No. 51078020190334YC) and Zingiber officinale Roscoe (No. 51078020191020YC) were obtained from Jiangyou City, Sichuan Province, China. The geographical location of Jiangyou is within 31°32′26″-32°19′18″ north and 104°31′35″-105°17′30″ east. Material authentication for TCM identification was carried out by Professor Gang Zhang of Shaanxi University of Chinese Medicine. The samples were deposited at the Herbal Medicine Museum of the same university.

Fetal bovine serum (FBS) was purchased from BI (United States). Phosphate buffer saline (PBS) and Dulbecco's modified Eagle medium (DMEM) were procured from Gibco (United States). Penicillinstreptomycin mixture and Cell Counting Kit-8 (CCK-8) from Shanghai Bivuntian Co., Ltd. (Shanghai, China). Dimethyl sulfoxide (DMSO) and trypsin were also procured from Gibco (United States). The assay kits for malondialdehyde (MDA), superoxide dismutase (SOD) apoptosis, atpase, creatine kinase (CK), mitochondrial permeability transition pore (MPTP), lactate dehydrogenase (LDH) and glutathione peroxidase (GSH-PS) were all obtained from Boster Biological Technology Co., Ltd. (Wuhan, China). Cyt-C, β-action, GADPH, Casp9, PI3K, AKT, Bax, Bcl-2 and phosphorylated(P)-AKT, GSK3β were also purchased from Boster Biological Technology Co., Ltd. (Wuhan, China). 6gingerol (202,003), aconitine (No. A0608), mesaconitine (A0196) and hypaconitine (A0609) were all purchased from Chengdu Munst Biotechnology Co., Ltd. Standard purity was set as more than 98%. Methanol and triethylamine were purchased from Shaanxi Weitong Chemical Co., Ltd.

Dried ginger-aconite decoction Preparation

Aconite and dried ginger were mixed at a 1:1 ratio. They were soaked in water for 0.5 h, then were boiled twice for 1 h each time. The filtrates were collected via gauzes, combined and concentrated to 1 g/ml to obtain the extract. For this study, 100 g of aconite and 100 g of dried ginger were prepared. Both components were completely immersed in water for 0.5 h. Then, 1.6 L water was added, letting the mixture boil for 1 h twice. The extract was then collected, filtered with gauze, and concentrated to 200 ml. The supernatant was obtained after centrifugation of the solution at 3,000 r/min, sterilized with 0.22 μ m aqueous microporous membrane, and sealed.

Network Pharmacology

Screening of Dried ginger-aconite decoction Active Components and Collection of Targets

The chemical constituents of aconite and dried ginger were examined from the Traditional Chinese Medicine Integrated Database (TCMSP, https://tcmspw.com/tcmsp.php) and the Comparative Toxicogenomic Database (CTD, http://ctdbase.org/), with aconite and dried ginger as the keywords. Active components of DAD were screened via oral bioavailability (OB)

and drug-like quality (DL) (Cao et al., 2018), with DL \geq 0.18 and OB \geq 30% as the thresholds.

The primary compounds of aconite and dried ginger are alkaloids and volatile oil, both of which are irreplaceable and have good pharmacological activity. Thus, the following nine compounds were supplemented: deoxyaconitine, aconitine, hypaconitine, mesaconitin, 6-gingerol, 8-gingerol, 10-gingerol, 6-shogaol, and zingerone. The targets of all active compounds were obtained and imported into the Universal Protein (UniProt) database (https://www.uniprot.org/) to standardize their names.

Predicting Targets of DAD Against MI/RI

With "myocardial ischemia-reperfusion injury" as the keywords, MI/RI targets in the disgenet database (https://www.disgenet.org/) limited to "Homo sapiens" were obtained. The interactions of the DAD and MI/RI targets were considered as the potential therapeutic targets. The protein-protein interaction (PPI) of the common targets was accomplished in the string database (https://string-db.org/); the parameter organism was set to Homo sapiens, while the other basic settings were set as default. Using the Cytoscape 3.7.0 software, compound-target (C-T) and PPI were constructed.

Pathway and Functional Enrichment Analysis

The database for Annotation, Visualization and Integrated Discovery (DAVID) v6.8 (www.david.ncifcrf.gov/) provides a comprehensive set of functional annotation tools for researchers to understand the biological meanings behind extensive lists of genes. It was employed to undertake pathway enrichment analyses using the Gene Ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes (KEGG) databases. Pathway terms with p < 0.05 were deemed significant. Using the Cytoscape 3.7.0 software, compound-target-pathway (C-T-P) was constructed.

In vitro Experiment HPLC Method for Component Analysis

DAD was filtered through a 0.22 μ m nylon membrane prior to HPLC analysis. An HPLC System (Thermo, United States) was used to separate the components of DAD. All components were separated by Waters Bridge C18 (4.6 mm \times 150 mm, 5 μ m) and a C18 guard. Flowrate was set at 1.0 mL, min⁻¹. The column temperature was 30°C. The wavelength was set at 237 nm. The mobile phases were (A) methanol and (B) triethylamine aqueous solution, with gradient elution of 0–15 min (A: B = 30:70), 15–40 min (A:B = 65:35) and baseline (A:B = 30:70).

Grouping and Modeling

Rat myocardial cells (H9C2) were purchased from Wuhan Punosai Life Science and Technology Co., Ltd. (Wuhan, China). The cells were cultured in DMEM with 10% FBS, 100 U/ml penicillin and 100 μ l/ml streptomycin. They were maintained inside a humidified incubator with 95% air and 5% CO₂ at 37°C. They were subjected to experimental procedures when they reached an 80% confluence level of population. They were classified into five groups: control group, Hypoxia/reoxygenation(H/R) group, DAD low-dose group

(0.125 mg/ml), DAD medium-dose group (0.25 mg/ml), and DAD high-dose group (0.5 mg/ml). For all experiments, the cells were rendered quiescent by serum starvation for 24 h before treatment. Following pretreatment with DAD at varied doses for 24 h, the cells for all groups-except for the control group and the H/R group-were incubated in DMEM and glucose-free DMEM, respectively and then placed inside a hypoxia chamber (Stem Cell Technologies, San Diego, CA, United States). The chamber was flushed with 95% (v/v) N₂ and 5% (v/v) CO₂ at a flowrate of 15 L/min for 10 min, and maintained at 37°C to induce hypoxia injury. After hypoxia for 12 h, reoxygenation was conducted by replacing the medium to DMEM that contained 4.5 mM glucose (pH 7.4) and by subsequent incubation in a CO₂ incubator (5% (v/v) CO₂, 95% (v/v) air) for 2 h (Wang et al., 2018).

Survival Rate of H9C2 Cells

CCK8 assay was applied to determine the influence of DAD on the survival rate of H9C2 cells that were damaged by oxygen. The cells were briefly seeded onto 96-well plates and then cultured until they adhered. Afterward, the cells were treated with DAD at varied concentrations (0.125 mg/ml, 0.25 mg/ml, 0.5 mg/ml). Model group and control group were given DMEM (without glucose) and DMEM, respectively. Model according to the above method. Afterward, 10 μ l of CCK-8 was added, and the mixture was incubated for another 2 h. Absorbance was recorded at 450 nm, and the experiments were performed in parallel in triplicate.

Detection of Apoptosis Rate

The H/R damaged cells in each group were digested with 0.25% trypsin and centrifuged at 1,500 r/min for 5 min. The supernatant was discarded and the cells were collected. The collected cells were then resuspended with PBS (pH 7.2), washed with PBS twice, and centrifuged at 1,500 r/min for 5 min, before the supernatant was discarded. The precipitated cells were resuspended with 500 μ l of binding buffer, then 5 μ l of annexin V-FITC and 5 μ l of PI staining solution was added. After mixing, the cells were incubated at room temperature in the dark for 5–15 min. Finally, the apoptosis for each group was detected by flow cytometry (NovoCyte 452180529501, Thermo, United States).

Biochemical Testing

After H/R injury, the cells in each group were obtained. According to the manufacturer's protocols, the SOD, MDA, Na⁺-K⁺-ATP and Ca²⁺-Mg²⁺-ATP levels were detected by their respective commercial kits.

In vivo Experiment

Establishment and Grouping of MI/RI in Rat Models

Sixty Sprague-Dawley male rats were purchased from Chengdu Da Shuo Experimental Co., Ltd. (Sichuan, China). They were housed in a specific-pathogen-free (SPF) environment. The rats in DAD low-dose, DAD medium-dose and DAD high-dose groups were orally administered with 1.4 g/kg, 2.8 g/kg and 5.6 g/kg DAD once daily, respectively. Those in the positive control group were orally administered with 0.09 g/kg per day

of compound danshen dripping pills (CDDP), and those in the model, and sham group were orally administered with the same volume of 0.9% NaCl. A week later, all rats were operated, with the sham group only opening the chest without ligation. Left thoracotomy and pericardiectomy, followed by left anterior descending coronary artery ligation, were performed. After 40 min of ischemia, the ligature was opened for reperfusion for 2 h. The serum and heart tissue samples were prepared for future experiment. All animal experiments were performed in accordance with the Animal Care and Use Committee of the Institute of Materia Medica, China (No. TCM-2019–194,040-E08).

Detection of Myocardial Infarction Area in MI/RI Rats

Prior to the experiment, 2% TTC was placed in a 37°C thermostat for 0.5 h. Four rats were randomly selected from each group. Their hearts were removed, flushed with PBS, and rapidly frozen at -20°C. The specimens were uniformly cut into 1 mm slices under the line of ligature and placed in a 37°C, 2% TTC solution to dye for 20°min, and then fixed with 10% formaldehyde solution. Ultimately, the myocardial infarction area was white and the non-infarction area was red. The infarct area was calculated using ImageJ software (Media Cybernetics, Inc., Rockville, MD, United States). The applied equation was as follows,

$$Infarction \ Range = \frac{Infarction \ Range}{Left \ Ventricular \ Area} \times 100\%.$$

Immunohistochemical Staining

Immediately after reperfusion, the heart was removed and rinsed in precooled saline. The myocardium from the anterior wall of the left ventricle was removed. The heart was then fixed with precooled 4% paraformaldehyde and rinsed with water for 12 h. The specimens were dehydrated afterward. They were then immersed in xylene, and hematoxylin-eosin (H-E) staining was conducted after routine paraffin-embedded staining. Then, the slices were sealed with conventional resin, and the pathological changes in the myocardium were observed under an optical microscope (Olympus BX 41, Japan).

Myocardial Tissue Apoptosis Detection

After MI/RI modeling, the heart tissue was removed. The tissue sections were washed in a phosphate buffer solution, and fixed in a 4% paraformaldehyde solution. They were then cut into paraffin sections with a thickness of 4 μm , and proteinase K was added. After a strict color rendering according to the kit instructions, five visual fields were randomly selected for shooting, and the color images of ten independent fields were randomly captured and digitized. The cells with clear nuclear markers were defined as TUNEL positive. Image J software was used for recording, and the apoptosis rate was calculated. The applied equation was as follows:

Apoptosis index =
$$\frac{\text{Number of TUNEL positive cells}}{\text{Total number of cardiomyocytes}} \times 100\%$$
.

Biochemical Testing

After reperfusion, the rats were intraperitoneally anesthetized using chloral hydrate (30 mg/kg), and the blood samples were

TABLE 1 | Information on the 16 active compounds in the DAD.

Herbal name	TCMSP ID	Compound	ОВ	DL
Aconite	MOL002395	Deoxyandrographolide	56.3	0.31
Aconite	MOL002398	Karanjin	69.56	0.34
Aconite	MOL002424	aconitine	7.87	0.23
Aconite	MOL000538	hypaconitine	31.39	0.26
Aconite	MOL002089	mesaconitin	8.7	0.25
Aconite	MOL002388	Delphin_qt	57.76	0.28
Aconite	MOL002392	Deltoin	46.69	0.37
Dried ginger	MOL002467	6-gingerol	35.64	0.16
Dried ginger	MOL002459	10-gingerol	19.14	0.28
Dried ginger	MOL002495	6-shogaol	31	0.14
Dried ginger	MOL002516	zingerone	25.23	0.05
Dried ginger	MOL000359	sitosterol	36.91	0.75
Dried ginger	MOL002464	1-Monolinolein	37.18	0.3
Dried ginger	MOL002501	[(1S)-3-[(E)-but-2-enyl]-2-methyl-4-oxo-1-cyclopent-2-enyl] (1R,3R)-3-[(E)-3-	62.86	0.3
		methoxy-2-methyl-3-oxoprop-1-enyl]-2,2-dimethylcyclopropane-1-carboxylate		
Dried ginger	MOL002514	Sexangularetin	35.64	0.16
Dried ginger	MOL000358	beta-sitosterol	36.91	0.75

obtained from the abdominal aorta. The samples were left standing at room temperature for 30 min and then centrifuged at 3,000 r/min for 15 min. The serum was collected and stored at -80°C until used. Based on the manufacturer's protocols, the GSH-Sp, MDA, CK and LDH levels were detected by the respective commercial kits.

Detection of MPTP Open Holes in Myocardial Tissues

The fresh myocardial tissue just removed was rinsed with PBS; the excess water on the surface of the myocardial tissue was absorbed using a filter paper. The proper part of the entire heart tissue was taken; its mass was accurately measured, and the tissue homogenate was prepared using a mass-to-volume ratio of 1:9. The entire operation needed to be conducted in an ice bath. Finally, the tissue homogenate was centrifuged for 3,500 r/min for 10 min. The supernatant was collected and stored at -80° C for later use. The openness of the MPTP holes in the homogenate was determined according to the kit instructions.

Western Blot Analysis (in vivo and in vitro)

The myocardial tissue and the H9C2 cells were lyzed by RIPA buffer (Shanghai Weiao Biological Technology Co., Ltd., China) containing cocktail protease inhibitors (1:100) and a protein phosphatase inhibitor (1:50) for 30 min on ice. The protein concentration in the supernatants was determined by BCA assay (Shanghai Weiao Biological Technology Co., Ltd., China). Protein samples were loaded with 10% SDS-polyacrylamide gel (Shanghai Weiao Biological Technology Co., Ltd. China), and then electrophoretically transferred onto PVDF (Millipore, Billerica, MA, United States). The membranes were blotted with 5% fatfree milk in a TBST buffer for 2 h at room temperature and then incubated at 4°C overnight with the following primary antibodies: anti-Caspase-9 (1:600), anti-Bax (1:500), anti-Bcl-2 (1:500), anti-Cyt-c (1:500), anti-PI3K (1:500), anti-Akt (1:1,000), anti-p-Akt (1: 1,000), anti-p-GSK-3β (1:1,000), and anti-GAPDH (1:1,000). The membrane was rinsed thrice on the second day and then incubated with HRP-conjugated secondary antibodies for 1 h at room temperature. The blots were imaged under an enhanced chemiluminescence (ECL) system. The target band molecular weights and the net optical density were analyzed using the AlphaEase FC software (Alpha Innotech, United States).

Statistical Analysis

All data were expressed as mean \pm standard deviation (SD). GraphPad Prism 7 software was employed to ascertain statistically significant differences. The differences among multiple groups were assessed using one-way analysis of variance (ANOVA). The difference between the means was considered statistically significant when p < 0.05.

RESULTS

Network Pharmacology

DAD Active Compounds and Target Screening

From aconite and dried ginger, 16 compounds (**Table 1**) were retrieved from the TCMSP database, and 171 targets were retrieved from the TCMSP and CTD databases (**Figure 1A**). A total of 966 targets of MI/RI were obtained from the DisGeNet databases. A total of 80 targets (**Table 2**) were obtained through the intersection of the 966 MI/RI targets and the 171 putative targets of aconite and dried ginger. These 80 mutual targets were identified as potential therapeutic targets for DAD against MI/RI (**Figure 1B**). The C-T network included 187 nodes (16 for potential bioactive components and 171 for protein targets). Among the bioactive components, aconitine (DAD, degree = 48), 6-ginger (DAD, degree = 31) and mesaconitine (DAD, degree = 25), hypaconitine (DAD, degree = 24) exhibited the greatest correlation with MI/RI. These could be the key components of DAD against MI/RI.

PPI Network Analysis

To examine the potential interactions of the 80 targets, String 11.0 database was used to build a PPI network. The minimum

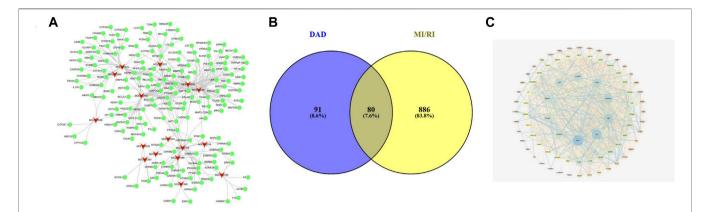


FIGURE 1 | The networks of dried ginger and aconite decoction anti-Ml/Rl. (A) The compound-target network of DAD. The red nodes represent active compounds and the green nodes represent targets. The target surrounding the active components are proportional to their degree. (B) Overlap of DAD and Ml/Rl targets. The blue circles represent DAD targets and the yellow circles represent Ml/Rl targets. The shaded area is the target of DAD anti-Ml/Rl. (C) The protein-protein interaction network of protein targets obtained from STRING database and constructed by Cytoscape. The colors of the nodes are illustrated from blue to yellow to orange in descending order of degree values.

TABLE 2 | Targes information of DAD anti-MI/RI.

Target name	Full name of the target	Uniprot ID
MAPK3	Mitogen-activated protein kinase 3	P27361
CYP2C9	Cytochrome P450 2C9	P11712
CYP2C8	Cytochrome P450 2C8	P10632
CYP3A4	Cytochrome P450 3A4	P08684
ARNTL	Aryl hydrocarbon receptor nuclear translocator-like protein 1	O00327
CD36	Platelet glycoprotein 4	P16671
GATA4	Transcription factor GATA-4	P43694
ITGA2B	Integrin alpha-IIb	P08514
ITGB3	Integrin beta-3	P05106
MTOR	Serine/threonine-protein kinase mtor	P42345
OLR1	Ox-LDL receptor 1	P78380
S100B	Protein S100-B	P04271
TNF	Tumor necrosis factor	P01375
BAX	Apoptosis regulator BAX	Q07812
BCL2	Apoptosis regulator Bcl-2	P10415
BDNF	BDNF	P23560
CASP3	Caspase-3	P42574
MAPK1	Mitogen-activated protein kinase 1	P28482
CHAT	SH2 domain-containing protein 3C	Q8N5H7
CHRNA5	Neuronal acetylcholine receptor subunit alpha-5	P30532
IL1B	Interleukin-1 beta	P01584
IL6	Interleukin-6	P05231
NFKB1	Nuclear factor NF-kappa-B p105 subunit	P19838
TP53	Cellular tumor antigen p53	P04637
TRPA1	Transient receptor potential cation channel subfamily a member 1	075762
ABCB1	ATP-dependent translocase ABCB1	P08183
CYP1A2	Cytochrome P450 1A2, EC 1.14.14.1	P05177
GSK3B	Glycogen synthase kinase-3 beta, GSK-3 beta	P49841
CCND1	G1/S-specific cyclin-D1	P24385
PPARG	PPAR-gamma	P37231
PTGS2	Prostaglandin G/H synthase 2	P35354
BIRC5	Baculoviral IAP repeat-containing protein 5	O15392
GDF15	Growth/differentiation factor 15	Q99988
CASP8	Caspase-8	Q14790
NOS2	Nitric oxide synthase, inducible	P35228
CAT	Catalase	P04040
MMP2	72 kDa type IV collagenases	P08253
ADIPOQ	Adiponectin	Q15848
MMP9	Matrix metalloproteinase-9	P14780
MPO	Myeloperoxidase	P05164
PARP1	Poly [ADP-ribose] polymerase 1	P09874
		(Continued on following page)

TABLE 2 | (Continued) Targes information of DAD anti-MI/RI.

Target name	Full name of the target	Uniprot ID	
SOD1	Superoxide dismutase [Cu-Zn]	P00441	
SOD2	Superoxide dismutase [Mn], mitochondrial	P04179	
AKT1	RAC-alpha serine/threonine-protein kinase	P31749	
BECN1	Beclin-1	Q14457	
FAS	Tumor necrosis factor receptor superfamily member 6	P25445	
FN1	Fibronectin	P02751	
GHRL	Appetite-regulating hormone	Q9UBU3	
HIF1A	Hypoxia-inducible factor 1-alpha	Q16665	
NFKBIA	NF-kappa-B inhibitor alpha	P25963	
PRKCE	Protein kinase C epsilon type	Q02156	
RPS6KB1	Ribosomal protein S6 kinase beta-1	P23443	
NFE2L2	Nuclear factor erythroid 2-related factor2	Q16236	
HMOX1	Heme oxygenase 1	P09601	
DDIT3	DNA damage-inducible transcript 3 protein	P35638	
GCLC	Glutamatecysteine ligase catalytic subunit	P48506	
FABP4	Fatty acid-binding protein	P15090	
GCLM	Glutamatecysteine ligase regulatory subunit	P48507	
BCL2L1	Bcl-2-like protein 1	Q07817	
HMGCR	3-hydroxy-3-methylglutaryl-coenzyme a reductase	P00347	
IFNG	Interferon gamma	P01579	
LCAT	Phosphatidylcholine-sterol acyltransferase	P04180	
LPL	Lipoprotein lipas	P06858	
TGFB1	Transforming growth factor beta-1 proprotein	P01137	
TLR4	Toll-like receptor 4	O00206	
PTGS1	Prostaglandin G/H synthase 1	P23219	
PIK3CG	Pl3K-gamma	P48736	
F2	Prothrombin	P00734	
SCN5A	Sodium channel protein type 5 subunit alpha	Q14524	
F10	Coagulation factor X	P00742	
ACHE	Acetylcholinesterase, AChE, EC 3.1.1.7	P22303	
ADRB2	Beta-2 adrenergic receptor	P07550	
DPP4	Dipeptidyl peptidase 4	P27487	
ESR1	Estrogen receptor	P03372	
NR3C2	Mineralocorticoid receptor	P08235	
CHRM3	Muscarinic acetylcholine receptor M3	P20309	
PDE3A	cGMP-inhibited 3',5'-cyclic phosphodiesterase A	Q14432	
HTR2A	5-hydroxytryptamine receptor 2A	P28223	
SLC6A4	Sodium-dependent serotonin transporter	P31645	
PON1	Serum paraoxonase/arylesterase 1	P27169	

combined score between the targets was set as the medium confidence (0.400). The PPI network of the potential target was saved as a TSV file and then entered into Cytoscape 3.7.0 for visualization (**Figure 1C**). In the PPI network, targets with high degrees played a significant role in central correlation. The top 5 targets, which were ranked in terms of degree value, were acquired as the core targets. These targets were AKT1 (degree = 47), IL6 (degree = 41), TNF (degree = 38), MAPK3 (degree = 36) and TP53 (degree = 30).

GO Enrichment Analysis

The biological function of DAD against MI/RI was identified by GO enrichment of the 80 potential therapeutic targets. A total of 158 GO items were obtained from the GO enrichment analysis of 80 potential therapeutic targets, including 118 biological processes (BP), 22 cell components (CC) and 18 molecular functions (MF) (p < 0.05). To realize a brief

demonstration, only the top 10 significant GO entries were selected for further analysis. The top ten analyses for BP, CC and MF were selected respectively (Figure 2A), which indicated that DAD might regulate cell apoptosis, inflammation and mitochondrial energy metabolism to exert its therapeutic effects against MI/RI.

Pathway Enrichment

To examine the potential pathways of DAD on MI/RI, a pathway enrichment of the 80 potential therapeutic targets was conducted. The top 20 significantly enriched pathways are presented in **Figure 2B**. Among the potential pathways, PI3K/AKT signaling was the most prominently enriched based on the gene numbers. To further clarify and elucidate the molecular mechanism of DAD treatment on MI/RI, a C-T-P network diagram was drawn based on the top 20 signaling pathways, as well as the targets and compounds involved (**Figure 2C**). After integrating drug target

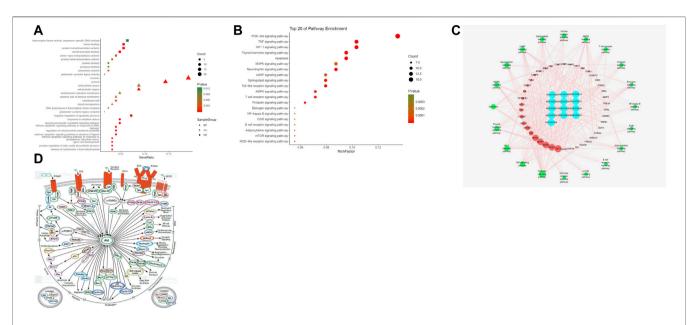


FIGURE 2 | (A) The gene ontology (GO) enrichment analysis for key targets. (B) The KEGG pathway enrichment analysis of key targets. (C) The compound-target-pathway network constructed by Cytoscape. The blue nodes represent active components in DAD, the red nodes represent putative targets, the green nodes represent the signaling pathways. Node's size is proportional to their degree. (D) PI3K/ Akt signaling pathway network (PI3K/Akt signaling pathway network is derived from https://www.cellsignal.cn/pathways-pathways-akt-signaling)

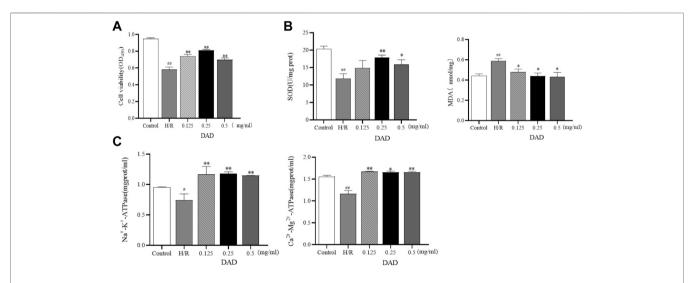


FIGURE 3 | Effects of dried ginger-aconite decoction (DAD) on survival rate and biochemical parameters of H9C2 cells damaged by H/R. **(A)** Effect on the survival rate of H9C2 cells. **(B)** Effect on oxidative stress factors MDA, SOD. **(C)** The effect on the activity of ATPase. Data were presented as mean standard deviation (SD). #p < 0.05, ##p < 0.01 vs. control group. *p < 0.05, **p < 0.01 vs. H/R group.

predictions, pathway and function enrichments, and network analyses, AKT1, PIK3G, MAPK3, MAPK1, NFKB, TNF, NFKBA, MTOR, GSK3β and TP53 were identified. These targets were highly associated with apoptosis and inflammation. Likewise, they were considered as the key targets of DAD against MI/RI. Interestingly, of the aforementioned targets, only GSK3β was downstream of the PI3K/AKT signaling pathway (**Figure 2D**). Thus, it was speculated that the anti-MI/RI effect of DAD might be

associated with its regulation of apoptosis and mitochondrial energy metabolism by targeting PI3K/AKT/GSK3 β signaling pathways with their relevant activators.

In vitro Experiments HPLC Analysis

Network pharmacology predicted that aconitine, 6-ginger, mesaconitine and hypaconitine in DAD were the potential active components of anti-MI/RI in DAD. The phytochemical composition

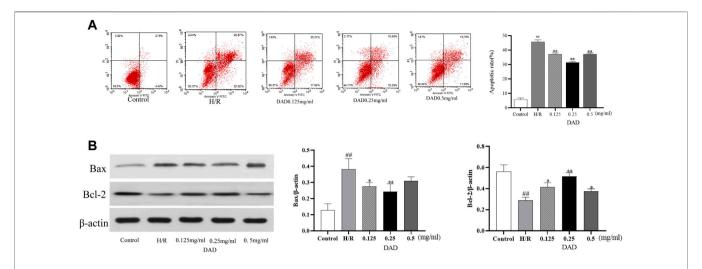


FIGURE 4 Effects of dried ginger-aconite decoction (DAD) on apoptosis rate and Bax/Bcl-2 expression of H9C2 cells after H/R injury. **(A)** The effect on apoptosis rate. **(B)** The effect on the expression of Bax/Bcl-2. Data were presented as mean standard deviation (SD) of three independent experiments. #p < 0.05, ##p < 0.01 vs. control group. *p < 0.05, **p < 0.01 vs. H/R group.

of DAD was assessed using HPLC. As shown in **Supplementary Figure S1**, DAD contained aconitine, 6-ginger, mesaconitine.

H9C2 Cells' Survival Test Results

The effects of DAD were initially assessed based on the cell viability of the H9C2 cells damaged by H/R. It was found that the exposure of H9C2 cells to H/R injury had led to a decrease in cells (p < 0.01). Compared to the control group, the survival rate of the H/R group was only 58%. When the H9C2 cells were pretreated with 0.125–0.5 mg/ml DAD, cell viability was significantly restored (p < 0.01). DAD (0.25 mg/ml) had the greatest effect on cell survival rate, which increased by 25% (p < 0.01), compared to the H/R group (**Figure 3A**). These data suggest that DAD pretreatment may provide protection against H/R-induced cardiomyocyte injury.

Results of Biochemical Testing

The outcome of cardiomyocyte hypoxia was insufficient oxygen as required by the mitochondria, which would lead to mitochondrial damage, reduced ATP production and aggravated oxidative damage of the cardiomyocytes. SOD is an oxygen free radical scavenger in human body (Khatua et al., 2012; Ling et al., 2019). The final product of oxidative damage is MDA, which can damage the mitochondria. The change in MDA can reflect the degree of oxidative damage of the cells (Mao et al., 2008; Radmanesh et al., 2017). The enzymatic activities of Na+-K+-ATP and Ca2+-Mg2+-ATP-indirectly reflect Changes in the amount of ATP (Zhu et al., 2019). After pretreatment with varied DAD doses, the MDA levels of H9C2 cells damaged by H/R could be reduced to varied degrees, as well as increased the activities of SOD, Na⁺-K⁺-ATP and Ca²⁺-Mg²⁺-ATP. In the administration group (Figure 3B-C), DAD (0.25 mg/mg) manifested the best therapeutic effect (p < 0.05). These results imply that the protective effect of DAD on H/R-damaged H9C2 is related to the mitochondria.

Effect of DAD on the Apoptosis Rate of H9C2 Cells With H/R Injury

As discussed, ischemia and hypoxia aggravate the oxidative damage of cardiomyocytes and eventually induce the apoptosis of cardiomyocytes. H/R injury significantly increased the apoptosis rate of the H9C2 cells, which increased by 35% compared to the control group (p < 0.01). after DAD preconditioning. The apoptosis rate of the H9C2 cells damaged by H/R significantly decreased, while the apoptosis rate of the DAD group (0.25 mg/kg) decreased by 18% (p < 0.01) compared to the H/R group (**Figure 4A**).

Western Blot Analysis

Network pharmacological analysis implied that the molecular mechanism of the anti-MI/RI effect of DAD might be associated with apoptosis. The mammalian BCL-2 family member Bcl-2 was an anti-apoptotic protein, while Bax protein induced apoptosis by enhancing cytochrome c (Cyt-C) release from the mitochondria (Aamazadeh et al., 2020; Lin et al., 2020). Therefore, the two targets of Bax and Bcl2 (Bax and Bcl2 belonged to the targets of DAD in anti-MI/RI) were validated in vitro. Compared to the control group, the expression of Bax had significantly increased and the expression of Bcl-2 had significantly decreased after the H9C2 cells were damaged by H/R (p < 0.01). Compared to the H/R group, the expression of Bax in the H9C2 cells damaged by H/R had significantly decreased, while the expression of BCL2 had significantly increased when the H9C2 cells were pretreated by DAD (p < 0.01). In the administration group (Figure 4B), DAD (0.25 mg/mg) manifested the best therapeutic effect. In vitro studies were found consistent with network pharmacology, with DAD being shown to resist MI/RI by reducing myocardial cell apoptosis. In vitro studies were found consistent with network pharmacology, with DAD being shown to resist MI/RI by reducing myocardial cell apoptosis.

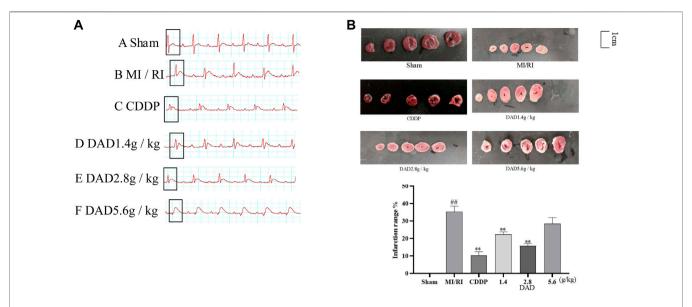


FIGURE 5 | Changes of electrocardiogram in MI/RI rats and effects dried ginger-aconite decoction (DAD) on myocardial infarction area in MI/RI rats. **(A)** After modeling, ECG changes in Sham group, MI/RI group, CDDP group and DAD (1.4 g/kg, 2.8 g/kg, 5.6 g/kg) groups. **(B)** Effects on infarction range reduction of I/R injured rats. Data were presented as mean standard deviation (SD). $^{\#}p < 0.05$, $^{\#}p < 0.01$ vs. sham group. $^{*}p < 0.05$, $^{**}p < 0.01$ vs. MI/RI group.

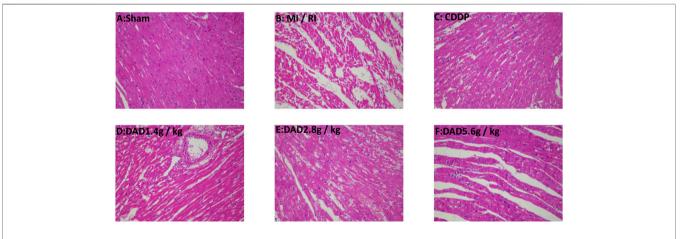


FIGURE 6 | Representative myocardial tissue histopathological sections on the effects of dried ginger-aconite decoction on myocardial infarction size in MI/RI rats (200x). Myocardial tissue injury was assessed by hematoxylin-eosin (H&E) staining.

In vivo Experiments

Results of ECG and Myocardial Infarction Area in MI/RI Rats

The electrocardiogram test results (**Figure 5A**) of rats presented that the ST segment was elevated after reperfusion for each group compared to the sham operation group, indicating that the model had been successfully established. Compared to the sham group, the MI/RI group had significantly increased the infarct size (45%) of the myocardial tissue (**Figure 5B**), (p < 0.01). Compared to the MI/RI group, the infarct size of the myocardial tissue for each administration group had significantly reduced. The lowest infarct size was 9.2% in the CDDP (positive) group. Among the three DAD groups (p < 0.01), the MI area of rats in the DAD (2.8 g/kg) medium dose group was the lowest (19.3%) (p < 0.01).

Meanwhile, although the high dose of DAD (5.6 g/kg) did not manifest a significant reduction in infarct size, a protective trend of infarct size reduction could be perceived.

Histopathological Examinations

The degree of myocardial injury could be determined by histopathological examinations (Zhou et al., 2020). In the sham group, the myocardial tissue was intact, with a clear texture and regular arrangement of the myocardial fibers, and without apparent cell swelling and fracture; the nuclei material was evenly distributed, without apparent pathological changes. In contrast, in the MI/RI group, the texture of the myocardial tissue was blurred, the shape of the myocardial fiber was disordered, the myocardial tissue was faulted, the interstitium was severely

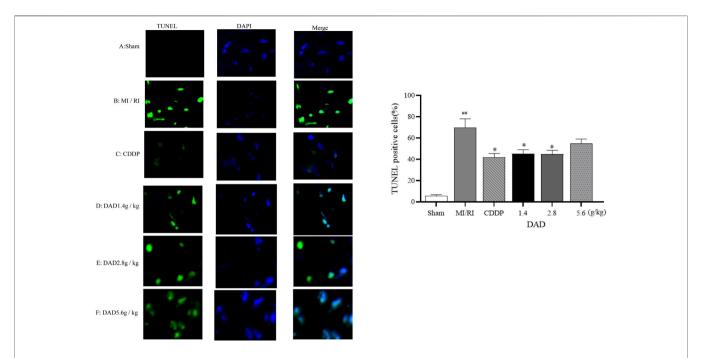


FIGURE 7 | Effects of dried ginger-aconite decoction (DAD) on apoptosis of myocardial cells in MI/RI rats. Apoptosis of cardiomyocytes (green) and DAPI (nuclei Blue). Representative images were shown, and the scale bar indicated 20 μ m. The percent of apoptosis cells were calculated for statistical analysis. Data were presented as mean standard deviation (SD). $^{\#}p < 0.05$, $^{\#}p < 0.01$ vs. sham group. $^{*}p < 0.05$, $^{**}p < 0.01$ vs. MI/RI group.

swollen, the nuclear morphology was changed, and some of the nuclei had disappeared. DAD treatment (1.4, 2.8 and 1.4 g/kg groups) partially attenuated the myocardial tissue histopathological damages, with the greatest improvement realized in the 2.8 g/kg group (**Figure 6**).

Effect of DAD on Myocardial Cell Apoptosis in MI/RI Rats

TUNEL assay was applied to evaluate the effects of DAD on the apoptosis of myocardial tissue cells in MI/RI rats. Compared to that of the sham operation group, the apoptosis rate (70%) of the MI/RI group had significantly increased (p < 0.01). DAD (1.4, 2.8 and 5.6 g/kg) treatment had significantly mitigated the increased percentage of apoptotic cells compared to the model group (p < 0.01). Among the three DAD groups, the 2.8 g/kg group exhibited the lowest apoptosis rate (45%). Meanwhile, although a high dose of DAD (5.6 g/kg) did not significantly reduce the apoptosis rate, a decreasing trend in such rate was observed (**Figure 7**).

Results of Biochemical Testing

Myocardial enzymes are vital indicators in the clinical detection of heart health (Radhiga et al., 2012; Xiang-Qian et al., 2019). The activity of the LDH and CK enzyme sharply increased after myocardial injury. The expressions of LDH and CK significantly increased in the MI/RI group (p < 0.01), suggesting that serious heart damage might occur. After treatment, the activities of CK and LDH decreased in each dose group of DADs (1.4, 2.8 and 5.6 g/kg), while the activities

of the 2.8 g/kg group had significantly decreased (p < 0.01) (**Figure 8A**). Oxidative stress injury is a key mechanism of I/R injury. Under ischemia and hypoxia conditions, the mitochondria of cardiomyocytes are damaged, the permeability of the mitochondria membrane is transformed (**Figure 8B**), and reactive oxygen species are released into the cytoplasm through the damaged mitochondria. SOD and GSH-Px are known as free-radical scavengers *in vivo*. Remarkably, after MI/RI, mitochondrial swelling degree and MDA had increased alongside a decreased GSH-Px activity. After treatment with varied DAD (1.4, 2.8 and 5.6 g/kg), the degree of mitochondrial swelling and the degree of elevated MDA level among MI/RI rats were reduced, while the activity of GSH-Px, SOD were restored (**Figure 8C**). Among the three DAD groups, DAD (2.8 g/kg) manifested the best therapeutic effect (p < 0.05).

Promotion of PI3K/AKT/GSK-3β by DAD

As a unique molecular target in the mitochondria, Cyt-C can activate apoptosis factors such as CASP9 and can lead to the apoptosis of damaged myocardium (Gao et al., 2016). Considering that the anti-MI/RI mechanism of DAD has been shown to be associated with apoptosis *in vitro*, the network pharmacologically predicted pathway and the related mitochondrial targets *in vivo* were further validated, namely the PI3K/AKT/GSK-3 β pathway and the mitochondrial targets–Cyt-C and CASP9. Western blot analysis presented that the expression of PI3K/AKT/GSK-3 β was inhibited (p < 0.05), and that the expression of Cyt-C and CASP9 was significantly increased in the MI/RI group compared to the

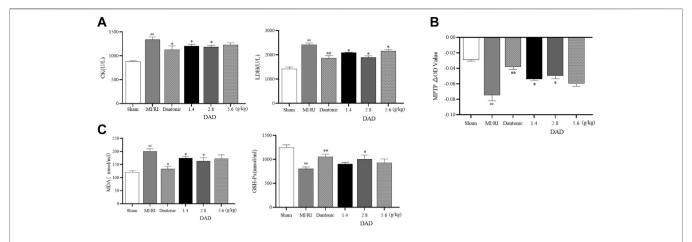


FIGURE 8 | Effects of dried ginger-aconite decoction (DAD) on biochemical indices and MPTP conversion pores in MI/RI rats. **(A)** Effects on activities of myocardial enzymes CK, and LDH. **(B)** Effects on mitochondrial transformation pore MPTP. **(C)** Effect on oxidative stress factors MDA, and GSH-Px. Data were presented as mean standard deviation (SD). #p < 0.05, ##p < 0.01 vs. sham group. *p < 0.05, **p < 0.01 vs. MI/RI group.

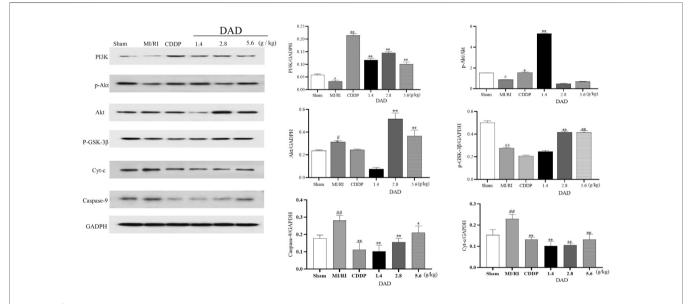


FIGURE 9 | Experimental validation of key signaling pathways and mitochondrial key targets in vivo. Dried ginger-aconite decoction(DAD) activates the Pl3k/Akt/ GSK-3 β signaling pathway and inhibits the expression of Cyt-C and CASP9. Data were presented as mean standard deviation (SD) of three independent experiments. $^{\#}p < 0.05$, $^{\#}p < 0.01$ vs. sham group. $^{*}p < 0.05$, $^{*}p < 0.01$ vs. MI/RI group.

sham group (p < 0.05). After DAD intervention, the expression of PI3K/AKT/GSK-3 β was significantly activated, and the expressions of Cyt-C and CASP9 were significantly decreased in the DAD groups compared to the MI/RI group (**Figure 9**). Among the three DAD groups, DAD (2.8 g/kg) manifested the best therapeutic effect (p < 0.05).

DISCUSSION

MI/RI is not only a primary cause of death among patients with cardiovascular and cerebrovascular diseases, but can also seriously affect the prognosis of patients with ischemic heart diseases. While the effects of DAD against MI/RI have been

demonstrated, its exact mechanism is vague. In this case, pharmacological approaches are adopted to explore relevant molecular pharmacological mechanisms and validate them empirically.

Sixteen active components and 171 targets of DAD were obtained using OB and DL parameters as significant evaluation indices and supplements of significant components. A higher degree of the compound in the C-T network denotes a greater significance. This study found that the degree values of aconitine, 6-ginger, hypaconitine and mesaconitine were among the top. These could be the key components of DAD against MI/RI. The HPLC method was used to determine the above components in DAD that were predicted by network pharmacology. We found that DAD contained aconitine, 6-

ginger, mesaconitine, which was consistent with the results of network pharmacology.

Through network pharmacology, it was found that BP that was highly correlated with DAD anti-MI/RI was the negative regulation of the apoptotic process, the lipopolysaccharidemediated signaling pathways, the regulation of mitochondrial membrane potential, the inherent apoptotic signaling pathway as a response to DNA damage, the external apoptotic signaling pathway lacking ligand, and release of cytochrome C from mitochondria. An analysis of the C-T-P network revealed that DAD anti-MI/RI acted on multiple targets and signaling pathways. The core targets of the active compounds in DAD were determined, namely AKT1, PIK3G, MAPK3, MAPK1, NFKB, TNF, NFKBA, MTOR, GSK3ß and TP53. As with BP, these targets were associated with apoptosis and inflammation. Various studies have likewise confirmed that apoptosis is the key mechanism of anti-MI/RI (Zhang et al., 2018b; Li et al., 2020b). Apoptosis plays a vital function in MI/RI prognosis. Studies have determined that the inhibition of myocardial cell apoptosis during MI/RI can mitigate the enlargement of the infarct area and can effectively protect cardiac functions (Geng et al., 2020). Significantly, PI3K/AKT/GSK-3β, an apoptotically-related signaling pathway, has the highest anti-MI/RI correlation in DAD (Chen et al., 2017). Therefore, DAD may play an anti-MI/RI function by inhibiting myocardial apoptosis through the PI3K/AKT/GSK-3β signaling pathway. To further validate this hypothesis, in vivo and in vitro experiments are conducted to validate its mechanism on network pharmacological prediction.

Mitochondria is the energy factory of the cells and is also the site of ATP synthesis (Wang et al., 2020). On a physiological level, a stable mitochondria provides ATP to the body; when it is damaged (i.e., by hypoxia injury), it can produce superoxides and reactive oxygen species, leading to adverse stimuli like calcium overload and oxidative stress, and further inducing apoptosis and necrosis in cells (Latini et al., 2015). The abnormal openness of MPTP, as a key regulator of mitochondrial functions, can induce mitochondrial structure disorders, which influence mitochondrial functions and eventually result to cell apoptosis. Under normal physiological conditions, MPTP remains closed, while Ca²⁺ overload and excessive oxidative stress can induce it to open (Tait and Green, 2010). Cyt-C generally exists in the space between the inner and outer membranes of the mitochondria, and cannot cross the outer membrane to reach the cytoplasm under physiological conditions (Joseph and Levine, 2015). When the MPTP is abnormally open and causes damage to the mitochondrial membrane structure, Cyt-C is released from the mitochondria into the cytoplasm and acts as a vital pro-apoptotic factor. It binds to the apoptotic protease activator 1 in the synergistic role of deoxyadenosine triphosphate. Caspase-9 is activated, eventually leading to apoptosis (Mace et al., 2014). Interestingly, in vitro studies have depicted that DAD reduces apoptosis and increases ATPase activity in H/R-damaged H9C2 cells. Meanwhile, in vivo studies have presented that DAD can reduce myocardial injury in MI/RI rats, with the rate of apoptosis of myocardial cells, the oxidative damage, the degree of mitochondrial MPTP opening, and the expressions of Cyt-C and CASP9 likewise all reduced. Therefore, as predicted by

network pharmacological analysis, it was verified that DAD could reduce cardiomyocyte apoptosis both *in vivo* and *in vitro*.

The PI3K/AKT/GSK-3β signaling pathway is a fundamental pathway in MI/RI. Phosphatidylinositol 3-kinase (PI3K, a lipid kinase) can specifically catalyze the phosphorylation of the phosphatidylinositol-3 hydroxyl group (Stokes and Condliffe, 2018). It phosphorylates PIP2 to produce PIP3 firstly (Zhang et al., 2017), and then activates AKT (Chen et al., 2014). Activated AKT can yield a series of phosphorylation cascade reactions and can regulate significant downstream effector molecules such as Glycogen synthase kinase-3β (GSK-3\beta) to exert their biological functions (Ya-Fei et al., 2010). GSK-3β is a serine/threonine kinase (Sun et al., 2011; Barré and Perkins, 2014), and is the most extensively studied downstream target of AKT. It can promote cardiomyocyte apoptosis through an intrinsic mitochondrial pathway (Yan et al., 2011); meanwhile, phosphorylated GSK3ß has no biological activity, which can reduce myocardial cell apoptosis. (Jun et al., 2011). The PI3K/AKT/GSK-3β signaling pathway plays a vital function in the growth, survival, apoptosis and proliferation of cells. Recent studies have presented that the activation of this signaling pathway can reduce body damage caused by hypoxia (Kaneko et al., 2016; Li et al., 2018; Jing et al., 2019). Interestingly, in vivo studies have indicated that DAD can activate the expression of the said signaling pathway.

The innovation of this study involves the prediction of active components, BP and mechanism of action of DAD against MI/RI using network pharmacology. This study has demonstrated that DAD plays an anti-MI/RI role by activating PI3K/AKT/GSK3β to reduce cardiomyocyte apoptosis. Nevertheless, the limitations of this study should be acknowledged. Firstly, DAD at its highest concentration has either no or minimal effect against MI/RI. In the dose-setting process, the clinical equivalent dose was selected as the medium-dose group. In Figures 3, 5-9, dose dependence was not found, which might be because the concentration gradient established was not large enough. Future studies may focus on the study of the "dose-effect" relationship of DAD in regulating SOD and MDA, as well as other indices. Moreover, most TCMs can play multiple therapeutic roles, and network pharmacology can predict DAD anti-MI/RI by inflammation relevant signaling pathways. Thus, further studies may explore inflammation-related signaling pathways and regulators. In addition, the active compounds neutralized in DAD have been identified by network pharmacology. However, the compounds that exert therapeutic effects are still unknown and deserve further study. Overall, the aforementioned limitations should continue to be studied in order to clarify the therapeutic mechanisms of DAD.

CONCLUSION

In this study, a comprehensive strategy that involved network pharmacological analysis, HPLC technology and experimental verification was adopted to determine the potential active components and molecular mechanisms of DAD against MI/ RI. Based on the TCMSP database and on core compounds, 16

active compounds of DAD were obtained. The presence of four of these components was identified in DAD by HPLC, in which the components were potential therapeutic ingredients as predicted by network pharmacology. Through the analysis of BP, hub targets and hub signaling pathways and experimental verification, it was concluded that DAD could play an anti-MI/RI role by inhibiting myocardial apoptosis via PI3K/AKT/GSK3 β . The experimental results were consistent with the network pharmacological predictions. Relatively, this study evidently clarified the anti-MI/RI mechanism of DAD, which could provide a certain basis for future studies on DAD.

DATA AVAILABLILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding author.

ETHICS STATEMENT

All animal experiments were carried out in accordance with the Animal Care and Use Committee of the Institute of Materia Medica, China (No. TCM-2019- 040-E08).

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AUTHOR CONTRIBUTIONS

FX, G-JD, and Y-YW performed the experiments, analyzed the data and wrote the manuscript. ML, BW, and P-FW designed the study. FG, LC, and A-PL revised the article. All authors have read and agreed to the final version of the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.609702/full#supplementary-material

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Estimation of Andrographolides and Gradation of Andrographis paniculata Leaves Using Near Infrared Spectroscopy Together With Support Vector Machine

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Andrographis paniculata (Burm. F) Nees, has been widely used for upper respiratory tract and several other diseases and general immunity for a historically long time in countries like India, China, Thailand, Japan, and Malaysia. The vegetative productivity and quality with respect to pharmaceutical properties of Andrographis paniculata varies considerably across production, ecologies, and genotypes. Thus, a field deployable instrument, which can quickly assess the quality of the plant material with minimal processing, would be of great use to the medicinal plant industry by reducing waste, and quality grading and assurance. In this paper, the potential of near infrared reflectance spectroscopy (NIR) was to estimate the major group active molecules, the andrographolides in Andrographis paniculata, from dried leaf samples and leaf methanol extracts and grade the plant samples from different sources. The calibration model was developed first on the NIR spectra obtained from the methanol extracts of the samples as a proof of concept and then the raw ground samples were estimated for gradation. To grade the samples into three classes: good, medium and poor, a model based on a machine learning algorithm - support vector machine (SVM) on NIR spectra was built. The tenfold classification results of the model had an accuracy of 83% using standard normal variate (SNV) preprocessing.

Keywords: near infrared spectroscopy, minimal processing, medicinal plant, Andrographis paniculata, quality grading, support vector machine

INTRODUCTION

Andrographis paniculata (Burm. F) Nees, popularly known as the "king of bitters," is an herbaceous plant in the family Acanthaceae. In China, India, Thailand, and Malaysia, this plant has been widely used for treating sore throat, flu, and upper respiratory tract infections (Jayakumar et al., 2013). Its major constituents are the group of diterpenoids designated as andrographolides. Andrographolides have a broad range of therapeutic activities, such as anti-inflammatory (Shen et al., 2002), antibacterial, antitumor, antidiabetic, antimalarial, and hepatoprotective (Trivedi and Rawal,

2001; Jayakumar et al., 2013; Dai et al., 2019). Clinical trials suggest that *Andrographis paniculata* has a strong treating capacity of viral respiratory infections (Hu et al., 2018).

The genotype and agroecology of Andrographis paniculata determine the nature and quantity of the active molecules like andrographolides and hence the pharmacological activities (Jayakumar et al., 2013). It is important to estimate the most important active molecules, the andrographolides and classify Andrographis paniculata plants with respect to this group of marker molecule. Traditional classifications based on visual inspection of the morphological traits do not consider the active molecules at all. Thus, estimations of active molecules for pharmacognosy, physicochemical studies are mainly based on performance analytical techniques like high chromatography (HPLC), high performance thin layer chromatography (HPTLC), LC-MS/MS (Mukherjee et al., 2015). These techniques are time-consuming, complicated, labor-intensive, and expensive; moreover, they produce considerable quantities of wastes (Borraz-Martínez et al., 2019). Any field level quality control system should be able to handle a large number of samples fast, at a relatively low cost and reasonably dependable accuracy and precision.

Use of NIR Spectra for detection and estimation of specific chemical constituents has proved its worth in diverse fields of application. Its advantages are low cost, speed and simplicity of detection, need for minimal sample preparation and even nondestructive use of samples, feasibility of use at the field level and the feasibility of mechanizing the detection/ estimation system for large number of samples. NIR spectroscopy uses liquid and solid samples without any pretreatment. Even when sample extracts are used, NIR spectroscopy obviates the use of further costly chemicals, equipment and time that are required in standard techniques like HPLC. NIR spectroscopy has been successfully used in several areas, like, in the tea leaf quality assessment (Hazarika et al., 2018), in food safety assessment (Cen and He, 2007; Lee and Herrman, 2016; Kusumaningrum et al., 2018) environmental chemistry, microfluidics, biomolecules (Cho et al., 2009), cancer diagnostic agents, and forensic science (Muehlethaler et al., 2016) as well as explosive detection.

In this study, the feasibility of using NIR spectra for estimating andrographolides in *Andrographis paniculata* plant samples and grading the samples based on the estimates was investigated. The performance of NIR spectrum-based technique was examined both in samples of dry powdered leaves and methanol extracts of leaves. Methanol extracts were required for estimation through HPLC, the gold standard (Mukherjee, 2019). If NIR spectrum can estimate andrographolides with reasonable accuracy compared to HPLC, that itself will be a big advantage in saving cost, time, and make mechanization of large scale estimates feasible.

We also attempted to grade the *Andrographis paniculata* samples based on the content of andrographolides (IP 2014). As only a small portion of the spectra responds to the andrographolides, a low cost portable spectrometer with customized range can be employed for simple gradation of the samples without the need for highly accurate estimation, and is likely to be used as a ready-to-apply tool by the traders for

breeding and improvement of cultivars for obtaining higher drug yield (Raina et al., 2013).

MATERIALS AND METHODS

Plant Material

Plant material (leaves) of *Andrographis paniculata* was collected from West Medinipur, East Medinipur, Purulia, South 24 Parganas, Hooghly, and Kolkata district of West Bengal, India. Plant material were identified and authenticated by Dr S. Rajan, Field botanist, the medicinal plant collection unit, Ooty, Tamil Nadu, Govt. of India. The voucher specimens of 18 samples (specimen no. SNPS/JU/2018/12–29) were deposited at School of Natural Product Studies, Jadavpur University, Kolkata, India for future reference.

Based on the content of andrographolides, *Andrographis paniculata* samples were graded into 3 categories: good quality, medium quality and poor quality. Plants having high andrographolides content (>2.50%) (Raina et al., 2013)were considered to be of good quality and placed in grade I; those with <1%, the non-acceptable level according to the Indian Pharmacopia (IP 2014), were placed in grade III. The intermediate types (\geq 2.5% and \leq 1%) were placed in grade II.

Chemical Analysis

Chemicals and Reagents

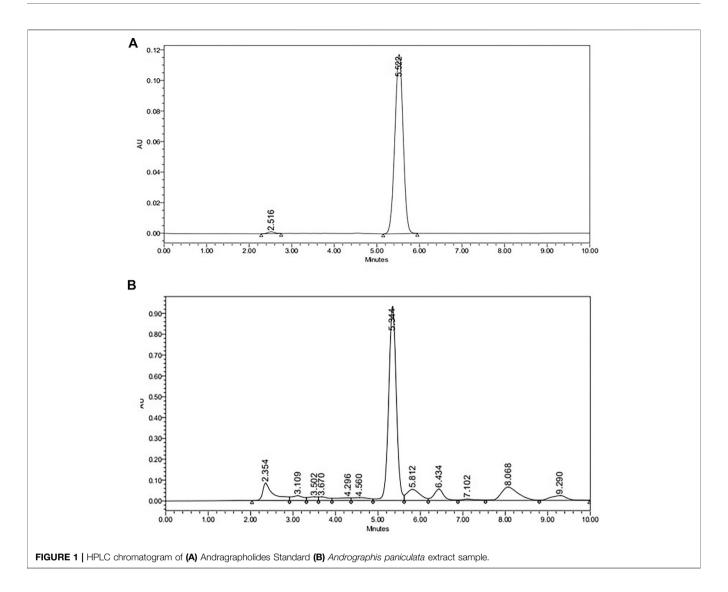
Andrographolides standard (>95% HPLC) was obtained from Sigma Aldrich. Methanol (HPLC grade), glacial acetic acid (HPLC grade), petroleum ether and ethyl acetate (analytical grade) and all other solvents (AR grade) were procured from Merck, India. Quantitative estimation was performed with Empowers software using the external standard calibration method.

Extraction

The air-dried (at room temperature) samples of 18 plants were powdered to a moderately coarse texture (180–355 μm) by a mechanical grinder. Methanolic extracts were made from the powdered samples (50 g in 80 ml of methanol) using rotary shaker at 150 rpm for 10 mins. Each sample was extracted thrice. The extracts were filtered and dried by vacuum evaporation using a rotary evaporator at 50°C and high pressure. The dried extract (10 mg) was dissolved in methanol and filtered through 0.22 μm membranes to get the stock solution (10 mg/ml). The stock solution was diluted to get 1 mg/ml sample concentration for HPLC.

High Performance Liquid Chromatography Analysis

The Reverse phase HPLC (RP-HPLC) system (Waters, United States of America) equipped with a rheodyne 7725i injector having 20 μ L loop, 3 Lines degasser (Volume 400 μ L), LC-30AD pump, C18 column (5 μ m particle size, 250 \times 4.6") UV/Vis detector was used for the analysis. The method developed was isocratic with the mobile phase of Methanol: Water (1% acetic acid) - 60:40 v/v/v. A Milli-Q academic water purification system (Bedford, MA, United States of America) equipped with



0.22 µm Millipak express filter. The pH of the solvent B was adjusted at 2.4 by using 1% (v/v) glacial acetic acid for better ionization. The mobile phase was filtered through 0.45 mm pore size (Millipore) membrane filter followed by sonication to degas the solvent. Whatman syringe filters (NYL 0.45 µm) were used for the filtration of the sample. The temperature of the column was kept at 25°C and the injection volume was 20 µL. The total run time was set at 10 min. The flow rate was set at 1.0 ml/min and the $\lambda_{\rm max}$ was set at 230 nm for maximum absorption of the compound. Quantitative estimation was performed with Empower 2 software programs using the external calibration method. Typical chromatograms of andrographolides standard and Andrographis paniculata extract sample are shown in Figure 1.

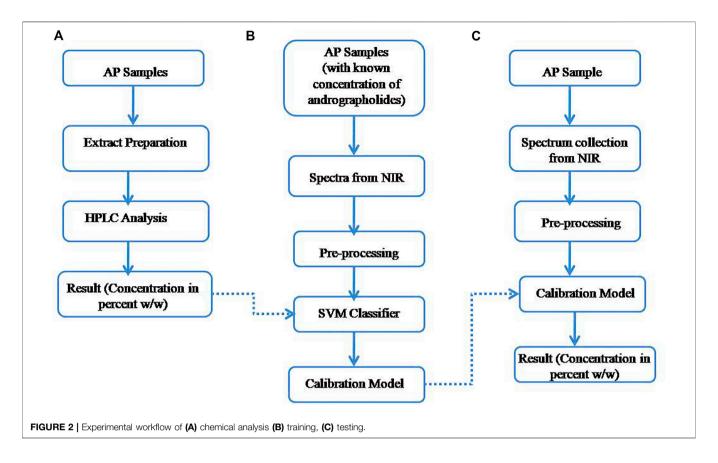
Method Validation

The RP-HPLC method was validated on the basis of the International Conference on Harmonization guidelines (ICH Q2 (R1) Guideline) (ICH Harmonized Tripartite Guideline, 2005). Method specificity was determined by

comparing the retention time of both the standard and test samples. Limit of Detection (LOD) and Limit of Quantification (LOQ) were calculated based on the equation: LOD = $3.3~\sigma/S$ and LOQ = $10~\sigma/S$, where σ is the residual standard deviation of regression and S is the slope of the calibration curve. The accuracy of the method was determined as percent recovery by the assay of known added amount of analyte in the sample. The samples were spiked with three different concentrations of standard compounds in triplicate. The precision of the analytical method was assessed by measuring six replicates of each of three different concentrations of the reference compounds. The results were represented as %RSD of intra-day and interday analysis.

Experimental Setup and Near Infrared Spectroscopy Spectra Acquisition

A DWARF-Star NIR spectrometer (StellarNet Inc., United States of America) coupled with an upward looking



diffuse reflectance accessory RFX-3D was used to acquire the diffuse reflectance spectra of the medicinal plant samples. The scanning range was from 900 to 1700 nm, and a RS50 (50 mm diameter White reflectance standard, halon>97%) was used as a calibration reference. The sample (after drying and grinding) was placed in a standard quartz plate of 1 mm thickness at the top of RFX-3D. RFX-3D was integrated with a 5 W halogen bulb and three fiber connectors to the spectrometer each positioned 120° in a circle to eliminate the need to rotate for coarse grain or non-uniform samples. Each sample was scanned 16 times with integration time of 300 ms and then the averaged spectrum was used for analysis. The S/N ratio was 4,000:1, wave-number accuracy was within ± 0.01 cm⁻¹, and the resolution was set as the resolving resolution of 2.5 nm. The temperature was kept at about 25°C during the whole experiment. Figure 2 explains the workflow of the chemical analysis, and the training, and testing steps with NIR spectrum.

In the Stellarnet spectrometer used in our study, the data points were collected from 900 to 1700.5 nm with a gap of 1.75 nm. Thus there were (1700.5-900)/1.75=459 points for each spectrum. Fifteen (15) replicates were taken for each sample; thus, in total, $459\times18\times15$ spectral data points were obtained for 18 samples.

DATA ANALYSIS

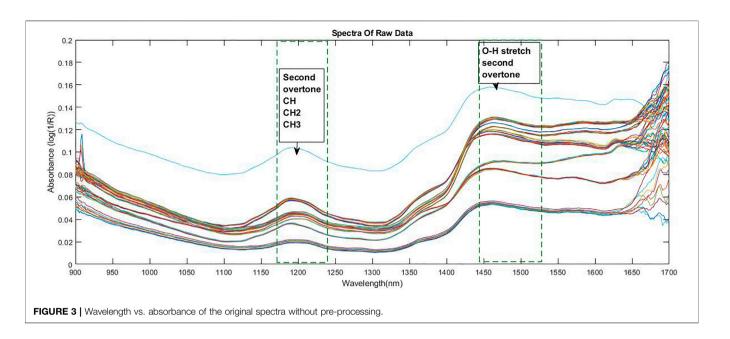
Both raw and pretreated spectral data obtained from the NIR instrument with the *Andrographis paniculata* samples were analyzed. To reduce the effect of scattering, data was pretreated with standard normal variate (SNV) method. The chemometric methods - principal component analysis (PCA), linear discriminant analysis (LDA) and support vector machine (SVM) were applied for clustering and classification.

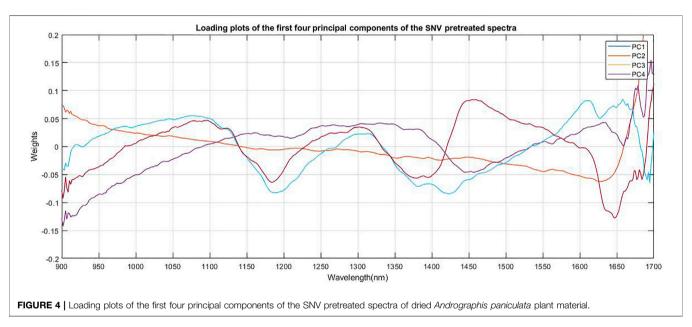
Preprocessing

In order to reduce the effect of base line variation, and scattering of light, standard normal variate (SNV) preprocesing technique was used on NIR spectra. The method removes the offset by subtracting the mean value of the full spectrum and brings all the spectra to the same scale dividing by the standard deviation of the spectrum (Barnes et al., 1989).

Principal Component Analysis

Principal component analysis (PCA) (Pearson, 1901) was used in order to visualize the multivariate data, by transforming the data along orthogonal axes, and the first two axes were plotted to observe the discrimination between the samples. Here, each point in the PCA plot corresponds to one spectrum.





Linear Discriminant Analysis

For reduction of features, Linear Discriminant Analysis (Fisher, 1936) was also used to visualize the samples in a lesser dimension hyper-plane. LDA maximizes separation between the samples. Only the first two axes were considered for visualizing the data. Class information was used to plot the data. PCA and LDA were implemented in Matlab V10.0 (Mathworks Co., United States of America).

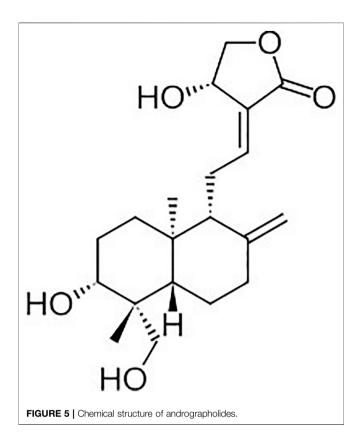
Support Vector Machine

Support vector machine (SVM) is a machine learning algorithm (Cortes and Vapnik, 1995). We have used radial basis function (RBF) as the kernel function. In this study, the two parameters of

SVM - γ (RBF kernel width) and c (SVM cost factor) were obtained based on the minimal classification error through a two-dimension grid search coupled with a leave-ten-out cross validation.

Full-spectrum data was directly used as the input of SVM to build the gradation model. The search range for γ was set from 10^{-6} to 10 with 15 values spaced uniformly for c from 10^{-3} to 100 with 11 values spaced uniformly. The optimal parameter combination of γ and c were obtained as 0.0001 and 100, respectively.

Support vector machine (SVM) was implemented in R studio. The accuracy of classification was estimated on the basis of the tenfold cross-validation method, where nine subsets were used for training and one subset for testing.



RESULTS AND DISCUSSION

Interpretation of Spectroscopic Characterization

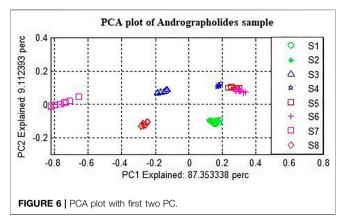
Original and Preprocessed Spectra

The graphical representation of the wavelength vs. absorbance of the raw spectra without any pre-processing is shown in **Figure 3**. The spectra obtained using the dried leaf powder shows absorption peaks at 1200 nm (C-H Second overtone region due to presence of CH2, CH) and 1472 nm (O-H second overtone region due to presence of R-OH group) (Reuben et al., 2018).

Loading Plot

The loading plot of the spectra is shown in **Figure 4**. The relative contributions of each PC to the explained variation were large for the first few components, with 97.2% of the variation explained by the first four components for andrographolides (PC1 = 55.89%, PC2 = 21.82%, PC3 = 15.94%, and PC4 = 3.56%).

The first two principal components (PCs) showed strong absorption peaks at 1100 and 1300 nm (C-H Second overtone region due to presence of CH3). The loading plot of PC2 (Figure 4) a showed another absorption peak at 1450 nm (O-H Second overtone region due to presence of R-OH group) and loading plot of PC1 showed another absorption peak at 1650 nm (C-H first overtone region due to presence of CH3). The loading plot of PC4 (Figure 4) had major



absorption peaks at 1400 nm (O-H second overtone, associated with water) and 1650 nm (C-H first overtone region due to presence of CH3, CH2, CH). These are all related to the most abundant structural groups present in the andrographolides (**Figure 5**).

Plot of Principal Component Analysis

PCA was performed on the raw and preprocessed spectra to examine the qualitative differences among the three varieties of the samples. **Figure 6** presents the PCA score plot derived from the raw spectra of *Andrographis paniculata* samples. The first and second principal components (PCs) accounted for 90.67% and 7.89% of the total variance, respectively. Samples of the same variety have been observed to appear as clusters, and no overlaps were observed among the three samples.

Plot of Linear Discriminant Analysis

Figure 7 displays the Linear Discrimination Analysis plot applied to the whole data matrix after preprocessing using Standard Normal Variate (SNV). The discrimination is better than PCA.

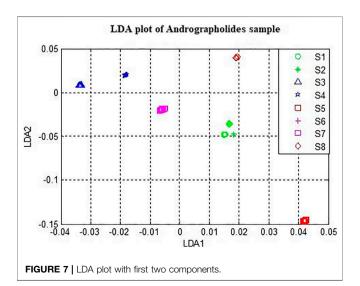


TABLE 1 | Result of HPLC and NIR and the grades of the 18 samples.

Serial no	Sample ID	HPLC method (w/w %)	Prediction	Grade	
			Extract (w/w %)	Powder (w/w %)	
1	SNPS/JU/12	2.50	2.45	2.25	II
2	SNPS/JU/13	2.20	2.10	2.00	II
3	SNPS/JU/14	1.5	1.45	1.44	II
4	SNPS/JU/15	0.53	0.47	0.41	III
5	SNPS/JU/16	0.54	0.54	0.49	III
6	SNPS/JU/17	0.55	0.50	0.44	III
7	SNPS/JU/18	0.93	0.90	0.89	III
8	SNPS/JU/19	2.90	2.89	2.46	1
9	SNPS/JU/20	2.65	2.62	2.52	1
10	SNPS/JU/21	1.71	1.70	1.65	II
11	SNPS/JU/22	2.57	2.54	2.32	1
12	SNPS/JU/23	2.72	2.62	2.52	1
13	SNPS/JU/24	2.68	2.31	2.14	1
14	SNPS/JU/25	2.30	2.28	2.29	II
15	SNPS/JU/26	1.57	1.80	2.07	II
16	SNPS/JU/27	1.79	2.24	2.05	II
17	SNPS/JU/28	1.59	1.54	1.44	II
18	SNPS/JU/29	2.03	2.13	2.12	II
	Correlation coefficient with respect to HPLC results		0.97	0.94	
	"t" value		0.27	1.78	
	"p" value		0.79	0.09	

TABLE 2 | Result of 10-fold cross-validation.

Cross validation folds	% Classification on
	SNV preprocess data
1	75
2	95
3	90
4	75
5	80
6	90
7	81
8	75
9	81
10	85
Average	83

Support Vector Machine Model

For analysis on the spectra obtained from the ethanol extracts of 18 samples, the support vector model was used for regression on the data pretreated with SNV data. The results of HPLC analysis, NIR predicted values and the corresponding grades are shown in **Table 1**. The of correlation coefficients and paired two tailed "t" statistic results of three pairs of among three sets of estimates: NIR estimates of methanol extract, NIR estimates of powdered samples, and the estimates from HPLC analysis, are given in **Table 1**.

Eighteen data patterns were considered for the tenfold cross-validation method. In this method, a total of ten train-test trials were conducted, and the total data set was divided into ten subsets. Out of these ten subsets, one subset (10% of data) was used as the test set, and the other nine subsets (90% of data) were used as the training set. The classification rates were then

averaged over these folds for estimating the classifier performance. The classification rate and the total misclassified pattern on 18 NIR data are shown in **Table 2**.

From the results of the tenfold cross-validation method, the average classification rate is found to vary from 75% to 95% and the average accuracy is obtained as 83% with SNV preprocessing. This result is quite encouraging, even though the data set is quite small with respect to the number of classes.

CONCLUSION

In this paper, a methodology has been proposed to grade Andrographis paniculata samples using NIR spectroscopy and SVM classifier based on the content of marker molecules. andrographolides. Relative accuracies estimating the andrographolides by NIR spectra of methanol extracts of the samples, and powdered leaf samples were compared taking the estimates obtained from HPLC analysis as the standard. The accuracy of estimation based on extracts was a little higher than the powder leaf samples. But it did not change the grading pattern of the samples. Support vector machine was used to grade the samples into three classes-Class I (best quality), Class II (intermediate quality) and Class III (poor quality). The average classification accuracy of tenfold cross validation of SVM was obtained as 83%. Thus, NIR based estimation of powdered leaf samples combined with SVM classifier can be a low-cost solution to grade the samples rapidly. A small range portable NIR instrument would serve as a field-lab deployable instrument for gradation of Andrographis paniculata samples by the industry.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

AUTHOR CONTRIBUTIONS

DS: Conceptualization, Methodology Development, Coding, Writing. SB: Data curation, HPLC analysis. SNJ: Sample collection, and extraction. RM: Coding and data analysis. NIR

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data analysis. Investigation. SGD: Coding and data analysis. NIR data analysis. KM: Conceptualization, Methodology Development. AB: Improving data interpretation, Reviewing and Editing. RB: Validation, Supervision, Writing, Reviewing and Editing. PM: Conceptualization, Supervision, Reviewing and Editing.

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In-Vitro α-amylase, α-glucosidase Inhibitory Activities and In-Vivo Anti-Hyperglycemic Potential of Different Dosage Forms of Guduchi (Tinospora Cordifolia [Willd.] Miers) Prepared With Ayurvedic Bhavana Process

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Guduchi (Tinospora cordifolia [Willd.] Miers) is a flagship rejuvenating herb of Ayurveda with reported anti-diabetic potential. In the present study, different dosage forms of Guduchi stem (growing on neem tree) were developed by adopting Ayurvedic pharmaceutical process of Bhavana (levigation). Guduchi Churna (GC) was subjected to 07 times Bhavana separately with its own extracted juice, decoction and potable water, and dosage forms namely Svarasa Bhavita Guduchi Churna (SBGC), Kwatha Bhavita Guduchi Churna (KBGC), and Jala Bhavita Guduchi Churna (JBGC) were prepared. The present study was aimed to evaluate the role of Bhavana on the potentiation of therapeutic properties of Guduchi. Sequential solvent extracts (5, 10, 15 and 25%) of GC, SBGC, KBGC and JBGC were prepared in different solvents [phosphate buffer, hexane, dichloromethane (DCM), chloroform] and screened for the α -amylase and α -glucosidase inhibitory activity. The results revealed that phosphate buffer and DCM extracts of SBGC exhibited strong α-amylase inhibitory potential (>80% inhibition at 25% concentration) followed by KBGC, JBGC and GC with reference to the standard acarbose. In α -qlucosidase inhibitory activity, maximum inhibition was observed in DCM and chloroform extracts of SBGC (>85% inhibition at 25% concentration), followed by KBGC (>80% inhibition at 25% concentration), JBGC and GC. In vivo anti-hyperglycemic studies were carried out by oral glucose tolerance test in Swiss albino mice. Test drugs (JBGC, KBGC, SBGC) treated groups showed marginal decrease of blood glucose levels in normo glycemic mice. However, the blood glucose level in test drug JBGC, KBGC and SBGC treated groups was still within normal range in overnight fasted mice. In oral glucose tolerance test, among all dosage forms SBGC (51.08%) produced pronounced anti-hyperglycemic effect followed by KBGC (42.57%) at a dose of 520 mg/kg. The GC, JBGC, KBGC and SBGC samples

were also standardized using berberine (a well established anti-diabetic compound) as a marker compound by HPTLC fingerprint analysis. Findings of the present study indicate that SBGC and KBGC can be used in the treatment of diabetes mellitus and gives supporting evidence to Ayurvedic claims that the *Bhavana* process has pharmaceutico-therapeutic significance in Ayurvedic drug development.

Keywords: tinospora cordifolia, guduchi, bhavana, α-amylase, α-glucosidase, anti-hyperglycemic, hypoglycemic

INTRODUCTION

Diabetes mellitus (DM) is a chronic metabolic disorder caused by a failure in insulin production or a decrease in insulin sensitivity and function, affecting the lipid and carbohydrate metabolism. Hyperglycemia, an inevitable ramification of diabetes, is linked with several deleterious effects associated with this disease (Sharma et al., 2015a). DM is exponentially growing worldwide and leading cause of morbidity and mortality in low- and middle-income countries (Olowoyo et al., 2018). Based on current report of International Diabetes Federation (IDF) the global number of diabetic people (aged 18–99 years) will increase to 693 million by 2045 (Cho et al., 2018). Most of the conventional anti-diabetic drugs are reported to have side effects in long term use and have certain limitations, and options from natural products especially herbal medicine are being searched to meet the need (Sharma et al., 2015a).

Guduchi (Tinospora cordifolia Willd. Miers.; Family: Menispermaceae) is a renowned, deciduous, extensively spreading, climbing, herbaceous vine, distributed throughout the tropical Indian subcontinent and China, ascending to an altitude of 300 m. Mainly three Tinospora species are available in India, namely T. cordifolia, T. malabarica/T. sinensis and T. crispa. Though these species are closely related with their morphology and chemical properties, amongst them, the level of berberine (a well established anti-diabetic compound) is reported higher in T. cordifolia. The name - T. cordifolia is ascribed to the Ayurvedic plant Guduchi in Ayurvedic Pharmacopoeia of India and the traditional practitioners also consider T. cordifolia as the genuine source for Guduchi (Srinivasan et al., 2008; Nidhi et al., 2013). Guduchi is traditionally used in Indian Ayurveda medicine to treat wide range of diseases such as fever, diabetes, urinary disorders, anemia, jaundice, asthma, stress, allergy, skin disorders, arthritis, liver disorders etc., (Saha and Ghosh, 2012; Sharma et al., 2014a). Several reports substantiate its high anti-diabetic potential (Sharma et al., 2015a). Time by time its different traditional formulations like Churna (fine powder), Kwatha (decoction), Satva (sedimented starchy aqueous extract) and Ghana (solidified aqueous extract) were developed according to its need, and their anti-diabetic potential is evident from several studies (Sharma et al., 2013a; Sharma et al., 2013b; Sharma et al., 2015b; Gade, 2017).

Bhavana (levigation or wet-grinding of powdered drugs with juice/decoction/solution of plant, animal or mineral origin) is a unique traditional method of transformation of raw material/substances and process of herbal drug manufacturing, affecting the physicochemical and biological properties of a dosage form.

Bhavana is one of the most commonly carried out pharmaceutical process in Ayurveda, having multi-dimensional pharmaceutico-therapeutic implications and various popular traditional herbal or herbo-mineral formulations are being prepared by this process. Bhavana process is claimed to make quicker and augmented action with possible reduction in therapeutic dose of the drug under process (Sharma and Prajapati, 2015; Sharma et al., 2017). Churnakriya is a type of Bhavana, wherein Bhavana of juice/decoction of the same drug is given usually with the motto of augmentation of properties of the drug being levigated and, hence, to potentiate the therapeutic action (Acharya, 2004). By adopting Churnakriya method of Bhavana, the potency of single herbs like Guduchi can be improved.

To the best of our knowledge, to date, there is no scientific evidence on the inhibitory effects of any dosage form or formulation of Guduchi on carbohydrate hydrolyzing enzymes. Also, no reports are available exploring anti-hyperglycemic potential of Bhavita dosage form of Guduchi. Considering all these, the present study was planned to validate the classical uses of Guduchi and its preparations in diabetes and understand the role of Bhavana in herbal drug potentiation, especially whether Bhavana process could augment the therapeutic potential of Guduchi Churna (GC) to manage glycemic levels. GC was subjected to 07 times Bhavana separately with its own extracted juice, decoction and potable water, and the dosage forms namely Svarasa Bhavita Guduchi Churna (SBGC), Kwatha Bhavita Guduchi Churna (KBGC), and Jala Bhavita Guduchi Churna (JBGC) were prepared. The third trial preparation JBGC was prepared (by subjecting Bhavana to GC with potable water) to obtain the same particle size reduction as in first two groups and to understand the effect of Bhavana. These preparations were comparatively evaluated for *in-vitro* α -amylase, α -glucosidase inhibitory activities and in-vivo anti-hyperglycemic potential with High Performance Thin Layer Chromatography (HPTLC) profiling.

MATERIALS AND METHODS

Preparation of Test Formulations

JBGC, KBGC and SBGC samples were prepared by adopting classical Ayurvedic pharmaceutical guidelines of *Bhavana* process (Sharma and Prajapati, 2015; Sharma et al., 2017) in the department of Rasa Shastra and Bhaishajya Kalpana, Institute for Postgraduate Teaching and Research in Ayurveda, Gujarat Ayurved University, Jamnagar, Gujarat, India.

For preparation of Guduchi Churna (#80 sieve), Guduchi Svarasa, and Guduchi Kwatha, mature fresh medium sized

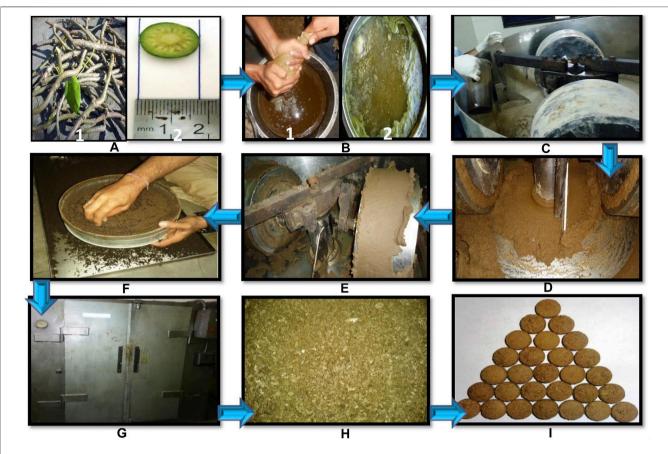


FIGURE 1 | Unit operating process of Svarasa Bhavita Guduchi Churna (SBGC), Kwatha Bhavita Guduchi Churna (KBGC), and Jala Bhavita Guduchi Churna (JBGC) samples preparation by traditional Bhavana method. (A)- (1) fresh Guduchi stems (2) chopped/crushed, (B)- (1) expressed juice (for SBGC batch) (2) decoction was prepared (for KBGC batch), (C)- wet grinding of Guduchi Churma with liquid media (Guduchi juice for SBGC batch, Guduchi decoction for KBGC batch, and potable water for JBGC batch) in edge-runner, (D)- soft and fine mass formed during grinding, (E)- observation of Subhavita Lakshana (Confirmatory tests for completion of levigation), (F)- wet granulation, (G)- hot air over drying, (H)- dry granules, (I)- preparation of tables.

diameter (1.6–2.0 cm) stems of *Guduchi*, climbing on neem (*Azadirachta indica*) tree were collected in monsoon season from the same vicinity (from non polluted, wild area of 'Moti Panchasara' village of Jamnagar district, Gujarat) to avoid any phyto-geographical differences. The physical impurities and outer exfoliating skin were removed and washed thoroughly with potable water. The collected plant material was authenticated (voucher specimen no- Phm/6,198) by the concerned authority in the Pharmacognosy laboratory of the institute.

Fresh *Guduchi* stems were taken to prepare different dosage forms as per classical Ayurvedic guidelines i.e., *Sadaiva ardra prayojyeta* (always use in fresh state) (Shastri, 2005; Sharma et al., 2012). *Guduchi* stems growing with the support of neem tree were selected, because it is believed to be the best as the synergy between these plants enhances its efficacy (Kinghorn, 2003; Bhalerao et al., 2012). Medium diameter or thumb sized stems from the same plant with uniform maturity was selected for study, as this is advocated to use for preparing *Guduchi*-based formulations (Acharya, 2008). Ayurvedic guidelines advocate collecting stems of medicinal plants in rainy/spring season. These ancient claims are supported by recent reports that the

concentration or percentage of total alkaloids and the antidiabetic biomarkers, tinosporaside and berberine of *Guduchi* are bit higher in rainy/monsoon season (Sharma et al., 2013c; Choudhry et al., 2014). Therefore the same harvesting time was selected for *Guduchi* collection.

In pharmaceutical process, three different batches of SBGC, KBGC, and JBGC were prepared. GC was subjected to 07 times Bhavana separately in edge-runner with Guduchi Svarasa (fresh expressed juice of Guduchi stems) - for SBGC batch, Guduchi Kwatha (decoction of Guduchi stems) - for KBGC batch) and potable water - for JBGC batch. The whole unit operating process involved in the preparation of SBGC, KBGC, and JBGC is exemplified in Figure 1. The whole pharmaceutical process of 07 times Bhavana for each formulation SBGC, KBGC, and JBGC was completed in the same season therefore excluding possibility of major changes in environmental conditions. The duration of wet grinding for each cycle of Bhavana was kept constant to 9 h so as to maintain homogeneity in pharmaceutical processing among the batches of three formulations. The finished products were collected, weighed and their compressed tablets (500 mg each) were prepared and stored in air-tight sterile glass containers along with small pieces of cotton in them.

In-Vitro α -Amylase and α -Glucosidase Inhibitory Studies

Chemicals and Reagents

Soluble starch (Merck), 3, 5-dinitrosalicylic acid (DNSA) (S D fine-chem Ltd.), phosphate buffer (0.02 M), hexane, dichloro methane (DCM) (S D fine-chem Ltd.), chloroform (S D fine-chem Ltd.), porcine pancreatic α -amylase (PPA) (Sigma-Aldrich) and acarbose (Bayer pharma) were used.

Test Materials

From the tablets of preparations, 5, 10, 15 and 25% of GC, JBGC, KBGC and SBGC solutions were prepared in different solvents (phosphate buffer, hexane, dichloro methane, chloroform).

α-Amylase Inhibitory Activity

The α -amylase inhibitory activity was determined according to the standard methods (Kumar et al., 2010; Sudha et al., 2011). 200μL of phosphate buffer was mixed with 200 μL of alphaamylase solution and 500 µL of various concentrations of test samples (5-25%) separately, were incubated at room temperature for 15 min and followed by addition of 200 µL of starch solution (1%) in all test tubes and further incubated for 10 min at 37°C. The enzymatic reaction was stopped by adding 400 µL of freshly prepared DNS reagent and placing in boiling water bath for 5 min. The mixture was allowed to cool, diluted with 15 ml of distilled water and absorbance was determined at 540 nm (Double beam systonic spectrometer-2201). The control samples were also prepared accordingly without any plant extracts and were compared with the test samples containing various concentrations of the plant extracts prepared with different solvents. The results were expressed as % inhibition.

α-Glucosidase Inhibitory Activity

The α -glucosidase inhibitory activity was determined using the standard method (Chougale et al., 2009; Tripathi, 2014). The enzyme solution was prepared by dissolving 0.5 mg α -glucosidase in 10 ml phosphate buffer (pH 7.0) containing 20 mg bovine serum albumin. It was diluted further to 1:10 with phosphate buffer just before use. Test sample solutions (5,10,15, and 25%) were prepared and 5 µL each of the sample solutions or DMSO (sample blank) were then added to 250 µL of 20 mM p-nitrophenyl-α-D -glucopyranoside and 495 μL of 100 mM phosphate buffer (pH 7.0). It was pre-incubated at 37°C for 5 min and the reaction started by addition of 250 μL of the enzyme solution, after which it was incubated at 37°C for exactly 15 min 250 µL of phosphate buffer was added instead of enzyme for blank. The reaction was then stopped by addition of 1000 µL of 200 mM Na2CO3 solution and the amount of p-nitrophenol released was measured by reading the absorbance of sample against a sample blank (containing DMSO with no sample) at 400 nm using UV visible spectrophotometer. The results were expressed as % inhibition.

Data Analysis

Experimental data of α -amylase and α -glucosidase inhibitory activity was expressed by multivariate analysis, principal

component analysis (PCA) with the help of Unscrambler software (Sharma et al., 2013c).

In Vivo Anti-Hyperglycemic Studies Experimental Animals

Swiss albino mice of either sex weighing 30 ± 5 g were obtained from animal house attached to Pharmacology laboratory of Institute for Postgraduate Teaching and Research in Ayurveda, Gujarat Ayurved University, Jamnagar, Gujarat, India, for experiments and maintained under standard experimental and husbandry conditions.

The animals were housed in each cage made of poly-propylene with stainless steel top grill. The dry wheat (post hulled) waste was used as bedding material and was changed every morning. The animals were exposed to 12 h light and 12 h dark cycle with the relative humidity of 50–70% and the ambient temperature during the period of experimentation was $22 \pm 03^{\circ}$ C. Animals were fed with Amrut brand rat pellet feed supplied by Pranav Agro Mills Pvt. Limited and drinking water *ad libitum*. The experiments were carried out after obtaining permission from Institutional Animal Ethics Committee (IAEC Approval number: IAEC/13/2013/01/PhD).

Dose Selection and Schedule

The clinical dose of *Bhavita Guduchi Churna* was taken based on available references as 4 g/day (Sharma et al., 2014c; Shingadiya et al., 2017). The dose for experimental study was calculated by extrapolating the human dose to animals (520 mg/kg) based on the body surface area ratio by referring to the tables of Paget and Barnes (Paget and Barnes, 1964). The test drugs were suspended in distilled water with suitable concentration and administered according to the body weight of the animals by oral route with the help of gastric oral cannula.

Instruments Used

One touch Glucometer (Lifeline Surgicals, New Delhi, India) with *Ez Smart* strips, weighing scale, disposable needle and syringe, mono pan balance and mortar and pestle.

Experimental Study

The hypoglycemic activity and anti-hyperglycemic activities were carried out by modifying previously described method of Pilkhwal et al. (2010). The selected mice were acclimatized for 7 days prior to experiments. The animals were divided randomly into relevant groups of six animals each. Then both activities were evaluated for the test drugs as per the following protocols:

Hypoglycaemic Activity

Swiss albino mice of either sex were randomly divided into five groups of six animals each. The first group received distilled water and served as water control group (10 ml/kg, po). Second group served as standard control group to which glibenclamide (0.65 mg/kg) was administered. Third, fourth and fifth groups were received JBGC, KBGC and SBGC respectively in the dose of 520 mg/kg, orally.

The animals were fasted overnight prior to the experiment and in the morning the fasting initial reading of blood sugar level (BSL) was measured with the help of One Touch Ez Smart CE0537 Glucometer, by using One Touch Ez Gluco test strips as per user's guideline by collecting the blood sample from tail vein under aseptic conditions. Then the water, test drug and standard drug were administered to respective groups. The BSL was recorded after 1, 2, 3 and 5 h of test drug administration for assessing the hypoglycemic effect after drug administration.

Anti-Hyperglycaemic Activity

The selected animals were randomly divided into five groups of six animals each. First group served as glucose control group to which glucose solution (5 g/kg, po) was administered. Second group served as standard control group to which glibenclamide (0.65 mg/kg, po) was administered. Third, fourth and fifth groups were received JBGC, KBGC and SBGC respectively in the dose of 520 mg/kg, oral.

Animals were fasted overnight prior to the experiment and in the morning the fasting initial BSL was measured as mentioned in hypoglycemic activity. Test drugs and reference standard drug were given to the respective group of animals as per the body weight. After 1 h of drug administration, glucose (5 g/kg, po) solution was administered to all groups orally by dissolving it in distilled water. Thereafter BSL was recorded at 30, 60, 90 and 120 min of post glucose overload for accessing the antihyperglycemic activity of test drug (Malalavidhane et al., 2000; Sachdewa et al., 2001; Kingsley et al., 2013).

Statistical Analysis

Results were presented as Mean \pm SEM, difference between the groups was statistically determined by Student paired 't' test with initial values of respective groups and unpaired 't' test with control group. The data also assessed through Anova followed by Dunnet's multiple 't' test. The level of significance set at p < 0.05. The level of significance was noted and interpreted accordingly.

High Performance Thin Layer Chromatography Studies

All chemicals utilized were of analytical grade and acquired from Merck Ltd. Berberine chloride hydrate, CAS number -14,050-10G; purity 90% was purchased from Sigma Aldrich (St. Louis, MO, United States). 5 g of each GC, SBGC, KBGC and JBGC formulation was refluxed with 50 ml of methanol for around 2 h. The subsequent solutions were filtered and concentrated using a rotary evaporator. The resultant extracts i.e., 240 mg (GC); 137 mg (SBGC); 200 mg (KBJC) and 100 mg (JBJC) were transferred in to 50 ml volumetric flask. The standard Berberine chloride hydrate 10 mg was dissolved in 10 ml methanol and finally standard concentration 1000 µg/ml was made. The calibration curve prepared with different volumes of standard stock solution (1, 2, 3, 4, 5, 7 µL) were spotted on HPTLC plate (20 × 10 cm) for berberine chloride hydrate followed by spotting (3, 4, 2, 1.8 µL) GC, JBGC, SBGC and KBJC respectively sample stock solutions in triplicate. Samples were applied as bands 4 mm wide keeping 12-mm distance from the left edge using Camag Linomat V applicator with a 100 µL test syringe at a steady application rate of 150 nL s⁻¹. The mobile

phase used was n-hexane, ethyl acetate, glacial acetic acid and methanol (10:1.1:1.1:2.5, v/v). After development, the plates were dried and observed in CAMAG TLC Visualizer at 254 nm. The developed plate was then scanned at 254 nm using CAMAG TLC densitometric Scanner 3 incorporated with WinCATS 1.4.8 programming (Doshi et al., 2014; Kamboj and Saluja, 2017).

RESULTS

α-Amylase Inhibitory Activity

The test formulations in different solvents were studied for inhibitory activity of α - amylase enzyme (**Figure 2**). It is evident from graphs that maximum α - amylase inhibition was demonstrated by SBGC, followed by KBGC, JBGC and GC formulations in comparison to the standard acarbose. In phosphate buffer saline SBGC formulation showed maximum activity (87%) which is comparable with acarbose (90%).

α-Glucosidase Inhibitory Activity

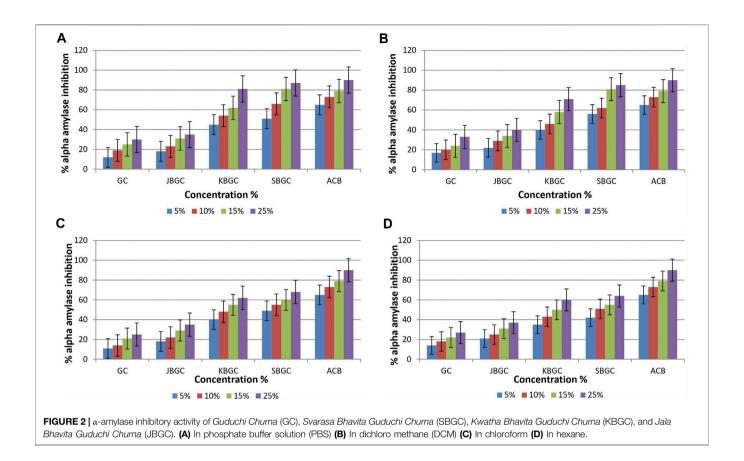
Data with respect to effect of GC, JBGC, KBGC and SBGC on α -glucosidase inhibitory activity are represented in **Figure 3**. It is evident from the graphs that maximum inhibition was demonstrated by DCM and chloroform extracts of SBGC, followed by KBGC, JBGC and GC in comparison to standard acarbose. Maximum inhibition (89%) was reported by SBGC formulation at 25% solution of DCM.

Differences Among the High, Medium and Low α -Amylase Inhibitory Activity Groups

To better screen the fuzziness and integrity of the various concentration and polarity codified Guduchi samples differentiating their α -amylase inhibitory activity (Figure 4), in the experimental samples, % of inhibitory outcome were separated five groups, high (≤54%), medium (≤43%) and very low (≥21%). An overview of the differences in the respective concentrations (5, 10, 15 and 25%) samples was obtained using unsupervized PCA, which takes into account all variables (Figures 4A, Figures 4B). The 1st and 2nd principal components explained 91 and 1% of the total variance respectively. In score plot, we can observe clear separation between SBGC and KBGC, while there was not clear separation of GC and JBGC because of α -amylase activity as a continuous variable. The SBGC samples have high content of active marker compounds may have great potential for preventing postprandial hyperglycemia followed by KBGC, JBGC and GC medicaments in comparison to standard acarbose.

Differences Among the High, Medium and Low α -Glucosidase Inhibitory Activity

The experimental findings of the various concentration and polarity codified *Guduchi* samples differentiating their α -glucosidase inhibitory activity (**Figure 5**), in the experimental samples, % of inhibitory outcome were separated five groups, high (\leq 52.4%), medium (\leq 39%) and very low (\geq 14%). An overview of



the differences in the respective concentrations (5, 10, 15 and 25%) samples was obtained using unsupervized PCA, which takes into account all variables (**Figures 5A, Figures 5B**). The first and 2nd principal components explained 99 and 1% of the total variance respectively. In score plot, we can observe clear separation of between GC and KBGC, while there was not clear separation of SBGC and JBGC because of α -glucosidase activity as a continuous variable. Furthermore, DCM and chloroform extract of SBGC with a high amount of active marker compounds may have more synergy and supra additive therapeutic effect, followed by KBJC, JBGC and GC in comparison to standard acarbose.

Hypoglycemic Activity

Table 1 and **Figure 6** represent the results of SBGC, KBGC, JBGC formulations on glucose concentration in normal fasted mice. All test formulations has produced a marginal hypoglycemia during the experimental studies. However the glucose concentrations were restored to that of pretreatment level (0 h). GB treated group leads to significant decrease in blood glucose level at almost all the time intervals in comparison to control group and maximum protection was observed at 3rd hour with 45.20%.

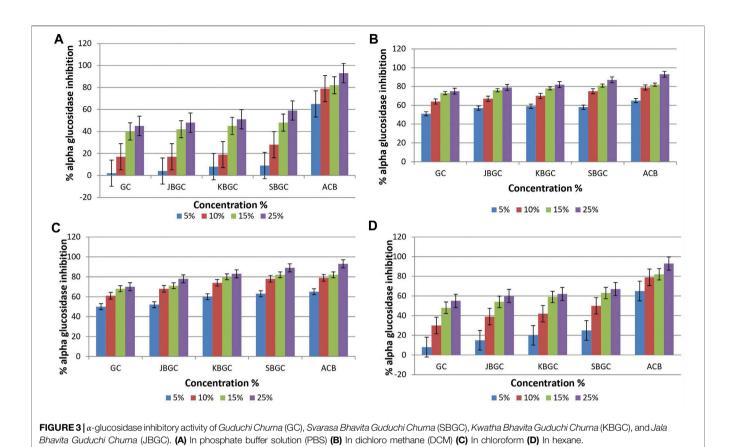
Anti-Hyperglycemic Activity

The effects of JBGC, KBGC and SBGC formulations in glucose tolerance test in mice are presented in **Table 2** and **Figure 7**. All formulations are shown significant activity at an oral dose of 520 mg/kg. The maximum protection was observed at 90 min

after glucose load. Among all formulations SBGC and KBGC were produced maximum protection at 90 min. Glibenclamide was used as standard and produced maximum protection at 90 min with percentage protection of 62.60%. The maximum glucose concentration was observed at 60 min with glucose concentration of 236.6 mg/dl. The percentage protection at 90 min produced by JBGC, KBGC and SBGC is 38.46, 42.06 and 56.56 respectively when tested at dose of 520 mg/kg, these results are comparable in activity produced by glibenclamide at a dose of 0.65 mg/kg. SBGC produced significant antihyperglycemic effect at all-time intervals in comparison to control group. Overall, SBGC produced pronounced antihyperglycemic effect followed by KBGC and JBGC.

High Performance Thin Layer Chromatography Studies

The developed mobile phase consisting of n-hexane, ethyl acetate and methanol (10:1.1:1.1:2.5, v/v) gave better, sharp and well defined peak resolution for standard (berberine chloride hydratea well-known anti-diabetic compound) as well as a test samples. The developed HPTLC method resolved the standard compound at $R_{\rm F}$ value of nearly about 0.28 \pm 0.02 for berberine chloride hydrate for confirming the presence in coded extract visualized by band parallel to standard spot along with other resolved components in the developed TLC plate. The TLC plates were scanned at 254 nm and to identify of berberine chloride hydrate



in the sample chromatogram was confirmed by three-dimensional (3D) chromatogram (**Figure 8**) obtained after densitometric scanning. The calibration curve was linear range of (200–1,400 ng/spot) for berberine chloride hydrate. The linear regression of the berberine chloride hydrate standard was determined with $R^2 \pm \mathrm{SD} = 0.991 \pm 3.21\%$ with regression line; y = 7.336x + 459.8. The quantification of berberine chloride hydrate in the respective codified samples is depicted in **Table 3**. The peak corresponding to berberine chloride hydrate and berberine from the codified samples solution had the same retardation factor ($R_{\mathrm{F}}=0.28\pm0.02$).

DISCUSSION

This study was carried out not only to validate the traditional uses of *Guduchi* and its preparations in diabetes (Sharma et al., 2014b) but also to initiate search for newer pharmacophores with specificity toward pancreatic α -amylase or α -glucosidase. Structurally as well as mechanistically, PPA is closely related to HPA (human pancreatic α -amylase) (Brayer et al., 1995). Hence, sequential solvent extracts of different formulations of *Guduchi* viz. GC, JBGC, KBGC and SBGC were screened for the presence of PPA inhibitors, the lead extracts quantified for PPA inhibition under *in-vitro* conditions. Primary screening for α -amylase inhibition was performed based on starch-iodine color complex formation. Different extracts of GC, JBGC,

KBGC and SBGC were prepared in various solvents such as phosphate buffer, DCM, chloroform and hexane extracts. All these extracts were screened, and all of them tested positive for PPA inhibition by chromogenic DNSA method. It was noted that phosphate buffer and DCM extracts of SBGC exhibited strong PPA inhibitory potential (>80% inhibition, in 15 and 25% concentrations) followed by KBGC, JBGC and GC. In α -glucosidase inhibitory activity, maximum inhibition was shown by DCM and chloroform extracts of SBGC (>85% inhibition, in 15 and 25% concentrations), followed by KBGC (>80% inhibition, in 15 and 25% concentrations), JBGC and GC.

In both α -amylase and α -glucosidase inhibitory activities, a dose/concentration dependent effect was observed on increasing the concentrations of the extract solution, suggesting a competitive type of inhibition. Our results suggests that extracts of GC, JBGC, KBGC and SBGC act effectively as PPA inhibitors leading to a reduction in starch hydrolysis and hence eventually to lowered glucose levels. Also, a good discrimination among respective codified samples is easily obtained from PCA analysis, may be due to supra-additive active metabolite load in context of α -amylase and α -glucosidase inhibitory activity. Our study shows that SBGC followed by KBGC were effectively inhibiting α -amylase and α -glucosidase enzyme and therefore it may be used as hypoglycemic agents in the management of post prandial hyperglycemia. The study suggests that one of the targets for hypoglycaemic property of *Guduchi* is α -amylase and α -glucosidase inhibition, where SBGC demonstrated a highly

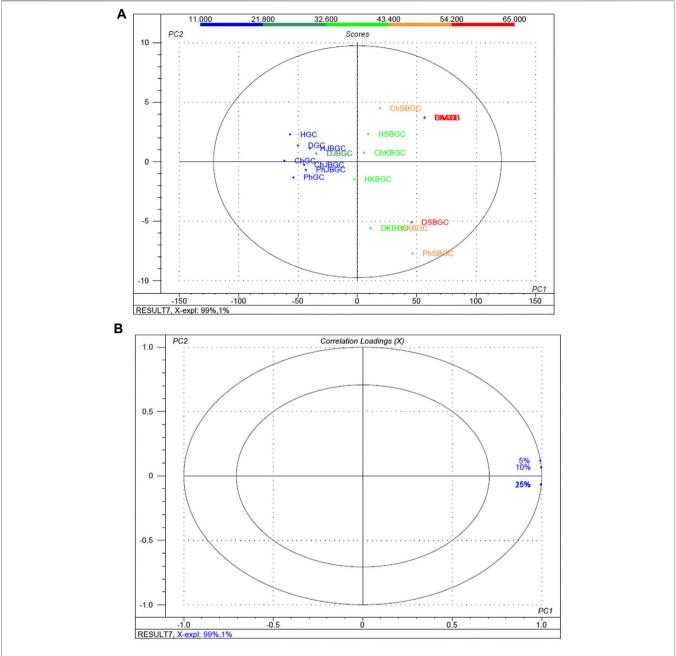


FIGURE 4 | Multivariate statistical analysis of codified different polarity *Guduchi* samples (Ph: phosphate buffer solution, D: dichloro methane, Ch: chloroform, and H: hexane) based on an unsupervized PCA model. **(A)** Unsupervized PCA score plot **(B)** Loading plot of α -amylase inhibitory activity of GC, JBGC, KBGC, SBGC formulations and various concentrations.

promising and effective strategy for diabetes, which may serve as a lead for isolation and characterization of compounds responsible for it.

Taking leads from encouraging enzyme inhibitory results, *in-vivo* experiments were carried out to understand the effects of extracts on glycemic levels of experimental animals. An ideal antihyperglycemic agent should decrease the elevated blood glucose levels and should maintain the normal blood glucose levels (Venkatesh et al., 2003). The decrease in blood glucose levels below the normal i.e., hypoglycemia, is the major side effect of insulin and oral hypoglycemic agents. In the

present investigation, all extracts were tested for their hypoglycemic activity and the results showed partial hypoglycemia in normal mice, where as glibenclamide showed maximum protection (45.20%.) at 3rd hour.

Glucose tolerance test is a preliminary method to assess the ability of drug to reduce the increased blood glucose levels or not (Kingsley et al., 2013). In this screening method, the animals are loaded with challenging dose of glucose (5 g/kg) after 60 min of test, standard drug administration. After glucose load, the raise in

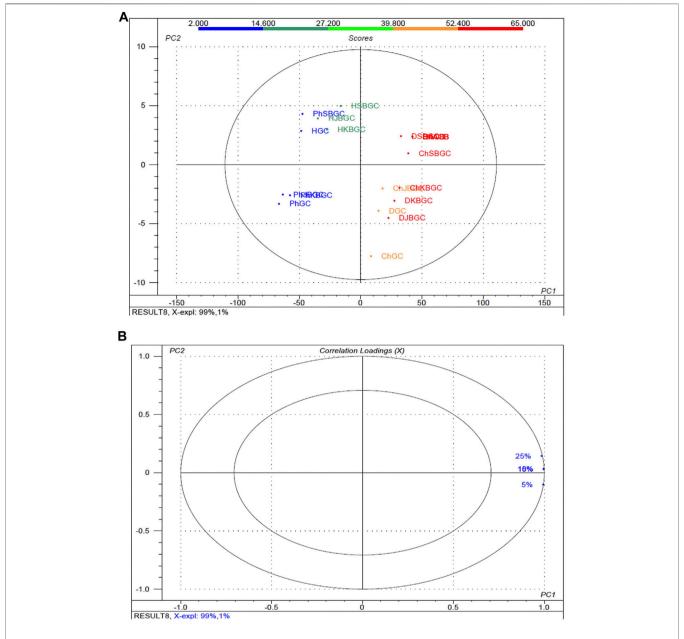


FIGURE 5 | Multivariate statistical analysis of codified different polarity *Guduchi* samples (Ph: phosphate buffer solution, D: dichloro methane, Ch: chloroform, and H: hexane) based on an unsupervized PCA model. **(A)** Unsupervized PCA score plot and **(B)** Loading plot of α -glucosidase activity of GC, JBGC, KBGC, SBGC formulations and various concentrations. The ellipse represents the Hotelling T₂ with 95% confidence.

glucose concentration is observed from 30 min and reached maximum at 60 min and decreased by 120 min. SBGC, KBGC, and JBGC extracts produced significant activity at 90 min, however, the maximum significant (p < 0.01) activity was produced at 520 mg/kg by SBGC, KBGC, and JBGC is 56.56, 42.06 and 38.46 respectively. SBGC produced significant anti-hyperglycemic effect at all-time intervals in comparison to control group. Overall, SBGC produced pronounced anti-hyperglycemic effect followed by KBGC and JBGC. The standard glibenclamide (10 mg/kg) produced a significant maximum protection at 90 min (62.60%). The observed

promising results of the test drugs on glycemic levels could be due to the increased concentration of the anti-diabetic phytoconstituents during *Bhavana* process. It also has been reported that the anti-diabetic activity of this plant is primarily due to improving the entry of glucose into the peripheral tissues and organs like the liver and decreasing the activity of phosphorylase in the liver, thereby it may prevent the release of glucose into the blood (Puranik et al., 2010). The same mechanism may be involved in the observed activity profile; however further detailed studies are needed to understand the exact pharmacodynamics involved.

TABLE 1 | Effect of JBGC, KBGC and SBGC on blood sugar level in normal overnight fasted Swiss albino mice at various time intervals.

Blood alucose I	evel ((ma/	dI)
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Groups	Initial (mg/dl)	1 h (mg/dl)	2 h (mg/dl)	3 h (mg/dl)	5 h (mg/dl)
wc	109.83 ± 2.24	106.00 ± 2.80	99.50 ± 1.70*	88.83 ± 1.90*	78.83 ± 1.85*
JBGC	107.60 ± 1.32	101.80 ± 1.49 (4.12)	98.80 ± 4.85* (0.7)	92.92 ± 2.65**	90.10 ± 2.39*
KBGC	106.16 ± 3.05	$104.50 \pm 1.46^*$ (1.41)	99.00 ± 3.59* (0.5)	86.33 ± 4.01* (2.81)	80.33 ± 2.42*
SBGC	102.50 ± 1.01	93.00 ± 3.51** (12.26)	86.00 ± 5.46* (13.56)	80.16 ± 3.92* (9.76)	75.66 ± 4.520* (4.02)
GB	103.64 ± 4.82	90.5 ± 2.32* (14.62)	74.17 ± 1.25* (25.45)	48.67 ± 2.26* (45.20)	57.33 ± 4.84** (27.27)

WC, Water control; JBGC, Jala Bhavita Guduchi Churna; KBGC, Kwatha Bhavita Guduchi Churna; SBGC, Svarasa Bhavita Guduchi Churna; GB, Glibenclamide as standard control. *p < 0.05, **p < 0.01 are in comparison with initial blood glucose levels of the mice (0 h) in the respective group. Figures in parenthesis indicate the percentage decrease.

Values are mean ± S.E.M; n = 6.

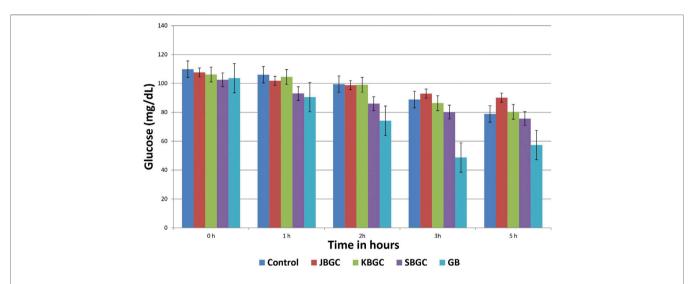


FIGURE 6 | Effect of Svarasa Bhavita Guduchi Churna (SBGC), Kwatha Bhavita Guduchi Churna (KBGC), and Jala Bhavita Guduchi Churna (JBGC) on BSL in normal fasted mice.

TABLE 2 | Effect of JBGC, KBGC and SBGC on blood sugar level in glucose overloaded Swiss albino mice at various time intervals.

Blood glucose level (mg/dl)

Groups	0 min	30 min	60 min	90 min	120 min
GC	86.66 ± 2.84**	180.83 ± 3.84**	236.6 ± 4.49**	189.0 ± 2.3**	134.5 ± 2.89**
JBGC	80.1 ± 1.62**	160.9 ± 2.89**	184.6 ± 2.62**	116.3 ± 1.26**	93.4 ± 3.42**
		(11.11)	(21.99)	(38.46)	(30.55)
KBGC	84.4 ± 3.97**	143.8 ± 4.56**	165.8 ± 3.12**	109.5 ± 3.15**	88.8 ± 1.94**
		(20.47)	(29.94)	(42.06)	(33.97)
SBGC	79.6 ± 4.58**	131.2 ± 1.97**	116.7 ± 4.23**	82.1 ± 1.59**	82.2 ± 3.04**
		(27.44)	(50.67)	(56.56)	(38.88)
GB	82.42 ± 5.12**	104.17 ± 2.68**	101.5 ± 3.58**	70.67 ± 1.36**	61.33 ± 2.33**
		(42.39)	(57.10)	(62.60)	(54.40)

GC, Glucose control; JBGC, Jala Bhavita Guduchi Churna; KBGC, Kwatha Bhavita Guduchi Churna; SBGC, Svarasa Bhavita Guduchi Churna; GB, Glibenclamide as standard control. *p < 0.05, **p < 0.01 are in comparison with initial blood glucose levels of the mice (0 h) in the respective group. Figures in parenthesis indicate the percentage decrease. Values are mean ± S.E.M; n = 6.

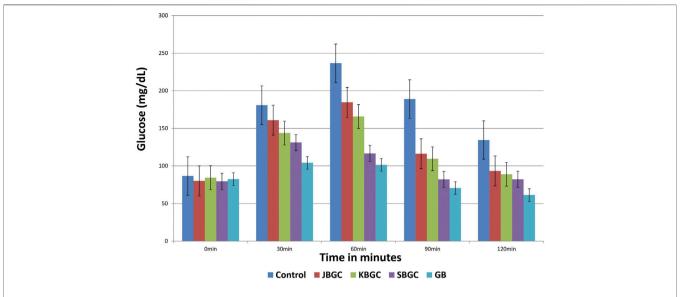
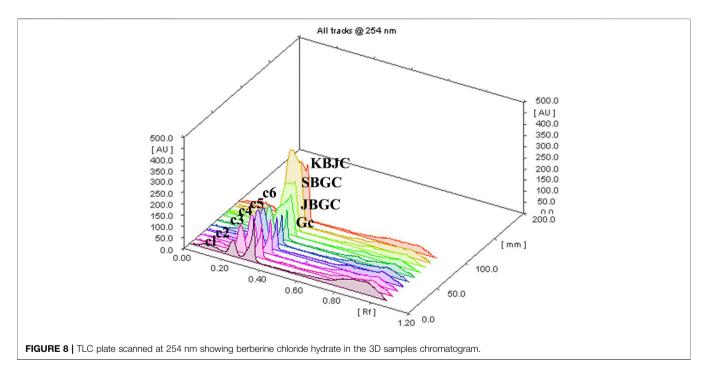


FIGURE 7 | Effect of Svarasa Bhavita Guduchi Churna (SBGC), Kwatha Bhavita Guduchi Churna (KBGC), and Jala Bhavita Guduchi Churna (JBGC) on BSL in glucose overloaded mice.



In view of the potential anti-diabetic importance of *Guduchi*, and promising results obtained in present study from *in-vitro* and *in-vivo* investigations, an attempt has been made to chromatographically quantify the berberine level in *Bhavita Guduchi* samples (SBGC, KBGC, and JBGC). The isoquinoline alkaloid 'berberine' has been tested and used successfully in experimental and human diabetes. It is reported to exhibit significant antioxidant and anti-hyperglycemic activity, inhibits FOXO 1 (Forkhead Box O1 Protein), which integrates insulin signaling with mitochondrial function, and activates AMPK (AMP-activated protein kinase), thus decreases

the levels of blood sugar, cholesterol and maintains the blood pressure (Sharma and Batra, 2013). Berberine salts are also reported as bioavailabity enhancer (Cui et al., 2019). On the flip side, isolation of another anti-diabetic compound Tinosporaside, an 18-norclerodane glucoside, is a tedious and more reductionist way to sample cleanup (Puratchimani and Jha, 2007), which would be a distoration of Ayurvedic holistic principle. In the present study, HPTLC method was developed for the determination of berberine chloride hydrate in *Guduchi* formulations, which showed the presence of berberine chloride hydrate in SBGC (32%) > KBGC (25.3%) > JBGC

TABLE 3 | The berberine chloride hydrate present in different codified samples.

Samples (coded methanolic extract)	Conc ⁿ prepared (mg/ml)	Spotting volume (μL)	Berberine chloride hydrate determined (ng/spot)	Extractive value (%)	% Marker in extract	% Of marker in raw powder (g)
GC	2.74	3	963.44	2.74	11.72	0.32
JBGC	2	4	2024.63	2	25.30	0.51
SBGC	4	2	2,563.14	4	32	1.28
KBGC	4.8	1.8	1,222.23	4.8	14.14	0.59

GC, Guduchi Churna; JBGC, Jala Bhavita Guduchi Churna; KBGC, Kwatha Bhavita Guduchi Churna; SBGC, Svarasa Bhavita Guduchi Churna; GB, Glibenclamide as standard control.

(14.14%) > GC (11.72%) respectively in increasing way. In HPTLC, increased berberine level in *Bhavita* samples (in comparison to GC) signifies the role of *Bhavana* in increasing the concentration of phytoconstituents. The obtained HPTLC results also corroborate with the findings of *in-vitro* and *in-vivo* experiments, wherein *Bhavita* samples exhibited better results than crude *Guduchi Churna*, and specifically SBGC showed better activity profile among all other samples. The increased berberine level after *Bhavana* could be having the role as bioavailability enhancer or imparting a supra-additive effect. Therefore further investigations are required to understand the kinetic chemistry of *Bhavana* in adding of myriad of bioactive phytoconstituents or active metabolites during wet grinding process and its possible role in improving the absorption and bioavailability of drugs.

In Ayurvedic classics, only *Svarasa* (extracted juice) dosage form of *Guduchi* is mentioned to be used for diabetes and in Ayurvedic pharmaceutics the *Svarasa* dosage form is said to be more potent than *Kwatha* (decoction) (Sharma et al., 2014b). Also, the *Svarasa* is extracted whole juice that may have more extractive principles of the plant, while decoction is only aqueous soluble extract of the botanical. However owing to very short shelf life of *Svarasa* (3 h) (Gupta et al., 2011), other dosage forms of *Guduchi* (viz. *Churna* or *Kwatha*) are popular among traditional practitioners. Thus better activity profile of SBGC in present *in-vitro* and *in-vivo* experiments validates and substantiate the Ayurvedic claims to use *Guduchi Svarasa* in diabetes; and to prepare the *Svarasa Bhavita* dosage form appears to be an effective way to preserve the properties of *Svarasa*. Hence further shelf-life studies are required for better understanding.

Present findings endorse the use of these formulations of *Guduchi* to manage glycemic levels in type 2 diabetes management. Further *invivo* antidiabetic as well as clinical studies are warranted to substantiate these findings. More extensive works are also needed to explore these formulations for their antioxidant, cytoprotective, and immunomodulatory roles in the management of other pathological metabolic cascades involved in diabetes.

CONCLUSION

In this study, better α -amylase, α -glucosidase inhibitory activities and significant anti-hyperglycemic effect of SBGC and KBGC ascertain definite role of *Bhavana* in augmentation of bioefficacy of drugs and suggest promising potential of these *Guduchi* formulations for the management of type 2 diabetes. This corroborate with findings of HPTLC study, wherein the percentage of anti-diabetic compound 'berberine' was found increased in *Bhavita* samples (maximum in

SBGC, followed by KBGC and JBGC). The obtained results provide new leads to researchers to investigate these formulations appropos their pharmacokinetic and pharmacodynamic mechanistic roles, bioactivities on other therapeutic parameters as well as at clinical levels. This traditional Ayurvedic pharmaceutical concept of *Bhavana* can be utilized further in invention of new chemical moieties in the field of drug discovery and development.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/Supplementary Material, further inquiries can be directed to the corresponding author.

ETHICS STATEMENT

The animal study was reviewed and approved by Institutional Animal Ethics Committee, Institute for Postgraduate Teaching and Research in Ayurveda, Gujarat Ayurved University, Jamnagar, Gujarat, India (IAEC Approval number: IAEC/13/2013/01/PhD).

AUTHOR CONTRIBUTIONS

RS, GR and PP designed the study protocol. RS performed the Pharmaceutical study. RS and JM performed the experiments and analyzed the data. RS and RB wrote the manuscript. GR and PP contributed to the critical reading and revision of the manuscript. All authors contributed to the article and approved the submitted version.

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Metabolite Profiling of the Indian Food Spice Lichen, *Pseudevernia furfuracea* Combined With Optimised Extraction Methodology to Obtain Bioactive Phenolic Compounds

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Pseudevernia furfuracea (L.) Zopf (Parmeliaceae) is a well-known epiphytic lichen commonly used in Indian spice mixtures and food preparations such as curries. This study is an attempt to find the best extraction methodology with respect to extractive yield, total polyphenolic content (TPC), total flavonoid content and antioxidant activities of lichen P. furfuracea. Two phenolic compounds, atraric acid and olivetoric acid were isolated and quantified in their respective extracts with the aid of reverse phase high performance liquid chromatography (RP-HPLC). The highest concentration of both the compounds, atraric acid (4.89 mg/g DW) and olivetoric acid (11.46 mg/g DW) were found in 70% methanol extract. A direct correlation was also observed between the concentrations of these compounds with the free radical scavenging potential of the extracts which might contribute towards the antioxidant potential of the extract. Moreover, scanning electron microscopy and HPLC analysis which was used to study the effect of pre-processing on extraction process highlighted the capacity of a mixer grinder technique for improved separation of surface localized metabolites and enrichment of the fraction. An investigation of the chemical profile of the bioactive extract 70% methanol extract using UHPLC-DAD-MS lead to tentative identification of forty nine compounds. This extract was also assessed towards HEK 293T cell line for cytotoxicity analysis. Concentration range of 0.156 to 100 µg/ml of PF70M extract exhibited no significant cell death as compared to control. Further, the active extract showed protective effect against hydroxyl radical's destructive effects on DNA when assessed using DNA nicking assay. Based upon this, it can be concluded that optimization of extraction solvent, sample pre-proceesing and extraction techniques can be useful in extraction of specific antioxidant metabolites.

Keywords: lichen, antioxidants, atraric acid, olivetoric acid, UHPLC-MS, metabolomics profiling, *Pseudevernia furfuracea*, spatial localization

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INTRODUCTION

Bioactive secondary metabolites of natural origin are extremely useful in food, pharmaceutical, agrochemical, nutraceutical and cosmeceutical industries due to their multifaceted biological activities such as antioxidant, antimicrobial, anticancer and antifungal (Goel et al., 2011; Sisodia et al., 2013; Goel et al., 2014; Newman and Cragg, 2016; Goel et al., 2020). Related to this, natural product derived antioxidants have been shown to exhibit strong protective effects against a variety of chronic health problems by postponing the damage caused by oxidative stress (Liu 2003). Antioxidants and their associated benefits is currently a subject of intensive research due to an increase in lifestyle disorders associated with stress and in line with this some lichens have been explored for their antioxidant potential through the last decade (Manojlovic et al., 2012; Kosanic et al., 2013; Kosanić et al., 2014; Kumar et al., 2014; Zugic, 2016).

Lichens are the microbial association defined by a stable symbiotic relationship between a mycobiont (fungal partner) and a photobiont (photoautotrophic partner, usually a green alga or cyanobacterium) (Calcott et al., 2018). Traditionally, some of the lichens are consumed for their culinary qualities, and used for their preservative and medicinal properties (Upreti et al., 2005). Pseudevernia furfuracea is well-known foliose lichen, commercially used in the spice mixture, food preparation like curries and as preservative in food and herbal preparations (Güvenç et al., 2012; Kosanic et al., 2013; Aoussar et al., 2017). Despite a decade of study, the potential of lichens to yield novel unique metabolites have not been fully realised. However an increase in technological capacity has recently rekindled the attention of pharmaceutical industries and researchers to determine potential of lichens antioxidants (Crittenden, 1991; Nash, 1996). The ethnopharmacological importance and consumption of the lichens as a functional food has resulted in investigations focusing upon the discovery and identification of the naturally occurring compounds responsible for their bioactivity. Phenolic polyketides present in lichens have been reported to have strong antioxidant properties (Hidalgo et al., 1994; Odabasoglu et al., 2006). Moreover, it has been well documented that extraction procedures used to isolate these compounds are vital for determining extractive yield and total polyphenols and thus antioxidant potential of the extracts (Spigno and De Faveri, 2007; Ismail et al., 2019). Factors such as extraction solvents, sample processing techniques, particle size, extraction techniques have been shown to have an influence on extraction efficiency and subsequent bioactivity (Cacace and Mazza, 2003; Ng et al., 2012). Therefore, it was rationalized that the extraction procedure is an important prerequisite for the comprehensive exploration of the beneficial effects of the species.

This study is designed to determine the effect of different extraction solvents, different extraction techniques and different grinding methods on obtaining polyphenolic and flavonoid rich fractions and evaluation of their antioxidant potential from lichen. The purpose of the study was to find best extraction methodology with respect to extractive yield and antioxidant activities of obtained extracts in order to inform the food industry

at large. The main factors selected for their presumed influence on the extraction efficiency and antioxidant potential are polarity of solvent, grinding or processing method and extraction methods. Separation of the metabolites rich portion from the lichen matrix was afforded by a grinding method prior to the determination of spatial localization of metabolites responsible for bioactivity in sample. Moreover, two key metabolites were isolated and quantified in different extracts and was found to be directly correlated with the free radical scavenging potential. In order to fully understand the fundamental process which influences the sample processing techniques, scanning electron microscopy was used to identify the separated fractions obtained after grinding and residual components left after extraction process. Finally, UHPLC-DAD-MS was used to study the qualitative composition of active extract and as such this work forms a platform for the advancement of lichen based food in future products and to enable a better understanding of food research where lichen forms a part of the diet.

MATERIALS AND METHODS

Material

Lichen material was collected from a local vendor (Khari baoli, New Delhi, India) in November 2017. Khari baoli market is one of Asia's largest wholesale spice market selling all kinds of spice. Sample *Pseudevernia furfuracea* is being sold as a part of spice mixture (**Figure 1**). The sample was then washed in distilled water, dried at room temperature ($25 \pm 5^{\circ}$ C). The sample was identified by Prof. Prem Lal Uniyal and a voucher specimen (DUH 1401) was deposited in the herbarium of University of Delhi, Delhi, India.

Chemicals and Reagents

2,2-Diphenyl-1-picryhydrazyl (DPPH) radical, 2,2-azinobis (3ethylbenzothiazoline-6-sulphonic acid) (ABTS), Ciocalteu reagent, gallic acid, quercetin, aluminum chloride anhydrous, 2-thiobarbituric acid (TBA), deoxyribose, ethylenediaminetetraacetic acid (EDTA) disodium dihydrate, ascorbic acid, alamar blue and trolox were procured from Sigma-Aldrich (Sigma Aldrich India Pvt Ltd., Bangalore, India). Potassium persulphate and sodium bicarbonate were purchased from Sisco Research Laboratories Pvt. Ltd. (Maharashtra, India). Ferric chloride, hydrogen peroxide, orthophosphoric acid were purchased from Fischer Scientific (Mumbai India). All the solvents methanol, acetone, hexane, ethyl acetate, dichloromethane, and dimethyl sulphoxide were purchased from Merck Millipore (KGaA, Darmstadt, Germany). Chemicals and solvents used were of analytical and HPLC grade, respectively.

Grinding of the Lichen Samples

The raw sample was dried in an oven at 40°C before grinding and divided into two portions; the first portion of sample (200 g) was chopped with the help of scissors to get fine pieces. These fine pieces were then crushed with the help of pestle mortar and resulted into homogenised powder. Other portion of the raw



FIGURE 1 | Pseudevernia furfuracea as it is sold in the spice market khari baoli (New Delhi, India).

sample (50 g) was ground up with a mixer-grinder (Philips, HL-1606) at maximum rotation speed for 15 min. This process led to the separation of sample into two portions, cortex powder and medulla pieces. Both the fractions were analysed and tested separately for their surface morphology, bioactive contents and bioactivity assays.

Extraction of Lichen Samples

Lichen sample was extracted using three variables parameters which include different extraction solvents, different grinding methods and different extraction methods. **Figure 2** explaining the complete experimental design for the preparation of different extracts gives a clear overview of all the different extraction.

To analyse the effect of different extraction solvent, direct extraction was done using hexane, ethyl acetate, acetone, methanol, 70% methanol, water. On the other hand, in case of sequential extraction, solvents of increasing polarity (hexane followed by dichloromethane, ethyl acetate, methanol and 50% methanol) were used in serial manner (**Figure 2**). To understand the effect of pre-processing on extraction process, differently grounded sample as mentioned above (*Grinding of the Lichen Samples*) were extracted separately using optimized solvent (70% methanol) and reflux method. All the extractions were done in triplicate using reflux apparatus at 60°C. Similarly, different extraction methods including maceration, sonication, reflux

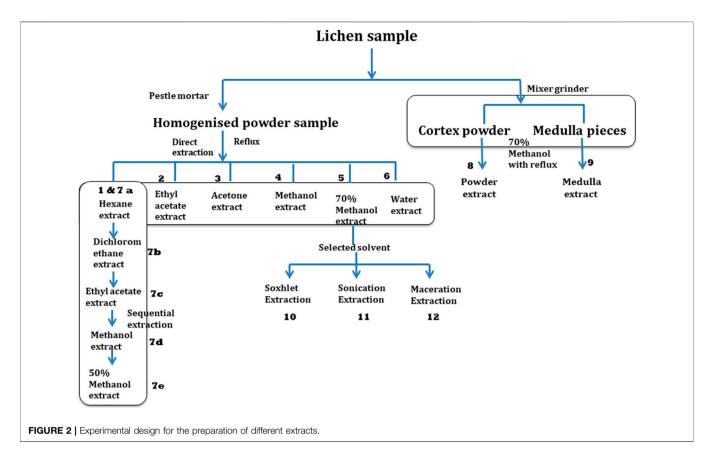
and soxhlet were used to access the effect of methodology on extraction yield and metabolic profiling.

Extraction yield in all the methods was calculated by following formula:

Total Yield (%) =
$$\left(\frac{\text{Total extract mass}}{\text{Mass of lichen}}\right) \times 100$$

Determination of Total Polyphenol and Total Flavonoid Contents

Total polyphenol content (TPC) and total flavonoid content (TFC) of the lichen extracts were measured using previously reported Folin-Ciocalteu's method (Singleton Vernon et al., 1999) and aluminum chloride method (Ordonez et al., 2006), respectively. The total polyphenol content of the extracts was expressed as mg of gallic acid equivalent (GAE)/g of dry lichen material on the basis of calibration curve of gallic acid (20–200 µg/ml; $R^2=0.99$). The total flavonoid content of the extracts was expressed as mg of quercetin equivalent (QE)/g of dry lichen material on the basis of calibration curve of quercetin (1–100 µg/ml; $R^2=0.99$). The absorbance for each methodology was determined using UV-Visible spectrophotometer-2450 (Shimadzu).



Evaluation of Free Radical Scavenging Potential

Free radical scavenging potential of the extract were evaluated by ABTS⁺ radical cation decolourisation assay, DPPH radical scavenging assay, hydroxyl radical scavenging potential using trolox as the standard.

ABTS Radical Scavenging Potential

The ABTS assay was performed in line with the previously described protocol by Re et al., with slight modification as follows (Re et al., 1999). The ABTS+ radical cation was prepared by mixing 7 mM ABTS aqueous solution with 2.45 mM potassium persulfate (final concentration) and allowing the mixture to stand in the dark at room temperature for 12-16 h before use. The working solution was prepared by diluting the stock solution with ethanol for an initial absorbance of about 0.70 ± 0.02 at 745 nm. Free radical scavenging potential was assessed by mixing different concentration (5-100 µg/ml) of sample and standard Trolox (1-20 μM; 0.25-5 μg/ml) with ABTS+ working standard to make a final volume of 1 ml. The decrease in absorbance was measured exactly after 6 min at 30°C. The half maximal inhibitory concentration (IC50) for test samples and Trolox was calculated by plotting the scavenging capacity against the concentration. The results were expressed as Trolox Equivalent Antioxidant Capacity (TEAC) µM Trolox/g DW.

1, 1-Diphenyl-2-picrylhydrazyl Radical-Scavenging Potential

Free radical scavenging potential of the samples was tested using a previously developed DPPH radical-scavenging protocol (Brand-Williams et al., 1995). The 0.2 mM solution of DPPH was prepared in 70% methanol and stirred overnight in the dark at room temperature before use. Free radical scavenging potential was assessed by mixing different concentration (10–300 µg/ml) of samples and standards Trolox (5–50 µM; 1.25–12.5 µg/ml) with DPPH solution to make a final volume of 1 ml. These samples were shaken well and kept in dark for 30 min at room temperature. The decrease in absorbance was measured (at room temperature) after 30 min at 517 nm. The results were expressed as Trolox Equivalent Antioxidant Capacity (TEAC) µM Trolox/g DW as mentioned above in ABTS assay.

Hydroxyl Radical Scavenging Potential

This assay was performed by previously described protocol described by Li (2013). Hydroxyl radical was generated by the Fenton reaction (Fe³+-ascorbate-EDTA-H²-Q² system). Samples (10–50 µg/ml) and standard Trolox (1–25 µM; 0.25–6.25 µg/ml) were mixed with 400 µL of phosphate buffer (0.2 M, pH 7.4) followed by 50 µl of deoxyribose (50 mM), 50 µl of Na²-EDTA (1 mM), 50 µl of FeCl³ (3.2 mM) and 50 µl of H²-Q² (50 mM). Addition of 50 µl of ascorbic acid (1.8 mM) initiates the reaction. Total volume of the reaction mixture was adjusted to 800 µl with buffer. The reaction mixture was incubated at 50°C for 20 min

followed by addition of 250 μ l of trichloroacetic acid (10%, w/w) for the termination of reaction. Chromogen was developed by addition of 150 μ l of TBA (5%, in 1.25% NaOH aqueous solution) and incubated at 105°C for 15 min. The mixture was cooled and absorbance was measured at 532 nm. The results were expressed as Trolox Equivalent Antioxidant Capacity (TEAC) μ M Trolox/g DW as mentioned above in ABTS assay.

Antioxidant Activity Using DNA Nicking Assay

Antioxidant activity of bioactive extract was also assessed by DNA damage protection assay. Analysis was performed using supercoiled pBSK plasmid DNA according to the method of Zhao et al. (2014) with slight modifications (Zhao et al., 2014). A mixture of plasmid DNA (0.5 μ g) and active extract PF70M in concentration range of 25–200 μ g/ml was incubated at room temperature for 10 min followed by addition of equal volume of Fenton's reagent (30 mM H₂O₂, 80 mM FeCl₃, and 50 mM ascorbic acid). Reaction mixtures were then allowed incubated for 30 min at 37°C. The DNA was examined on 1% agarose gel using ethidium bromide staining. Curcumin was found as positive control.

Isolation and Quantification of Metabolites by High Performance Liquid Chromatography

The isolation of metabolites was performed using column chromatography (CC) over silica gel (100–200#). The extracts was eluted using hexane/ethyl acetate (95:5 to 70:30, v/v) as eluent and yielded nine major fractions (A-I). Fraction B was further subjected to CC over silica gel (60–120#), using hexane/ethyl acetate (95:5 to 28:20, v/v) lead to isolation of pale yellow crystals (compound 1). Fractions F was subjected to preparative TLC and lead to isolation of pale yellow amorphous powder (compound 2). Both the isolated compounds were identified with the help of NMR and mass spectral analysis.

Chemical analysis of the lichen extracts was performed using a Waters HPLC system consisting of a 600 quaternary gradient pump with an online vacuum degasser, a 717 auto-sampler, and 2996 diode array detector. Separation of the compounds of interest was achieved using a reversed phase C₁₈Luna column (Phenomenex, Lorance, CA, United States, 150 mm × 4.6 mm, 5 μm) and a 10 μl injection volume. A five point calibration curve from standard solutions was prepared by 10 µl injections of 5-100 µg/ml. Commercial standards of lichen compounds were not available therefore abovementioned isolated compounds were used as standards for the quantification. An HPLC gradient was applied: A (0.8% orthophosphoric acid in water) and B (acetonitrile). The following gradient was used at a flow rate of 1 ml/min: initial, 100% A in 0-5 min; 100% B in 5-45 min, 100% A in 45-60 min. Presence of compounds in the extracts was confirmed by comparison of retention time and ultraviolet and visible (UV-Vis) absorption spectra (Chowdhary et al., 2019).

UHPLC-DAD-MS Analysis

A Thermo Scientific Dionex Ültimate 3000 UHPLC system hyphenated with a Thermo high resolution Q Exactive focus mass spectrometer (Thermo, Bremen, Germany) were used for analysis. Mass calibration for the Orbitrap[™] was performed once a week, in both negative and positive modes, to warrant a working mass accuracy lowers than or equal to 5 ppm. UHPLC and mass parameters were used as per previously described method for the analysis of lichen samples (Salgado et al., 2018). An HPLC gradient having eluent (A) 0.1% formic acid in water, eluent (B) 0.1% formic acid in acetonitrile was performed. The following gradient was used at a flow rate of 1 ml/min: 5% B in 0-5 min; 30% B in 5-10 min, 30% B in 15 min, 70% B in 20 min, 70% B in 25 min, 5% B in 35 min, 12 min for column equilibration before each injection. The injection volume was 10 μL. Analysis was performed on UHPLC C₁₈ column (Acclaim, 150 mm × 4.6 mm ID, 2.5 mm, Thermo Fisher Scientific, Bremen, Germany) operated at 25°C. The MS conditions were as follows: Spray voltage 2500 V (for ESI-); aux. gas unit flow rate 20; aux gas heater temperature 500°C; capillary temperature 400°C; sheath gas flow rate 75 units. Full scan range was set in negative mode with the resolving power of 70,000 FWHM (full width half maximum) at m/z 200. For the compounds of interest, a scan range of m/z 100–1000 was chosen; the automatic gain control (AGC) set at 3×10^6 and the injection time set to 200 ms. Scan-rate was set at 2 scans s⁻¹. A mixture of taurocholic acid sodium salt, buspyrone hydrochloride, and sodium dodecil sulfate (Sigma-Aldrich, Darmstadt, Germany), plus Ultramark 1621 (Alpha Aezar, Stevensville, MI, United States) dissolved in a mixture of acetic acid, acetonitrile, water and methanol, was used as calibration solution to ensure a working mass accuracy lower than or equal to 5 ppm. For confirmation purposes, a targeted MS/MS analysis was performed using the mass inclusion list, with a 30 s time window, with the Orbitrap spectrometer operating in negative mode at 17,500 FWHM (m/z 200). The AGC target was set to 2 × 10⁵, with the maximum injection time of 20 ms. The precursor ions were filtered by the quadrupole which operates at an isolation window of m/z 2. The fore vacuum, high vacuum and ultrahigh vacuum were maintained at approximately 2 mbar, from 105 and below 1010 mbar, respectively. Collision energy (HCD cell) was operated at 30 kv. Detection was based on calculated exact mass of target compounds, as shown in Table 3.

Cell Cytotoxicity/Viability Assay

The cytotoxicity for most bioactive extract (PF70M) extract was assessed toward HEK 293 T cell line using Alamar Blue (Resazurin), a cell metabolic activity reagent (Sigma) (Rampersad et al., 2012). The log phase cells were harvested and cell count was adjusted to $(1 \times 10^4/\text{well})$ in DMEM containing 10% fetal bovine serum (FBS) and incubated for 12 h under 5% CO_2 at 37°C in 96-well microplates. Next day, cells were incubated with varying concentrations of PF70M extract at 37°C for 24 h. Following this, 0.02% Alamar blue reagent was added and the cells were further incubated for 6–8 h under 5% CO_2 at 37°C. Fluorescence was measured with excitation wavelength at 545 nm and emission wavelength at 590 nm in Elisa plate reader (Power Wave HT Microplate Spectrophotometer–BioTek).

TABLE 1 | Extraction yield, total phenolics and antioxidant potential of P. furfuracea using different extraction solvents, grinding method and extraction method.

Experiment number	Extraction solvent/method/grinding technique	Extractive yield ±SE (wt%)	TPC ^a (mg GAE/ g DW)	TFC ^b (mg QE/ g DW)	TEAC ^c (μM TROLOX/ g DW)	Atraric acid ^d (mg/ g DW)	Olivetoric acid ^d (mg/ g DW)
1 and 7a	Hexane/reflux/pestle mortar	1.38 ± 0.44	0.70 ± 0.10	0.02 ± 0.00	1.66 ± 0.00* 0.45 ± 0.01** 19.33 ± 0.21***	Nd	Nd
2	Acetone/reflux/pestle mortar	4.04 ± 0.32	5.92 ± 0.38	0.22 ± 0.04	6.91 ± 0.16* 5.33 ± 0.07**	0.63	1.95
3	Ethylacetate/reflux/pestle mortar	3.7 ± 0.44	9.80 ± 0.60	0.10 ± 0.00	99.12 ± 1.14*** 7.62 ± 0.04* 4.65 ± 0.06**	1.20	1.44
4	Methanol/reflux/pestle mortar	7.83 ± 0.68	21.43 ± 0.11	0.24 ± 0.00	64.77 ± 0.74*** 25.97 ± 0.69* 13.94 ± 0.26**	0.72	2.56
5	70% methanol/reflux/pestle mortar	9.81 ± 0.41	32.38 ± 0.29	0.38 ± 0.00	260.31 ± 7.60*** 38.30 ± 1.53* 19.10 ± 0.60**	2.41	11.46
6	Water/reflux/pestle mortar	9.55 ± 0.95	5.84 ± 0.10	0.16 ± 0.01	353.06 ± 9.58*** 5.22 ± 0.00* 3.02 ± 0.09**	0.08	Nd
7	0	45.40 . 0.04			80.30 ± 5.47***		
7 7b	Sequential extraction Dichloro methane/reflux/pestle mortar	15.19 ± 0.24 2.64 ± 0.27	5.39 ± 0.10	0.07 ± 0.00	$7.10 \pm 0.04^{*}$ $2.45 \pm 0.07^{**}$	0.15	0.42
7c	Ethyl acetate/reflux/pestle mortar	2.23 ± 0.26	5.88 ± 0.07	0.03 ± 0.00	42.03 ± 0.19*** 4.96 ± 0.15* 2.96 ± 0.03**	0.14	0.69
7d	Methanol/reflux/pestle mortar	4.9 ± 0.11	10.65 ± 0.11	0.06 ± 0.00	32.56 ± 0.79*** 13.39 ± 0.24* 4.81 ± 0.11**	0.97	3.39
7e	50% methanol/reflux/pestle mortar	4.28 ± 0.56	3.86 ± 0.08	0.11 ± 0.00	$75.08 \pm 1.42^{***}$ $6.12 \pm 0.02^{*}$ $2.40 \pm 0.05^{**}$	0.43	0.69
8	70% methanol/reflux/mixer grider (cortex powder portion)	8.92 ± 0.08	28.07 ± 0.16	0.35 ± 0.00	59.16 ± 1.00*** 23.90 ± 0.05* 14.06 ± 0.13**	2.61	6.69
9	70% methanol/reflux/mixer grider (medulla pieces)	5.25 ± 0.19	14.87 ± 0.03	0.11 ± 0.00	302.39 ± 6.40*** 15.26 ± 0.09* 6.52 ± 0.03**	1.01	6.49
10	70% methanol/soxhlet/pestle mortar	11.06 ± 0.26	41.73 ± 2.37	0.44 ± 0.00	99.32 ± 1.76*** 47.57 ± 0.16* 22.48 ± 0.04*	4.89	8.35
11	70% methanol/sonication/pestle mortar	6.72 ± 0.42	18.39 ± 0.48	0.14 ± 0.00	388.33 ± 3.31*** 20.16 ± 0.03* 7.38 ± 0.08**	4.04	6.03
12	70% methanol/maceration/pestle mortar	7.04 ± 0.30	17.54 ± 0.00	0.12 ± 0.00	$127.58 \pm 1.22^{***}$ $23.28 \pm 0.08^{*}$ $8.25 \pm 0.14^{**}$ $176.15 \pm 1.13^{***}$	0.21	6.83

^aData expressed as mg of gallic acid equivalent (GAE)/g of lichen dry material.

The percent difference between treated and un-treated cells was calculated by following formula:

$$\%Viability = \left(\frac{RFU \text{ of treated sample}}{RFU \text{ of untreated}}\right) \times 100$$

Where RFU stands for relative fluorescence unit.

Statistical Analysis

Results are expressed as mean of triplicate data \pm standard error and Pearson correlation between polyphenol contents, flavonoid content, atraric acid and olivetoric acid concentration and antioxidant potential was established by IBM SPSS statistical software.

^bData expressed as mg of quercetin equivalent (QE)/g of lichen dry material.

^cData expressed as µM of Trolox equivalent/g of lichen dry material (*) TEAC assayed by ABTS method, (**) TEAC assayed by DPPH method, (***) TEAC assayed by OH scavenging method.

^dAmount represented in μg/g of the dry lichen material, nd-peak not detected.

RESULTS AND DISCUSSION

Effect on Extractive Yield

Different Solvent Treatment

The percentage extractive yield obtained from the solvent treatments ranged from 1.38 ± 0.44 to $15.19 \pm 0.24\%$ and the full data can be viewed in Table 1. The maximum extractive yield was obtained in 70% methanol followed by water and methanol and the key driver behind the increased extraction efficiency with 70% methanol is principally due to extraction of wide range of compounds (polar to non-polar) present in Pseudevernia furfuracea. The optimum extraction yield observed from the successive extraction is likely due to the better mass transfer from the substrate, which is clearly visible in the scanning electron microscopy (SEM) image (Supplementary Figure S1). The residue (a dense layer of platelets like crystals) left after each extraction can be observed and these crystals were washed off successively after each extraction. These findings suggest better extraction efficiency from the substrate and thus the driver of the highest extractive vield in the successive extraction (Supplementary Figure S1). Nevertheless, taking consideration, other factors such as time, resources required and nature of metabolites directed toward bioactivity, 70% methanol was found to be the most appropriate solvent for the efficient and rapid extraction of bioactive phenolic constituents.

Different Grinding Techniques

As lichen metabolites are not homogeneously distributed in the sample matrix, different types of grinding methods or sample processing technique may influence extraction yield, TPC, metabolites concentration and subsequently the antioxidant potential of extract. To understand this effect, two different grinding methods, a pestle mortar and a mixer grinder were assessed. Samples crushed in mortar pestle resulted in a homogenised powder and was considered as a whole thallus sample for extraction, represented in experiment 5 (Figure 2) affording the extraction yield of 9.81 \pm 0.41%. Whereas the total extractive yield obtained from the mixer grinder method (14.17 \pm 0.19%) which is the sum total of extractive yield of cortex powder sample (8.92 \pm 0.08%) and medulla pieces (5.25 \pm 0.11%) is far more than the yield obtained from sample ground using mortar pestle which generated the homogenous powder.

Different Extraction Techniques

The extraction techniques chosen for their putative influence on extraction efficiency with a single optimized solvent were identified as soxhlet, reflux, sonication and maceration. With the optimum solvent (70% methanol), the extractive yield was found to be best with soxhlet extraction (11.03 \pm 0.26%), followed by reflux (9.81 \pm 0.41%), then maceration (7.04 \pm 0.30%) and finally sonication (6.72 \pm 0.42%). The higher yield obtained with the soxhlet extraction may be attributed to the application of warm solvent and exhaustive extraction with fresh solvent in every siphon.

Determination of Total Polyphenolic Content and Total Flavonoid Contents

The total polyphenolic content of the extracts prepared with solvents of different polarities, different extraction and grinding methods were determined from regression equation of calibration curve and expressed in gallic acid equivalents. In terms of solvent influence the 70% methanol extract led to the maximum TPC $(32.38 \pm 0.29 \text{ mg of GAE/g of dry lichen material})$ followed by methanol, ethyl acetate, acetone, water and hexane. These results indicate that polar solvents such as the water component of the 70% methanol and methanol assist in the extraction of polyphenolics due to the hydroxyl moieties on the phenols. With the sequential extraction the methanol extract showed maximum TPC, followed by ethvl dichloromethane, 50% methanol and finally hexane. The low amount of TPC achieved in the 50% extract might be attributed to extraction of major polyphenol beforehand by methanol in the

Importantly, processing of the sample with different grinding methods led to separation of fractions providing one fraction rich in total polyphenol and flavonoid content. The sample ground with the mortar and pestle gave a uniform powder mixture (whole thallus) that produced a higher TPC content (32.38 \pm 0.29 mg of GAE/g of dry lichen material). On the other hand the sample ground in the mixer grinder gave two separate fractions; cortex powder having almost similar TPC content (28.06 \pm 0.16 mg of GAE/g of dry lichen material) as obtained in whole thallus sample and the medulla pieces providing lower TPC content (14.87 \pm 0.03 mg of GAE/g of dry lichen material).

In another set of experiments, comparison of extraction of total polyphenols with the optimized extraction solvent mixture (70% Methanol) was also carried out using four commonly used extraction techniques (soxhlet, reflux, sonication and maceration). **Table 1** shows the result of total polyphenol content obtained by four different extraction procedures. The results indicate that the maximum yield of total polyphenolics was achieved by soxhlet extraction followed by reflux, sonication and maceration. Exhaustive extraction of total polyphenols in soxhlet extracts is because of the repeated and continuous washing of the crude material and application of heat during extraction as compared to other extraction methods.

The total flavonoid content of the extracts prepared with solvents of different polarities, different grinding and extraction methods were determined from the regression equation of calibration curve obtained from quercetin and expressed in quercetin equivalents. The different solvents exhibited substantial differences in the TFC as depicted in **Table 1**. The TFC ranged from 0.02 ± 0.00 mg of QE/g of dry lichen material for hexane to 0.38 ± 0.00 mg of QE/g of dry lichen material for 70% methanol extract. In case of sequential extraction, 50% methanol extract has maximum flavonoid content $(0.11 \pm 0.00$ mg QE/g) followed by dichloromethane, methanol and ethylacetate. The mixer grinder processing of samples led to an improved separation of fractions rich in flavonoids. The TFC content of the cortex powder fraction $(0.35 \pm 0.00$ mg QE/g) is almost equivalent to the whole

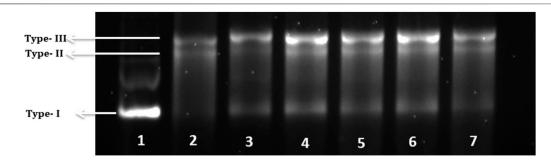


FIGURE 3 | DNA Nicking assay showing protective effect of PF70M extract against hydroxyl radical generated by Fenton's reagent. Lane 1: Native plasmid DNA pBSK without treated with Fenton's reagent; Lane 2: DNA treated with Fenton's reactant and 25 μg/ml Curcumin; Lane 4–7: DNA treated with Fenton's reactant and *Pseudevernia furfuracea* 70% methanol extract (200. 100. 50 and 25 μg/ml, respectively).

thallus sample (0.38 \pm 0.00 mg QE/g) whereas medulla pieces provided a lower TFC content (0.11 \pm 0.00 mg of QE/g of dry lichen material). When considering the different extraction methods the maximum TFC were afforded by soxhlet extraction (0.44 \pm 0.00 mg of QE/g of dry lichen material) followed by reflux, sonication and maceration.

Free Radical Scavenging Potential

To evaluate the free radical scavenging potential of different extracts, three types of assays were employed. The chemical composition of different extracts will have an influence depending on the test employed and therefore more than one assay was performed to get a thorough understanding of the extract's antioxidant potential. Antioxidant potential of the different samples were expressed as µM of Trolox equivalents per gram of dry lichen material as it is a more significant and descriptive expression. The results of antioxidant potential of different extract by ABTS, DPPH and OH scavenging assay are summarized in Table 1. Among the various solvents used, extracts obtained with 70% methanol exhibit higher antioxidant potential with highest TEAC value. With the different grinding techniques, the TPC, TFC and antioxidant potential obtained from cortex powder is comparable to the homogenised powder. Separation of surface metabolites in cortex powder portions provides an enriched fraction targeted to specific metabolites and also in terms of TPC, TFC and antioxidant potential. When comparing the different extraction methods, it was also observed that the extraction of the metabolites having maximum TPC, TFC and highest antioxidant potential was found via soxhlet extraction.

Antioxidant Potential

Lastly, a DNA nicking assay was used to understand the protective effect of specific extract against hydroxyl radical's destructive effects on DNA. Hydroxyl radicals generated using Fenton's reaction mixture resulted in degradation of supercoiled form of plasmid DNA (Lane 1, Type 1) into single stranded nicked and double stranded linear forms of DNA (Lane 2, Type II and III) (**Figure 3**). Results showed that presence of curcumin in $25\,\mu\text{g/ml}$ concentrations (Lane 3) protect the DNA in supercoiled form. Similarly, presence of PF70M extract at different

concentrations (200–25 μ g/ml, Lane 4–7, respectively) in the reaction mixture diminished the DNA damage. Thus, concentration-dependent intensification of native supercoiled DNA (Type 1) was observed.

Correlation of Antioxidant Potential With Total Polyphenolic Content and Total Flavonoid Content

The redox potential of the components such as polyphenols, phenolic acids and flavonoids is the determining factor for the antioxidant property of any food or herbal entity (Tembo et al., 2017). A statistical significant relationship was established between total polyphenol contents, total flavonoid content and TEAC values obtained from DPPH, ABTS and hydroxyl scavenging assays (**Table 2**). As a correlation between the TPC and antioxidant potential are marginally better when compared to the correlation between the TFC and antioxidant potential we suggest here that the phenolic compounds play a more significant role towards antioxidant potential than the flavonoids.

Spatial Localization of Metabolites Using High Performance Liquid Chromatography and Scanning Electron Microscopy Surface Morphology Using Scanning Electron Microscopy

As discussed earlier, samples ground in the mixer grinder lead to separation of fine powder (cortex) and coarser segments (medulla). These two portions were examined using SEM (EVO MA10, Carl Zeiss) to have a clear understanding of their surface morphology. This approach also helped to understand the spatial localization of some surface metabolites in sample. Microscopic observation of the two portions identifies some crystals like structure present on the surface (**Figure 4**). This result is consistent with the findings of Komaty et al., who have discussed the separation of cortex powder from medulla pieces and thus obtained atranorin localized on the cortex portion of *P. furfuracea* (Komaty et al., 2016).

TABLE 2 | Values of Pearson's correlation coefficients (r) for the TPC, TFC, TEAC (DPPH), TEAC (ABTS), TEAC (OH radical scavenging), Atraric acid and Olivetoric acid concentration

Correlations	TPC content (mg GAE/DW)	TFC content (mg QE/DW)	TEAC ABTS (uM Trolox/DW)	TEAC DPPH (uM Trolox/DW)	TEAC OH radical scavenging (uM Trolox/DW)	Atraric acid conc (mg/g DW)	Olivetoric acid conc (mg/g DW)
TPC content (mg GAE/DW)	1	0.874**	0.979**	0.979**	0.962**	0.873**	0.867**
TFC content (mg QE/DW)	0.874**	1	0.842**	0.920**	0.936**	0.846**	0.701**
TEAC ABTS (µM Trolox/DW)	0.979**	0.842**	1	0.972**	0.950**	0.824**	0.870**
TEAC DPPH (μM Trolox/DW)	0.979**	0.920**	0.972**	1	0.986**	0.863**	0.819**
TEAC OH radical scavenging (µM Trolox/DW)	0.962**	0.936**	0.950**	0.986**	1	0.827**	0.808**
Atraric acid conc (mg/g ^a W)	0.873**	0.846**	0.824**	0.863**	0.827**	1	0.672**
Olivetoric acid conc (mg/g DW)	0.867**	0.701**	0.870**	0.819**	0.808**	0.672**	1

^{**}Correlation is significant at the 0.01 level (2-tailed)

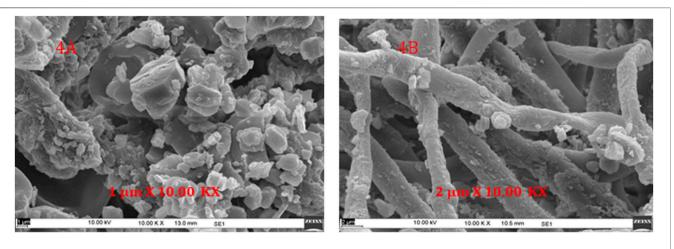


FIGURE 4 | Spatial localization of metabolites using SEM, Scanning electron microscope images of sample after grinding employing mixer grinder (A) Cortex powder (B) Medulla pieces.

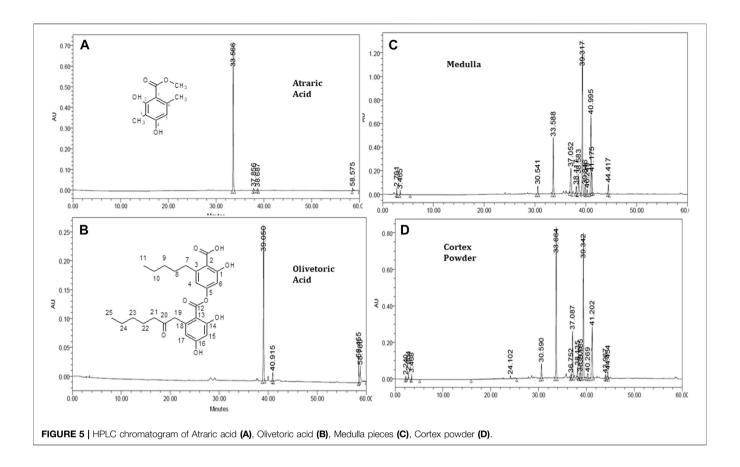
Determination of Atraric Acid and Olivetoric Acid by High Performance Liquid Chromatography

To further confirm this in our study, both of these portions were treated separately for extraction and identification of their respective metabolites. Characterisation of the some constituents in the extracts was performed with the two secondary metabodsllites that has been isolated namely atraric acid and olivetoric acid. These metabolites were characterized using NMR and mass spectroscopic data. Typical chromatograms of the standard compounds are shown in Figure 5. The calibration curves of atraric acid and olivetoric acid also showed good linearity ($R^2 = 0.9994$ and 0.9971, respectively). Quantification of these metabolites in all the extracts obtained using different extraction solvents, techniques and grinding methods was carried out using regression equation obtained from their calibration plots and results are presented in Table 1. In the case of different solvent extraction, the maximum concentration of both the compounds were found in the 70% methanol extract, matching the trend observed in total phenolic content study. With the different extraction methods,

the maximum concentration of atraric acid was achieved *via* soxhlet extraction and interestingly the concentration of olivetoric acid was higher in the reflux process. This highlights the importance of taking holistic approaches towards sample extract optimisation.

The concentrations of both the compounds were observed to be higher in the homogenised powder followed by the cortex powder and the medulla. A marginal difference of olivetoric acid was found between cortex powder and medulla pieces highlighting presence of olivetoric acid in both the portions equally and cannot be separated by this method. Interstingly the concentration of the atraric acid which has been reported as hydrolysis derivative of atranorin when come in contact with methanol or processed in the presence of methanol (Oettl et al., 2014) was found to be more concentrated in the powder compared to the cortex (**Figure 5**) thus highlighting the surface localization of atranorin and can be easily separated from the sample by simple pre-processing.

A good correlation was found between concentration of both compounds and TEAC obtained from ABTS, DPPH and OH



scavenging assay in all the three parameters (**Table 2**). These results indicate that these two metabolites might contribute strongly toward the antioxidant potential of this lichen.

Based on this information the importance of the lichen *Pseudevernia furfuracea* have been shown to have key metabolites that contribute strongly to the antioxidant profile of the food product. Lichens in general are underutilised in western food cuisine and this work shows that they may have an important place to in food products. In generally lichens have not been well studied in terms of their potential as a healthy food product and this highlights them as a viable avenue which could even lead to large scale production of them. For this to occur and for the successful application of them into food products it is clear that the way in which the sample is processed and if required the approach to biomolecule extraction is particularly important.

Identification Data (Nuclear Magnetic Resonance and Mass Spectra) of Compounds

Both the compounds were identified on the basis of nuclear magnetic resonance (NMR) data and high resolution mass spectrometry (HRMS) data reported previously.

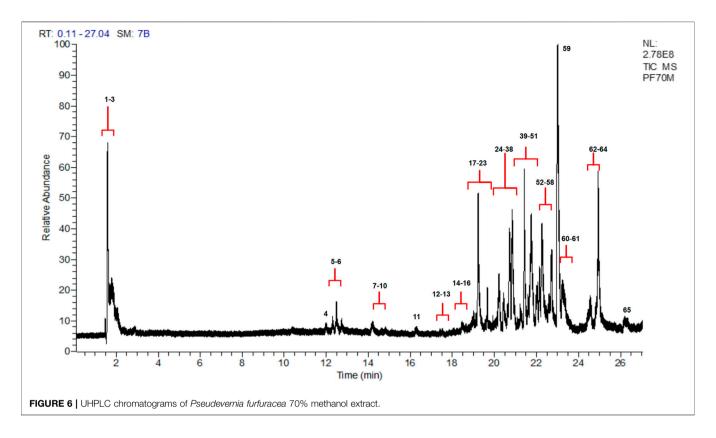
Atraric acid (1): Pale yellow crystal, $^1\text{H-NMR}$ (CDCl₃) δ : 2.16 (3H, s, 3-Me), 2.52 (3H, s, 6-Me), 3.95 (3H, s, -C=OOCH₃), 6.28 (1H, s, H-5), 12.40 (1H,s, 4-OH), 12.88 (1H, s, 2-OH); $^{13}\text{C-NMR}$ (CDCl₃) δ : 176.54 (-C=O), 166.74 (C-4), 164.06(C-2), 143.42(C-

6), 114.05(C-1), 112.45(C-3), 107.53(C-5), 54.56(C-OCH₃), 26.86(Me-C6), 10.48(Me-C3). (+)HRMS: 197.0807 [M + H]⁺. Obtained data was in good agreement with reported literature (Gormann et al., 2003).

Olivetoric acid (2): Pale yellow amorphous powder, $^1\text{H-NMR}$ (CDCl $_3$) δ : 0.93 (6H, t, 11-Me and 25-Me), 1.3 (8H, m, H-9,10, 23, 24), 1.5 (2H, dd, H-7), 2.4 (2H, t, H-21), 2.8 (2H, bs, H-19), 6.5 (4H, d, H-4,6,15,17),10.0 (1H,s, 16-OH), 10.5 (2H,s, 1-OH, 14-OH); $^{13}\text{C-NMR}$ (CDCl $_3$) δ : 163.21 (C-14), 162.69 (C-1), 158.39 (C-16), 142.06 (C-5), 132.72 (C-18), 104.13 (C-2), 103.02 (C-13), 100.92 (C-15), (+) HRMS: 473.54 [M + H] $^+$.

Composition of 70% Methanol Extract of Pseudevernia furfuracea Using UHPLC-DAD-MS

Electrospray Orbitrap is a rapid and state of art tool for the characterization of metabolites in various food and herbal commodity. Considering the metabolites profiling of 70% methanol extract, it has been subjected to UHPLC/ESI/MS/MS analysis to investigate the whole biochemical composition of stated extract. **Figure 6** shows the total ion current chromatograms (TIC) of 70% methanol extract and **Table 3** presented the list of all the compounds tentatively identified on the basis of their m/z of molecular ion [M-H]⁻ and respective mass information extracted through their MS and MS/MS spectra. Sixty five peaks were detected using UHPLC/ESI/MS/MS in the negative



mode. Of the forty nine compounds identified in this species the majority were depsides, depsidones, depsone, lipids, pulvinic acid derivative, diphenylether derivatives and dibenzofurans. Eight depsides moieties namely decarboxythamnolic acid, boninic acid, epiphorellic acid II, 4-O-methylolivetoric acid, dihydropicrolichenic acid, haemathamnolic acid isomer, squamatic acid and 2, 2' -di-O-methylanziaic acid, respectively were tentatively identified. Few of these compounds are in congruent with previous reported data (Torres-Benítez et al., 2017).

Along with depsides, eight depsidones moieties were identified namely menegazziaic acid (Salgado et al., 2018), loxodellonic acid, 3-hydroxyphysodic acid, methylphysodic acid (Le Pogam et al., 2015), physodic acid, acido-nor-8'-metilconstictico, physodic acid isomer and derivative physodic acid, respectively. Two depsone moieties identified as picrolichenic acid isomer and picrolichenic acid, both having [M-H]⁻ ions at m/z 441.1920 were also detected.

Two dibenzofuran (DBF) corresponding to peak 9 and 55 were identified as methyl porphyrilate and haemophaein, respectively. Besides, DBF, two pulvinic acid derivative namely pulvinic acid and vulpininc acid corresponding peak 33 and 61 were also identified. β -Alectoronic acid and 2'-O-methylphysodone belongs to category of diphenyl ether has also been detected. Peak 37 was identified as loxodinol (diphenyl ether) (Torres-Benítez et al., 2017).

As is often the case with biological samples several components are not fully elucidated however the mass spectral information generated here forms the basis for their further investigation.

Cytotoxicity Assay

PF70M extracts were tested for their toxic effect on HEK 293T cells by *in vitro* viability test method using Alamar blue as described in methods. The data obtained was plotted as bar graph depicting the percent difference between treated and untreated cells to evaluate the level of cellular viability (**Figure 7**). The results showed that after treatment with varying concentrations $(0.156-100\,\mu\text{g/ml})$ of PF70M extracts there was no significant cell death as compared to control cells as shown in **Figure 7** suggesting its safe application to host cells.

Conclusion

The chemical composition of lichen extracts mainly depends upon the method used for the extraction of metabolites. Studying various extraction processes using different solvents, methods and pre-processing techniques, we have found that 70% methanol extract using soxhlet method and mixer grinder technique is the most efficient combination for the enrichment of powder fraction targeting specific metabolites. Extract obtained using this combination resulted in a fraction rich in polyphenolic and flavonoids compounds that accounted for the significant antioxidant potential. The findings of the present work suggest that this lichen used in the form of spice mixture has also potential antioxidant effect. Also the safety of the active extract could be proved with the cytotoxicity and DNA damage protection assays. The antioxidant potential of the detected metabolites obtained from profiling of the active extract should be further explored in suitable cell based and in vivo models. Also, detailed studies for elucidation of mechanism

TABLE 3 | Biochemical composition of 70% methanol extract by UHPLC-DAD-MS analysis the negative ion mode.

Peak	Tentative identification	Molecular formula	Retention time (min.)	Theoretical mass (m/z)	Measured mass (m/z)	Accuracy (ppm)	Metabolite type	MS ions (ppm)
1	Arabic acid	C ₅ H ₉ O ₆	1.59	165.0399	165.0401	-1.2	Acid	147.0294; 113.0237; 129.0187
2	Atraric acid ^a	C ₆ H ₁₁ O ₇	1.58	195.0505	195.0508	-1.5	Acid	165.0401
3	Glucosylglycolate	C ₈ H ₁₃ O ₈	1.67	237.0610	237.0619	-3.8	Acid	207.0511; 147.0296
4	Derivative 2,4-Diformyl-3,5-	C ₉ H ₇ O ₆	11.99	211.0243	211.0247	-1.9	A	179.0349; 167.0336;
7	dihydroxytoluene o	Ogi 17O6	11.33	211.0240	211.0241	-1.3	^	149.0239
	2,6-Diformyl-3,5-dihydroxytoluene							
5	Orsellinic acid	$C_8H_7O_4$	12.31	167.0344	167.0347	-1.8	Α	123.0445
6	2,4-Dicarboxy-3-hydroxy-5-	$C_{10}H_{9}O_{6}$	12.48	225.0399	225.0404	-2.2	Α	181.0504; 167.0345;
7	methoxytoluene Unknown	_	14.19	_	_	_	_	149.0240 371.1017 339.0755
								278.1034 141.0917 135.1196
8	9,10,12,13-Tetrahydroxyhexadecanoic acid	C ₁₆ H ₃₁ O ₆	14.26	319.2121	319.2128	-2.2	L	301.2022
9	Methyl porphyrilate	$C_{17}H_{11}O_7$	14.82	327.0505	327.0513	-2.4	DBF	283.0612; 181.0498
10	9,10,12,13,14-Pentahydroxytricosenoic acid	C ₂₃ H ₄₃ O ₇	15.18	431.3009	431.3015	-1.4	L	_
11	Hexahydroxytetracosanoic acid	$C_{24}H_{47}O_8$	16.27	463.3271	463.3277	-1.3	L	389.1244
12	9,10,12,13-tetrahydroxynonadecanoic acid	C ₁₉ H ₃₇ O ₆	17.55	361.2590	361.2598	-2.2	L	_
13	Menegazziaic acid	C ₁₈ H ₁₃ O ₉	17.87	373.0560	373.0567	-1.9	D	329.0671; 167.0344; 149.0240; 151.0398
14 15	Hexahydroxytetracosenoic acid 9,10,12,13,14-Pentahydroxytricosanoic	C ₂₄ H ₄₅ O ₈ C ₂₃ H ₄₅ O ₇	18.46 18.66	461.3114 433.3165	461.3121 433.3171	−1.5 −1.4	L L	417.2859; 375.5755 329.0671; 389.2546
16	acid 9,10,12,13-Tetrahydroxyeicosanoic acid	C ₂₀ H ₃₉ O ₆	18.95	375.2747	375.2754	-1.9	L	361.2609
17	Unknown	——————————————————————————————————————	19.01	_	_	— —	_	467.2780 413.2912 375.2755 135.0389 119.0173
18	9,10,12,13,14- Pentahydroxytetracosanoic acid	C ₂₄ H ₄₇ O ₇	19.13	447.3322	447.3328	-1.3	L	433.3170
19	Unknown	-	19.22	_	-	-	_	481.2937 445.3171 389.2911 181.3367 109.1143
20	Olivetonic acid, 2,4-Dihydroxy-6-(2'-oxo-n-heptyl)-benzoic acid	C ₁₄ H ₁₇ O ₅	19.65	265.1076	265.1083	-2.6	А	247.0972; 221.1182
21	Loxodellonic acid	C ₂₃ H ₂₃ O ₈	19.74	427.1393	427.1400	-1.6	D	235.0975; 385.0932; 343.0970; 249.0767; 195.0662
22	9,10,12,13-Tetrahydroxypentacosanoic acid	C ₂₄ H ₄₅ O ₇	19.88	445.3165	445.3173	-1.8	L	417.3225
23	Hexahydroxyhexacosanoic acid	$C_{26}H_{51}O_{8}$	19.93	491.3584	491.3589	-1.0	L	445.3173; 345.2437
24	9,10,12,13-tetrahydroxydocosanoic acid	$C_{22}H_{43}O_6$	20.04	403.3060	403.3068	-2.0	L	375.2755
25	Unknown	_	20.13	_	_	_	_	309.0983 265.1081 237.0767
								190.0540 103.0760
26	9,10,12,13-Tetrahydroxydocosanoic acid	C ₂₂ H ₄₃ O ₆	20.23	403.3060	403.3067	-1.7	L	387.3123
27	Unknown	-	20.25	-	_	_	_ (Cor	451.2832 403.3066 345.2437 110.2839 108.2998 tinued on following page)

TABLE 3 | (Continued) Biochemical composition of 70% methanol extract by UHPLC-DAD-MS analysis the negative ion mode.

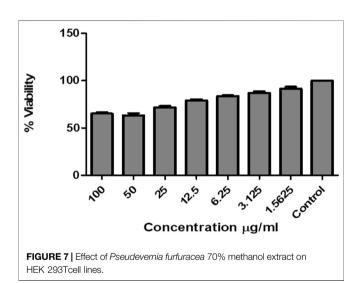
Peak	Tentative identification	Molecular formula	Retention time (min.)	Theoretical mass (m/z)	Measured mass (m/z)	Accuracy (ppm)	Metabolite type	MS ions (ppm)
28	9,10,11,12,13,14,15- Hexahydroxycosaenoic acid	C ₂₆ H ₄₉ O ₈	20.43	489.3427	489.3432	-1.0	L	429.3227
29	Decarboxythamnolic acid	C ₁₈ H ₁₅ O ₉	20.55	375.0716	375.0724	-2.1	d	167.0345; 209.0455
30	9,10,12,13,14	C ₂₆ H ₅₁ O ₇	20.66	475.3635	475.3641	-1.3	Ĺ	431.3376; 447.3331
00	Pentahydroxyhexacosanoic acid	026. 15107	20.00	0.0000			_	10110010, 11110001
31	Hexahydroxyoxooctacosenoic acid	C ₂₈ H ₅₃ O ₉	20.66	533.3690	533.3694	-0.7	L	475.3640
32	9,10,12,13-tetrahidroxytricosanoic acid	C ₂₃ H ₄₅ O ₆	20.72	417.3216	417.3224	-1.9	L	403.3067
33	Pulvinic acid	C ₁₈ H ₁₁ O ₅	20.80	307.0606	307.0615	-2.9	PAD	263.0715; 117.0342
34	Boninic acid	C ₂₅ H ₃₁ O ₈	20.85	459.2019	459.2026	-1.5	d	415.2128; 237.1130
		- 25 51 - 6						281.1033; 253.1078
								223.0974
35	Unknown	_	20.85	_	_	_	_	509.3247
								459.2026
								415.2129
								345.2437
								109.2090
36	Epiphorellic acid II	C ₂₆ H ₃₁ O ₉	20.92	487.1968	487.1974	-1.2	d	443.2076; 235.0977
								251.0930; 429.1917
37	Loxodinol	C ₂₅ H ₂₉ O ₉	20.98	473.1812	473.1819	-1.5	DE	429.1920; 237.0768
38	Unknown	_	20.98	_	_	_	_	263.0927
								243.0066
								221.0816
								209.0454
								104.0931
39	Olivetolcarboxylic acid	$C_{12}H_{15}O_4$	21.08	223.0970	223.0975	-2.2	Α	179.1074; 207.1027
40	4-O-Methylolivetoric acid	$C_{27}H_{33}O_8$	21.20	485.2175	485.2182	-1.4	d	441.2286; 279.1240
41	6-ethyl-6-n-pentylpentadecan- 4,5,7,8,15-pentol-15-acetate	$C_{24}H_{47}O_6$	21.20	431.3373	431.3381	-1.9	Aliphatic compounds	417.3233
42	Unknown	_	21.24	_	_	_		501.2130
	0							485.2180
								455.1588
								431.3380
								345.2438
43	9-Hydroxydocosapentaenoic acid	C ₂₂ H ₃₃ O ₃	21.32	345.2430	345.2439	-2.6	L	301.2536
44	Unknown	_	21.38	_	_	_	_	419.0988
								265.1083
								151.0396
								123.0446
								105.0337
45	Dihydropicrolichenic acid	$C_{25}H_{31}O_7$	21.42	443.2070	443.2077	-1.6	d	399.2177; 221.1184;
								151.0394
46	Haemathamnolic acid isomer	$C_{19}H_{15}O_{10}$	21.51	403.0665	403.0673	-2.0	d	371.0412; 209.0455;
								359.0778
47	Unknown	_	21.61	_	_	_	_	468.2028
								443.2077
								210.1328
								144.2105
								122.3307
48	Unknown	_	21.67	_	_	_	_	261.0770
								233.0817
								223.0975
								179.1075
10	O I hardway make man Proceedings	0 11 0	04.00	405 4010	405 46:5		5	151.0398
49 50	3-Hydroxyphysodic acid	C ₂₆ H ₂₉ O ₉	21.69	485.1812	485.1817	-1.0	D	441.1926; 247.0976
50	Acido-nor-8'-metilconstictico	C ₂₁ H ₁₉ O ₁₁	21.69	447.0927	447.0933	-1.3	D	209.0455; 403.1052
51	Squamatic acid	C ₁₉ H ₁₇ O ₉	21.74	389.0873	389.0880	-1.8	d	193.0140; 163.0396; 149.0239; 119.0497;
50	Mathylahyaadis asid	0 11 0	00.00	400 0010	400 0000	0.0	D	121.0289
52	Methylphysodic acid	C ₂₇ H ₃₁ O ₈	22.06	483.2019	483.2023	-0.8	D	453.0593; 345.2436
	Picrolichenic acid isomer	$C_{25}H_{29}O_7$	22.15	441.1913	441.1920	-1.6	Depsone	_
53 54	Dhyaadia aaid	\circ \circ	00 05	160 1000	160 1000	^ ^		105 1000, 017 0070
53 54	Physodic acid	$C_{26}H_{29}O_8$	22.25	469.1862	469.1866	-0.9	D	425.1969; 247.0973; 451.1762

TABLE 3 (Continued) Biochemical composition of 70% methanol extract by UHPLC-DAD-MS analysis the negative ion mode.

Peak	Tentative identification	Molecular formula	Retention time (min.)	Theoretical mass (m/z)	Measured mass (m/z)	Accuracy (ppm)	Metabolite type	MS ions (ppm)
55	Haemophaein	C ₂₇ H ₃₁ O ₇	22.42	467.2070	467.2076	-1.3	DBF	247.0975; 425.1970; 451.1762
56	β-Alectoronic acid	C ₂₈ H ₃₁ O ₉	22.60	511.1968	511.1971	-0.6	DE	369.1351; 247.0975; 263.0927; 467.2073
57	2,2'-Di-O-methylanziaic acid	C ₂₆ H ₃₃ O ₇	22.67	457.2226	457.2234	-1.7	d	265.1080; 413.2310; 427.2128; 443.2079
58	Physodic acid isomer	C ₂₆ H ₂₉ O ₈	22.73	469.1862	469.1868	-1.3	D	247.0976; 425.1968
59	Derivative physodic acid	$C_{25}H_{29}O_6$	23.00	425.1964	425.1973	-2.1	D	381.2068; 177.0945
60	Unknown	_	23.23	_	_	_	_	423.0492
								395.0543
								409.0699
								163.0394
								119.0497
31	Vulpinic acid	$C_{19}H_{13}O_5$	23.49	321.0763	321.0771	-2.5	PAD	_
2	Picrolichenic acid	$C_{25}H_{29}O_7$	24.55	441.1913	441.1920	-1.6	Depsone	359.1863
3	9-Hydroxydocosapentaenoic acid isomer	$C_{22}H_{33}O_3$	24.69	345.2430	345.2438	-2.3	L	301.2538
64	2'-O-Methylphysodone	$C_{26}H_{31}O_{6}$	24.92	439.2121	439.2126	-1.1	DE	
35	Unknown	_	26.25	_	_	_	_	555.2851
								537.2493
								389.2700
								239.2504
								119.2575

^aIsolated, identified and quantifed.

Where A = Aromatic; L = Lipid; D = depsidone; d = depsido; DE = diphenylether; DBF = dibenzofuran; PAD = pulvinic acid derivative.



behind these activities can further contribute in the better utilization of this lichen.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation, to any qualified researcher.

AUTHOR CONTRIBUTIONS

RK contributed toward the excecution of the experiments, drafting and editing of the article. XC contributed in the language corrections and editions. CA helped in getting the UPLC-MS/MS (Metabolite profiling) analysis done. RD contributed in the cytotoxicity assay. MG contributed towards the Design of study, plan of experiments, guidance, critical revision, final edition and approval of the article.

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Polyphenolic-Rich Compounds From Dillenia pentagyna (Roxb.) Attenuates the Doxorubicin-Induced Cardiotoxicity: A High-Frequency Ultrasonography Assisted Approach

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Cardiovascular complications are the foremost concern in patients undergoing anticancer therapy. There is an unmet need to address the problems arising from the drug-induced toxicity for the long-term benefit of the patients undergoing chemotherapy. Alternative medicines are gaining their prosperity in addressing the various drug-induced organ toxicity. Dillenia pentagyna Roxb (DP) is an ethnomedicinal plant rich in flavonoids and phenolic contents. In India & Nepal, DP is a common ingredient of traditional medicines used to treat multiple ailments like inflammation, cancer, and diabetes. However, its protective role against doxorubicin (Dox) induced cardiotoxicity remains unexplored. Herein, we investigated the potential effects of various extracts/fractions obtained from the DP's bark against Dox-induced cardiotoxicity, both in-vitro and in-vivo. The antioxidant content of the extracts/fractions was evaluated by using DPPH, ABTS and FRAP chemical assays. The results indicated that the hydroalcoholic (HA) extract of DP has intense anti-oxidant potential. Further fractionation of DP revealed that the phenolic-rich fraction (F1) has a high anti-oxidant potential. The protective effect of extract/fraction was also investigated in the H9c2 cell line following the Dox-induced cardiotoxicity model. We observed that the pre-treatment of extract/fraction in cardiomyocytes had exhibited increased cell viability. Fluorescence-based chemical assays indicated a decreased ROS levels in the treated groups in comparison to the Dox control group. The effect of DP was evaluated further in balb/c mice by the Dox-induced cardiotoxicity model. Non-

Abbreviations: DPPH, 2,2-diphenyl-1-picryl-hydrazyl; ABTS, 2,2'-azino-bis(3-ethylbenzo) thiazoline-6-sulfonic acid; TPC, Total phenolic acid; RIPA buffer; MTT, 3- (4,5-dimethylthiazol-2-yl) -2,5-diphenyl tetrazolium bromide; FRAP, ferric reducing antioxidant power; CM-H2DCFDA, chloromethyl derivative of 2', 7' -dichlorofluorescein (DCF); ROS, Reactive oxygen species; FACS, fluorescence-activated cell sorting; DMSO, dimethylsulfoxide; ESI, electronspray ionization; ATCC, American type culture collection; NCCS, National center for cell science; SOD-2, superoxide dismutase; Keap-1, Kelch-like ECH-associated protein 1; Nrf-2, nuclear factor erythroid 2-related factor 2; HO-1, hemeoxygenase; RSA, radical scavenging assay; BSA, bovine serum albumin; LCMS-QTOF, Liquid chromatograpy-quadrapole time of flight; HFUS- high frequency ultrasonography.

invasive techniques like high-frequency ultrasonography and electrocardiogram revealed that the mice pre-treated with DP had improved cardiac functionality (left ventricular ejection fraction and stroke volume) and normalized the electrocardiograms compared to the Dox control group. Further, biochemical analysis with the cardiac tissues revealed that the cytoprotective proteins like HO-1, SOD-2, and Nrf-2 were elevated in the DP treated groups compared to the Dox control group. Overall, our results suggested that the bioactive extract/fractions of DP helped alleviate the Dox-induced cardiotoxicity. LC-QTOF-ESI-MS analysis of DP and F1 indicated that polyphenolic anti-oxidant compounds like gallic acid, syringic acid, and sinapic acid could be responsible for the potent -cardioprotective effect. Future understanding of the pharmacokinetics and pharmacodynamic parameters can help translate from the bench to the bedside.

Keywords: doxorubicin, oxidative stress, cardioprotection, ultrasonography, dillenia pentagyna roxb

INTRODUCTION

Cancer is one of the significant public health concerns affecting nearly 18 million people, thereby leading to 9.6 million deaths worldwide (Bray et al., 2018). Current treatment strategies for cancer include targeted therapy (Ex: immunotherapy), photodynamic/thermal treatment, radiation, chemotherapy. Among them, chemotherapeutic drugs have shown a better prognosis in reducing the tumor burden and increasing cancer patients' overall life expectancy. Modern cancer therapies had increased the number of survivors. However, there is a surge in cardiac complications in patients undergoing various cancer therapies contributing to increased morbidity and mortality (Tan and Scherrer-Crosbie, 2014). Multiple drugs and therapies like Doxorubicin, Paclitaxel, monoclonal antibodies (Trastuzumab), and tyrosine kinase inhibitors (Imatinib), causes cardiotoxicity (Brown et al., 2015). Doxorubicin (Dox) is a widely used drug reported to induce oxidative stress-mediated necrosis in the cardiomyocytes (Xu et al., 2020). A single regime of Dox at a dose of 60-75 mg/m² for every three weeks is being used in the clinical application (Rugo et al., 2016). Increased dosage of Dox leads to its accumulation in cardiolipin (a phospholipid located in the inner mitochondrial membrane) of cardiomyocytes leading to the disruption of the electron transport chain, ultimately leading to the generation of ROS (Huang et al., 2015). Reports indicated that the Dox also reduces the functional capacity of the Nrf-2 gene, which is a critical regulator of the redox system (Wang et al., 2019). This affects the reduction of anti-oxidant enzymes like glutathione (GSH), and catalase (Peoples et al., 2019). Few Nrf-2 activators have been developed (Cuadrado et al., 2019); however, limitations like interference with drug's oncologic efficacy and low bioavailability had hindered their complete translation. Therefore, creating safe and highly effective therapeutics to mitigate the toxicity associated with the chemotherapeutic drugs will benefit cancer patients.

Plants are considered a vast source of natural anti-oxidants from ancient times. Many such sources have even become part of our dietary lifestyle due to polyphenols, vitamins, mineral content. They have high nutritional value and therefore gained importance in drug discovery over time. *Dillenia pentagyna* Roxb (DP) belongs to the family Dilleniaceae, commonly known as Nepali elephant apple, is a highly valued medicinal plant distributed in Asian countries. Fruits of it are edible and are cooked as a dish by the tribal people of North-East and central parts of India. The plant's bark and fruits have been traditionally used for treating inflammatory diseases, chest pain, and cancer (Sharma et al., 2001). The plant's seed and bark are also used against cancer by the Koch-Rajbanshi tribes of northeastern states in India (Yadav and Srivastava, 2014). Fruits of the plant possess flavonoid glycosides like naringenin 7-galactosyl and dihedral quercetin 5- galactoside (Saiful Yazan and Armania, 2014).

Preliminary *in-vitro* studies on the bark showed anti-oxidant content due to the presence of lupeol, betulin, and betulinic acids. Despite the therapeutic properties, the plant or its parts were not scientifically explored for beneficial effects in managing druginduced oxidative stress-mediated diseases/toxicity. In this regard, the current study intends to evaluate *Dillenia pentagyna* Roxb (DP) extract/purified fractions ameliorative effect against Dox-induced cardiotoxicity in both *in-vitro* and *in-vivo* studies. High-frequency ultrasonography assisted real-time monitoring of cardiac functional parameters was attempted. To the best of our knowledge, we are the first to understand the potential of DP against Dox-induced cardiotoxicity using high-frequency ultrasonography (HFUS).

MATERIALS AND METHODS

Chemicals

Doxorubicin (Dox), DPPH, ABTS, NBT, DTNB, and Lactate dehydrogenase (LDH) assay kit were purchased from Sigma Chemicals (St. Louis, MO, United States). Ascorbic acid was purchased from Hi-media. Creatine Kinase-MB (CK-MB) was procured from Accurex (Mumbai, India). Normal goat serum, Alexa Flour 488 goat anti-rabbit, and Hoescht's 33,258 were procured from Invitrogen. All primary (Nrf-2, SOD-2, Keap-1, and HO-1) and secondary antibodies used in this study were obtained from Cell Signalling Technology (Beverly, Massachusetts United States). LC-MS grade water and

acetonitrile were purchased from M/s JT Baker, United States. Ammonium acetate and formic acid were brought from M/s Sigma Aldrich, United States. All the chemicals were used as such without any modification and derivatization.

Cell Lines and Maintenance

Rat cardiomyocytes (H9c2 cell line) were procured from NCCS, Pune and colon cancer cell line (HCT-116) was procured from ATCC, United States. The cells were cultured in DMEM, and RPMI medium respectively enriched with fetal bovine serum (10% v/v), L-Glutamine (1%), and anti-anti (antibiotic and antimycotic) (100°U/ml) and was maintained at 37°C in a humidified air containing 5% $\rm CO_2$ in a sterile condition.

Animals

25–30°g male Balb/c mice were used to evaluate the bioactive DP's cardio-protective activity (hydro-alcoholic). Animals were procured from Palamur Biosciences (Hyderabad, India). All experiments were performed by following the Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA), India. The study was approved by the Institutional Animal Ethics Committee (IAEC), Guwahati, India (NIPS/NIPER/18/029). The animals have been housed in individually ventilated cages (IVC) under standard conditions (temperature $23 \pm 1^{\circ}$ C, 12 h light/dark cycle). Acute oral toxicity study was performed for the maximum dose of 2000 mg/kg for seven days as per Organization for Economic Co-operation and Development (OECD) guidelines.

Plant Material Collection

The bark of *Dillenia pentagyna* Roxb. was collected from Auxiguri village, Baksa district (91° 20.47′ E and 26° 39.49′ N), Assam in the month of April. The plant was authenticated from Bodoland University Herbarium, Kokrajhar, with accession number (BUH 0000142).

Preparation of Bioactive Extract

Bark was shade dried at room temperature and pulverized into fine powder through a grinding mill (MF 10 B S000, IKA, Germany). The fine powder was extracted with successive solvents with low polarity to high polarity index. The powder was first defatted with the hexane and macerated twice with each solvent for 24 h in an incubator shaker. The solvents were followed as chloroform (CH), ethyl acetate (EA), ethanol (EOH), and hydro-alcohol (HA) (1:1). The extracts were filtered using Whatman filter paper Grade-1 and subjected to dryness using a rotary evaporator (IKA RV 10, Germany).

IN-VITRO ANTI-OXIDANT ASSAYS

All the extracts were tested for preliminary anti-oxidant potential by using the following assays.

DPPH Radical Scavenging Assay

All the extracts and fractions of DP were tested for their free radical scavenging properties using a Spectramax I3X (Molecular

Devices, United States). 20 μ l aliquot of different concentrations of the extracts, fractions (1,000, 500, 250, 125, 62.5 and 31.25 μ g/ml) and the respective standard (Ascorbic acid 200, 100, 50, 25 and 12.5 μ g/ml) were added to 200 μ l of DPPH in methanol (0.2 mM). After 20 min of incubation, the absorbance of each solution was read at 517 nm. Results were expressed in percentage free radical scavenging activity (% RSA) with reference to ascorbic acid (Sridhar and Charles, 2019), and IC₅₀ values were calculated.

ABTS Radical Scavenging Assay

All the extracts and fractions of DP were tested to scavenge the cation radicals. To 20 μl of various concentrations of the test samples (1,000, 500, 250, 125, 62.5 and 31.25 $\mu g/m l$) or standard 200, 100, 50, 25 and 12.5 $\mu g/m l$), 200 μL of ABTS solution was added and incubated for 20 min. The resulting absorbance of these solutions was measured spectrophotometrically at 734 nm using Spectramax I3X. Analyses were done in percentage radical scavenging activity (% RSA). Ascorbic acid was employed as the reference standard (Abramovič et al., 2017), and IC50 values were calculated.

FRAP Assay

All the extracts and fractions of DP were tested for their ability to reduce Fe^{+3} to Fe^{+2} , which can be observed from light green to blue color at an absorbance of 700 nm. Ascorbic acid was used as a reference standard. 0.2 ml of each test sample of different dilutions (1,000, 500, 250, 125 and 62.5 $\mu g/ml)$ was added to 0.2 ml of PBS and 0.2 ml of 1% ferric chloride. The reaction was incubated for 20 min at 50 °C, and the reaction was stopped by adding 0.2 ml of 10% trichloroacetic acid, 0.5 ml of distilled water, and 0.2 ml of 0.1% ferric chloride. Absorbance was measured against a blank solution containing all the reagents except the test samples or standard. The value of FRAP was expressed in mg ascorbic acid equivalent (AAE)/Gram of extract (Müller et al., 2011).

Total Phenolic Content

Total phenolic content of all the extracts and fractions of DP were estimated by the Folin–Ciocalteu method. Bioactive fractions $100\,\mu l$ (1 mg/ml) and mixed thoroughly with 0.2 ml of Folin–Ciocalteu followed by adding 0.75 ml of sodium carbonate solution 75% (w/v) and incubated for 30 min and read at 765 nm. Results were expressed as mg of Gallic acid Equivalent (GA)/Gram of extract (Alizadeh Behbahani and Shahidi, 2019).

METHOD DEVELOPMENT FOR SEPARATION OF THE ACTIVE CONSTITUENTS

Flash Chromatography was used for the separation of active components. Solvent optimization was carried out initially using thin-layer chromatography (TLC) on Silica gel 60 F₂₅₄ (Merck, Germany) A range of solvents with different polarity indexes was used, and finally, methanol and water (9:1 ratio) was found to be optimal to separate maximum constituents. Later, the crude

extract was loaded onto the flash chromatography apparatus (Biotage Isolera one, Sweden), and the chemical components were eluted using the mobile gradient phase by reverse phase chromatography. The solvents used are methanol (A) and water (B) (A: B) 100–90% with a flow rate of 20 ml/min using a Sfar C18 30gD Duo 30um cartridge. Three fractions (named Fraction F1, F2, and F3) were collected and evaluated for *in-vitro* anti-oxidant potential, and further biological activity screening was performed.

In-vitro Cardioprotective Studies Cell Viability

Cells were seeded at the density of $1\times10^4/\text{well}$ and incubated for 12~h. Bioactive fractions were treated with different concentrations (6.25, 12.5, 25, and 50 µg/ml) for 24 h. MTT assay assessed cell viability followed by treatment with bioactive extract/fraction with or without Dox treatment. 0.5 mg/ml MTT was added to the cells and incubated for 4 h. DMSO was added to dissolve the insoluble formazan crystals and read the plate at 570 nm by Spectramax I3X (Van Meerloo et al., 2011).

Measurement of ROS and Superoxide Anion Radicals

Cells were plated 1×10^6 /well and pre-treated with bioactive fractions for 2 h, and Dox 40 μ M was given for 24 h. Cellular ROS generation was determined qualitatively by CM-H2DCFDA and evaluated using a fluorescence microscope (EVOS FL Auto two, Invitrogen). The fluorescein intensity was quantitatively assessed by a Flow cytometer (Life Technologies, Thermo fisher scientific, Singapore). Cellular Superoxide radical generation was defined by Mitosox red. H9c2 cells were subjected to the same treatment as ROS and superoxide radical was evaluated by a confocal microscope (Leica, Germany). Results were expressed as mean fluorescence intensity (MFI).

Bioactive Fraction/s and Dox on Cancer Cell Line

Cells were seeded at the density of 5×10^3 cells/well and incubated for 12 h. Bio-active fractions were treated with different concentrations 3.125.6.25, 12.5, 25 and 50 µg/ml for 24 h. Extracts were treated along with Dox (2.5 µM) for 24 h, and an MTT reagent was used to assess the cell viability. 0.5 mg/ml. MTT was added to the cells and incubated for 4 h. DMSO was added to dissolve the insoluble formazan crystals, and the plate was read at 570 nm by Spectramax I3X (Molecular Devices, United States of America).

In-vivo Studies

Experimental Design

Mice were divided into four groups, each group consisting of six animals. Group 1: Normal saline control. Group 2: disease control, received an intraperitoneal injection of Dox 2.5 mg/kg six times in two weeks. Group 3: Treated with the bioactive DP (100 mg/kg) per oral (p.o) daily once for fourteen days and an intraperitoneal injection of Dox 2.5 mg/kg six times in two weeks. Group 4: Given DP (200 mg/kg) (p.o) daily once for fourteen days and an i. p injection of Dox 2.5 mg/kg six times in two weeks of the study. Body weights of the mice were recorded at periodic

intervals during the study to evaluate the treatment's effect (Rugo et al., 2016).

Electrocardiographic Recording (ECG) and Analysis

The ECG was performed for different groups on day $14^{\rm th}$ (end of the experiment). Briefly, mice were anesthetized with 4% isoflurane and maintained anesthesia with 1--2% isoflurane and followed by insertion of electrodes through a needle in the right hind limb, right forelimb, left forelimb. The ECG was recorded for each mice and data was collected by AD Instrument, Australia. T wave elevation, p duration, and ST heights were analyzed using Lab Chart 8 software (AD Instrument, Australia) (Sheibani et al., 2020).

Analysis of the Cardiac Parameters by High-Frequency Ultrasonography Imaging

The animals underwent imaging to evaluate the cardiac functional parameters. The animals were anesthetized with 4% isoflurane in an anesthesia chamber and placed on a heating pad, and anesthesia was maintained using 1.5% isoflurane by a nasal mask throughout the experiment. Echocardiography was performed using a high-frequency (30 MHz) small animal imaging system (Vevo LAZR-X 3100, FUJIFILM Visual Sonics). The transducer used was MX400 with a mouse small cardiology application and the parasternal long-axis view (Gangrade et al., 2020; Tene et al., 2020). Cardiac functions like cardiac output, fractional shortening, and ejection fraction were calculated from B mode where left ventricular region of the heart was focused in a two-dimensional manner. Similarly, systolic volume, diastolic volume, left ventricular mass, left ventricular posterior wall thickness systolic (LVPW; s) left ventricular posterior wall thickness diastolic (LVPW; d) were measured for each animal from the M-mode image. Measurements were performed using digital image analysis software (Vevo Lab 3.1.1).

Assessment of Anti-Oxidant Enzymes

Serum was collected and stored at -20°C. CK-MB, LDH assays were measured with corresponding assay kits from Accurex and Sigma. Heart tissue was homogenized with Tissue lyser II (Qiagen, Germany) using 0.05M PBS pH 7.4 and centrifuged at 12,000 rpm at 4°C for 10 min, and the supernatant was collected and anti-oxidant parameters GSH (Owen and Butterfield, 2010), catalase, MDA was measured. Results were expressed per mg protein (Ohkawa et al., 1979).

Tissue Processing

The mice were sacrificed by cervical dislocation under mild anesthesia and the heart from each mice was collected. Organs were fixed and stored in neutral 10% formalin solution for 24 h. Tissues were dehydrated in grades of alcohol and embedded in paraffin blocks. Sections (5 μ m) were cut by using a microtome and placed on slides and stained with hematoxylin and eosin (H&E) staining. A light microscope analyzed the stained segments under 20x magnification (Koul et al., 2014).

Western Blot Analysis

The effect of DP in modulating the ROS mediated by the Dox induction was evaluated by western blot analysis of the homogenized H9c2 cells and heart tissue lysate. The cells and heart tissues were briefly collected and washed with ice-cold 1X PBS, followed by RIPA lysis buffer protein extraction (Battu et al., 2018). The supernatant was collected, and the protein concentration was determined by using the Bradford reagent at 595 nm. Equal protein concentrations were subjected to SDS-PAGE (10 and 12% Tris-Glycine gel) with a pre-stained protein molecular weight marker (Bio-Rad). The separated proteins were transferred to nitrocellulose membrane (Bio-rad) followed by blocking in 3% BSA (Hi-media) for 1 h at room temperature. Blocked membranes were incubated with the specific primary antibodies (Nrf-2, Keap-1, SOD-2, HO-1, a-tubulin, and β -actin) overnight at 4°C, washed three times with TBST followed by incubation with secondary antibody for 1 h at room temperature. Blots were developed by using Clarity substrate solution (Peroxide solution and enhancer solution (1:1) on a Chemiluminescence 17-200255 (Fusion F. Vilber 363) Lourmat) and densitometric analysis by ImageJ software (Bethesda, Maryland, United States).

LC-MS/MS Characterization

Hydroalcoholic extract of Dillenia pentagyna Roxb. and its fraction F1 was used for UHPLC-QTOF-ESI-MS analysis. Dried samples were mixed with methanol and water on an equal ratio (1:1). Samples were vortexed and sonicated for uniform mixing. Samples were filtered by a 0.22 µM syringe filter to remove the foreign article and to avoid cone choking during analysis. Plant metabolites identification was performed using UHPLC-QTOF (Agilent 1,290 Infinity II Binary pump, well plate autosampler, thermostatted column compartment, and Agilent 6545XT AdvanceBio QTOF LC/MS/MS. Agilent Poroshell 120 EC C18, 2.7 μ M, 2.1 \times 100 mm column was used in this study with 45°C. The autosampler temperature was kept at 6°C to avoid any degradation during the analysis. The mobile phase was used in gradient mode as A and B. A is composed of 95:5: Water: Acetonitrile with 0.1% formic acid and 10 mM Ammonium Acetate, and B is composed of 95:5 Acetonitrile: Water with 0.1% formic acid and 10 mM Ammonium Acetate. The flow rate was kept at 0.4 ml per minute. Mobile phase B was changed concerning time such as 0.00 min-2% B, 3 min-2%B, 15 min-95%B, 20 min-95%B, 20.1 min-2%B, 25 min-2% B, and the stop time was 25-min. QTOF MS was run in both positive and negative mode using the Agilent Jet stream option. Source conditions were composed of gas temperature-275°C, drying gas (nitrogen)-8 L per minute, nebulizer gas (nitrogen) -35psi, sheath gas temperature -300°C, sheath gas flow-11 L per minute. Fragmentation, capillary voltage, and nozzle voltage were set at 150, 3500, and 1000 V, respectively. The mass range was kept 100-1700 m/z with one spectrum per second acquisition rate time.

Statistics

Mean \pm SEM values were used for the expression of data unless mentioned otherwise. Statistical analyses of data were performed using the One Way ANOVA (GraphPad Software Inc., CA,

United States) followed by Tukey's post hoc test unless specified. Values of p < 0.05 were considered statistically significant.

RESULTS

Identification and Purification of the Anti-Oxidant Fractions

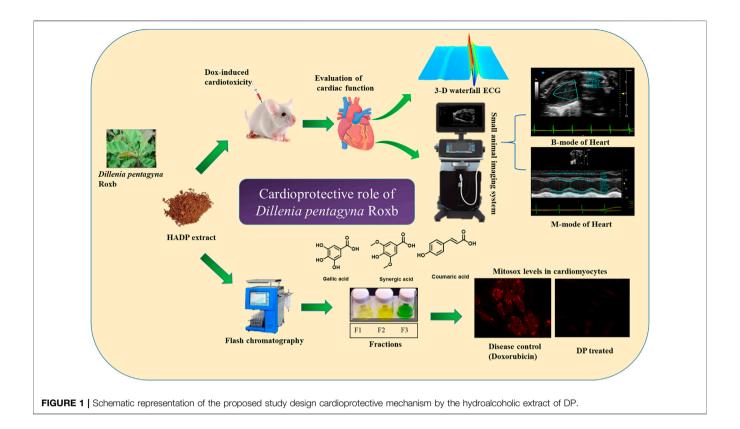
The bark powder obtained from the *Dillenia pentagyna* Roxb (DP) was subjected to polarity guided extraction and identified that the DP hydroalcoholic extract has a potent anti-oxidant property (**Supplementary Figure S1**). The generalized scheme of the study is depicted in the **Figure 1**. The DP hydroalcoholic extract was subjected to fractionation to obtain different fractions (F1, F2, and F3) (**Supplementary Figure S2**). Further analysis identified that fraction F1 has shown high anti-oxidant molecule content (DPPH, ABTS, and FRAP) compared to the respective control (DP), (**Figures 2A–C**). The total phenolic content analysis indicated that the bioactive DP and fraction F1 have high total phenolic content, as shown in **Figure 2D**.

Bioactive DP Hydroalcoholic Extract and Its Fraction F1 Alleviates the Dox-Induced Toxicity in Cardiomyocytes

Pre-treatment with the bioactive fractions (DP and F1) has shown no remarkable changes in the morphology of the H9c2 cardiomyocytes. The MTT assay result indicated that the cardiomyocytes treated with Dox exhibited $43.61 \pm 1.61\%$ of viability. In contrast, pre-treatment with the bioactive DP has alleviated the Dox's toxic effect in H9c2 cells in a dose-dependent manner. A similar protection effect was observed when the cardiomyocytes were treated with the fraction F1, as shown in **Figures 2E,F**, respectively, Maximum protection was observed at the higher concentration of the DP and F1 (12.5 μ g/ml). Meanwhile, bioactive extracts alone (without Dox) did not cause significant cytotoxicity (**Supplementary Figures S2A,B**).

Bioactive Fraction Attenuates the Dox-Induced ROS Production *In-vitro*

Dox causes cellular and mitochondrial damage by intracellular ROS generation. Hence, to evaluate the bioactive DP's role in modulating the cellular ROS generation, we have assessed the quantitative total cellular ROS level using a fluorescent dye DCFDA by FACS. Figure 3A represents the distribution of the DCFDA stained cell populations. As evidenced in Figure 3B, there is a right shift of the cell population in the Dox control group, indicating an overall increase in ROS level compared to the control group. When pre-treated with the bioactive DP and its fraction F1, the cardiomyocytes have shown ROS levels equivalent to the control group. The fluorescent microscope images also indicated a high fluorescence in the Dox group and basal amounts of intracellular ROS in the cardiomyocytes pre-treated with the bioactive DP and fraction F1, as shown in Figure 3C. The quantified bar graph represents their mean fluorescence



intensities (MFI) in **Figure 3D**. The Dox-treated group of cardiomyocytes has higher mean fluorescence intensity (MFI: 204 ± 2.0) than the control group (140 ± 9.0).

Whereas the pre-treatment with DP (12.5 μ g/ml) and F1 (12.5 μ g/ml) had significantly reduced the ROS levels (143.5 \pm 1.5 and 150 \pm 2.0, respectively). Mitochondrial superoxide was assessed using Mitosox red by a confocal microscope. The mean fluorescent intensity in Dox control remarkably increased compared with the control group, where pre-treatment with bioactive fractions attenuated the superoxide generation in mitochondria in **Figures 3E,F**. The results indicated that the cardiomyocytes, upon pre-treatment with the bioactive DP and its fraction F1 even after the induction with Dox, have successfully alleviated the increased ROS levels.

Bioactive Fraction Did Not Compromise the Anticancer Activity of Dox

Both the DP hydroalcoholic extract and fraction F1 were cotreated with Dox ($2.5\,\mu M$) in a cancer cell line (HCT116) to understand if they have any interference. We observed that the cancer cell death was similar in the groups treated with Dox alone and Dox combined with the DP hydroalcoholic extract and fraction (**Supplementary Figures S3C,D**). Overall, the results indicate that the DP hydroalcoholic extract and fraction F1 had not compromised the Dox anticancer property. However, considering the scalability, cost of production, and effort to green technology contribution, we have opted for the DP hydro alcoholic extract for the in-vivo studies.

In-vivo Cardioprotective Role of the Bioactive DP

Acute toxicity studies indicated that the bioactive DP was safe at a dose of 2000 mg/kg in mice, where no toxicity was observed for 14 days a single administration. Therefore, by following the OECD guidelines 425, we have chosen $1/20^{\rm th}$ (i.e., 100 mg/kg) and $1/10^{\rm th}$ (200 mg/kg) of the maximum tolerable dose for further studies.

Bioactive DP Hydroalcoholic Extract Attenuated the Myocardial Injury *In-vivo*

The cardioprotective effect of the bioactive fraction was evaluated in a Dox-induced cardiotoxicity mice model **4A**). Electrocardiogram measurements performed in the various groups to assess the impact of the bioactive DP. A significant decrease in the heart rate (bradycardia) was evidenced in the Dox treated group (394.3 ± 27.43) in comparison to the control mice $(499.04 \pm$ 40.49). However, the bioactive DP hydroalcoholic extract treated groups (382.7 \pm 59.4 & 447.04 \pm 74.7) have significantly improved heart rate than the Dox group. The heart rate of the DP hydroalcoholic extract-treated group was near to the control mice. In Figure 4B representative 3D and ECG images of T-wave elevation were observed in the Dox group. T-wave and ST height elevation was found in the disease control, where it was normalized in the treatment groups, as shown in Figures 4C-E.

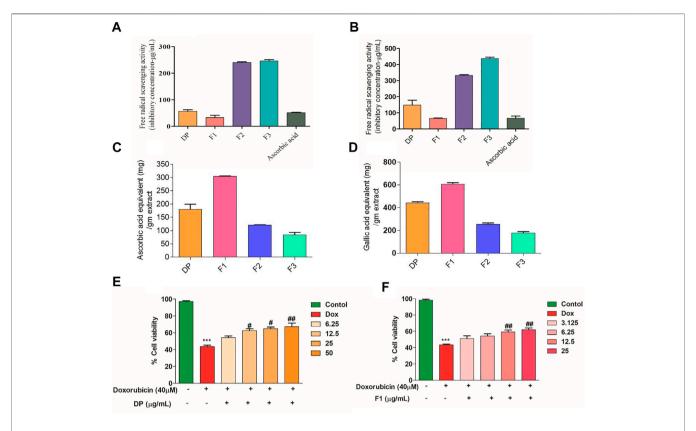


FIGURE 2 | IC_{50} values of the bioactive fractions in various antioxidant assays. **(A)** ABTS and **(B)** DPPH assay compared with ascorbic acid. **(C)** FRAP assay (equivalent ascorbic acid/gm extract) **(D)** Total phenolic content (Gallic acid equivalent/gm extract). **(E, F)** Cell viability of cardiomyocytes (H9c2) pre-treatment with DP and Fraction F1 along with Dox. Values were expressed as Mean \pm SEM (n = 3). The data were analyzed by One Way ANOVA using Graph Pad Prism. ***p < 0.001, and **p < 0.01 represents Control vs Dox control. *#*p < 0.01 and ***p < 0.001 represents Dox control vs Treatment groups.

Bioactive DP Hydroalcoholic Extract Alleviates Functional Heart Parameters

Figure 4F shows the representative M-mode images obtained from the parasternal long-axis view images by using a high-frequency ultrasonography-based electrocardiograph imaging system. The left ventricular (LV) posterior wall thickness, ejection fraction, fractional shortening, cardiac output, and stroke volume of the Dox treated group was decreased compared to the control group (Figures 4D-M). Simultaneously, the bioactive DP hydroalcoholic extract-treated groups have restored cardiac parameters and were found to be near the control group.

Bioactive DP Hydroalcoholic Extract Alleviates Functional Heart Parameters

The mice's body weights at the end of the study indicated that the disease control group had shown remarkably reduced body weights compared to the control group. The DP (100 and 200 mg/kg) pretreated groups had maintained the body weight to its initial values, as shown in **Figure 5A**. The heat index (HI), a ratio of heart weight to body weight, was lower in the Dox treated group when compared to the control group. The DP pre-treated group has values almost

near the normal saline group, as shown in **Figure 5B**. Further, key biomarker enzymes for tissue damage in the heart, i.e., Creatine Kinase isoenzyme-MB (CK-MB) and lactate dehydrogenase (LDH) levels were analyzed. The Dox alone treated mice group has shown an increase in both the enzymes' levels than the control group. This reveals that the Dox treated group elevated oxidative stress where lipid peroxidation causes tissue damage followed by enzymatic heart levels (LDH and CK-MB) increase.

Meanwhile, bioactive DP group mice have significantly reduced the levels compared to the control group, as shown in Figures 5C,D. This indicates the protective role of the bioactive DP in alleviating Dox-induced cardiac tissue damage. Also, the levels of anti-oxidant key regulators GSH and catalase were remarkably increased in the treatment groups, as shown in Figures 5E,F. The tissue MDA and nitric oxide (NO) levels were significantly elevated in the Dox treated groups compared to the control group. Bioactive DP treated groups have decreased the levels in a dose-dependent manner, as shown in Figures 5G,H. Histopathological study of the heart tissue in normal control mice exhibited apparent integrity of the myocardial cell membrane with no evident inflammatory cell infiltration, as shown in Figure 5I. The Dox treated mice group showed necrosis and filtration of the lymphocytes, macrophages, and inflammatory cells along with the vacuolization. In some of the myocytes, the myofibrils were disorganized and evident with clear

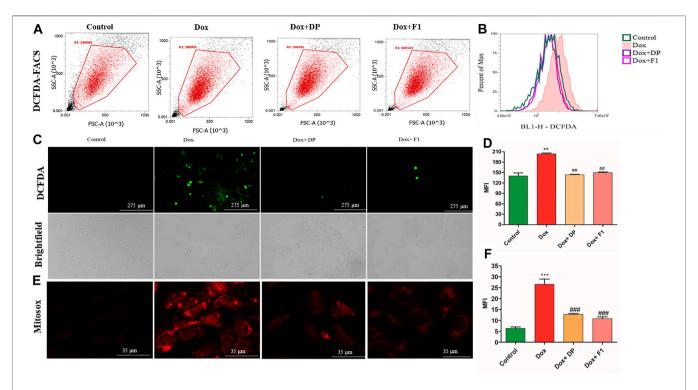


FIGURE 3 | *In-vitro* evaluation of the cardioprotective effect of the DP and fraction F1. **(A)** Quantitative analysis of ROS by DCFDA using flow cytometer. **(B)** Histogram overlay of DCFDA shift **(C)** Representative brightfield and fluorescent images of the DCFDA stained cells. **(D)** Mean fluorescence intensity of DCFDA. **(E)** Representative superoxide radical generation using Mitosox staining. **(F)** Quantitative measurement of mean fluorescence intensity (MFI) of Mitosox red. The data were analyzed by One Way ANOVA using Graph Pad Prism. ***p < 0.001, and **p < 0.01 represents Control vs Dox control. *#p < 0.01 and *#p < 0.001 represents Dox control vs Treatment groups (p = 3).

space, indicating intracellular edema. Pre-treatment of the bioactive DP (100 and 200 mg/kg) prevented the entry of the inflammatory cells and vacuole changes caused by the Dox treatment.

Bioactive Fractions Attenuate Dox-Induced Cardiotoxicity by Activating Nrf-2 Expression

Nrf-2, a key anti-oxidant transcription factor, plays a vital role in maintaining redox homeostasis under oxidative stress. **Figure 5J** showed treatment with DP alleviated the Dox-induced cardiotoxicity by activating the Nrf-2 expression where the subsequent downstream protein levels were increased *in-vitro*. We found that Keap-1 protein levels were decreased, and Nrf-2 levels were raised in the treatment group in a dose-dependent manner compared with Dox control *in-vivo* (**Figure 5K**). The quantitative analysis SOD-2 and HO-1 protein levels were increased in the treatment group compared with the Dox control group in both *in-vitro* and *in-vivo* shown in **Figures 5L,M**. Overall, results indicated that the bioactive fraction attenuated the Dox-induced cardiotoxicity by the Nrf-2 pathway.

LC-MS (LC-QTOF-ESI-MS) Analysis

Hydroalcoholic extract of DP and the fraction F1 were subjected to characterize the lead compounds responsible for the biological activity. Mass accuracy measurements were observed to be within

the limit of ±10 PPM. The obtained mass of the molecules/ metabolites present in the sample matches with the available literature, as shown in Tables 1-4. Chromatogram for the hydroalcoholic extract of DP and its fraction F1 have been portrayed in Figure 6A. The samples were screened for identification hits based on screening scores and the targeted identification of plant metabolites using a find-by-formula algorithm. However, it may be concluded that most of the molecules have been observed for the formate and acetate adduct form. Polyphenolic compounds gallic acid, benzoic acid, syringic acid, coumaric acid, protocatechuic aldehyde, mellein, 2hydroxy xanthone, sinapic acid are active chemical constituents in the hydroalcoholic extract and its fraction F1 as detected in the LC-QTOF-ESI-MS, negative mode (Tables 1, 3). However, coumaric acid, cinnamic acid, and umbelliferone are the common active chemical constituents in the hydroalcoholic extract and fraction F1 in the LC-QTOF-ESI-MS analysis in the positive mode, as portrayed in Tables 2, 4 and represented and the structures illustrated in Figure 6B. The proposed cardio protective mechanism of HC has been represented in the Figure 7.

DISCUSSION AND CONCLUSION

Recent progress in cancer therapy has increased patients' life expectancy and elevated the cardiac complications in them.

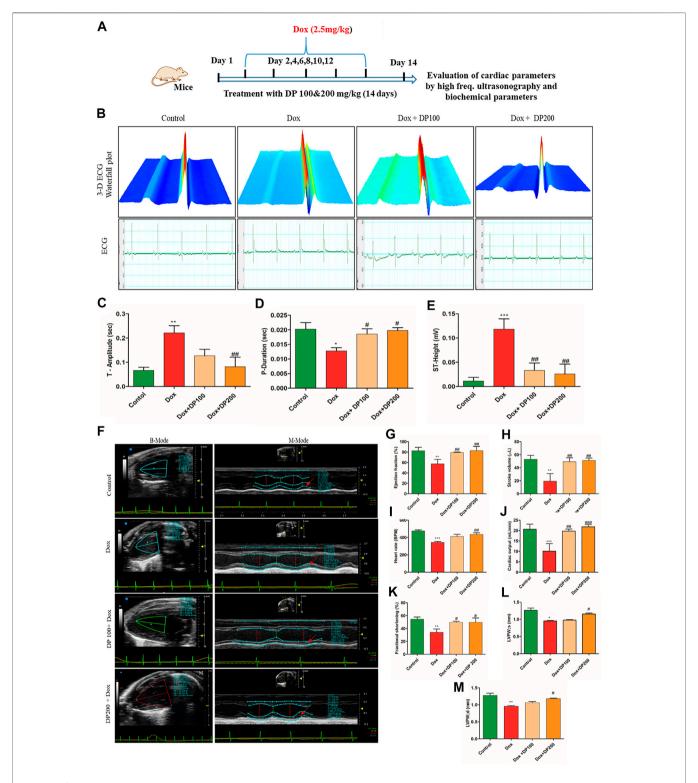


FIGURE 4 | Effect of DP extracts on the electrocardiogram. **(A)** Representative study design for cardioprotective model. **(B)** 3-D representative images of the electrocardiogram with elevated T-wave (I) Control (II) Dox control (III) Dox + DP100 and (IV) Dox + DP 200 **(C)** P-Duration **(D)** T- Amplitude **(E)** ST- Height, where n = 5. Effect of DP extract on *in-vivo* cardiac parameters by Vevo Lazer X 3100. **(F)** Representative images of M-Mode (I) control (III) Dox control (III) Dox + DP 100 and (IV) Dox + DP200. **(G)** Ejection fraction. **(H)** Stroke volume. **(I)** Heart rate. **(J)** Cardiac output **(K)** Fractional shortening **(L)** left ventricular posterior wall thickness (systole) **(M)** left ventricular posterior wall thickness (diastole), where n = 4. The data were analyzed by One Way ANOVA using Graph Pad Prism. ****p < 0.001, **p < 0.05 represents normal control vs disease control (Dox). **p < 0.05 **p < 0.01 and ***p < 0.001 represents disease control (Dox) vs treatment groups.

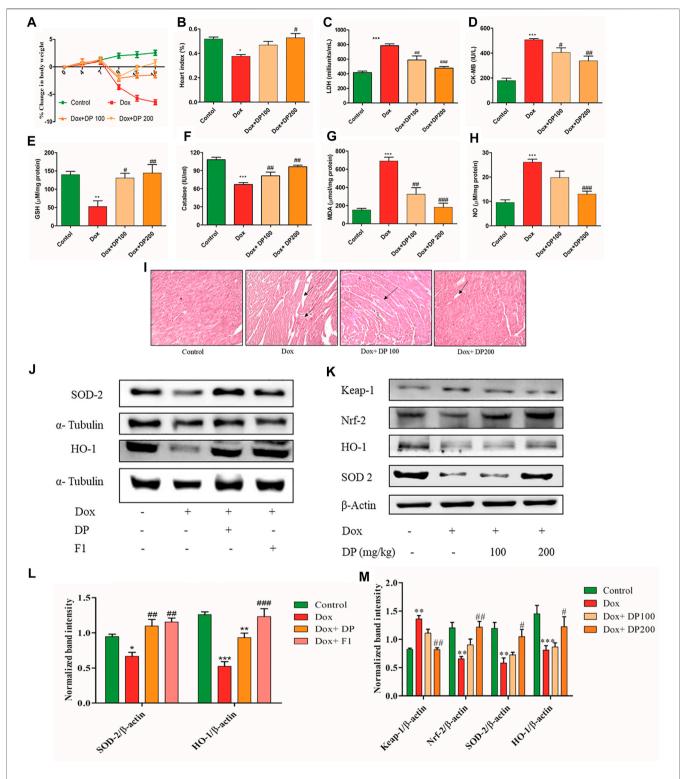


FIGURE 5 | Effect of DP extract on **(A)** percentage change in body weight **(B)** Heart index **(C)** LDH **(D)** CK-MB **(E)** GSH **(F)** catalase **(G)** MDA and **(H)** Nitric oxide, where n = 5. **(I)** Histopathology H&E staining of cardiac tissue. **(J)** ln-vitro western blot analysis of protein levels of SOD-2 and HO-1 in H9c2 cell line **(K)** ln-vivo western blot analysis of SOD-2, Keap-1, Nrf-2, and HO-1. **(L)** Quantitative analysis of relative protein levels of SOD-2 and HO-1. **(M)** Quantitative analysis of relative protein levels of KEAP-1, Nrf-2 SOD-2, and HO-1 expression respectively. The data were analyzed by One Way ANOVA and Two Way ANOVA using Graph Pad Prism. ***p < 0.001, **p < 0.001, **p < 0.005 represents normal control vs disease control (Dox). **p < 0.005 and **p < 0.001 represents disease control (Dox) vs treatment groups (p = 3).

TABLE 1 | QTOF-ESI-MS data of identified plant metabolites from hydroalcoholic extract of DP in negative mode [M-H]⁻ with the possible molecular formula.

S. No.	Retention time	Name	Molecular formula	Mean measured mass (Da) m/z	Mass (Da)	Diff (Tgt, ppm)	Reference
1	1.035	Gallic acid	C ₇ H ₆ O ₅	169.01	170.12	0.57	Uddin et al. (2020)
2	6.33	Benzoic acid	C ₇ H ₆ O ₂	167.03	122.12	3.47	Yang et al. (2018)
3	6.364	Syringic acid	C ₉ H ₁₀ O ₅	197.04	198.17	3.68	Ding et al. (2017)
4	6.081	Coumaric acid	C ₉ H ₈ O ₃	163.04	164.16	1.21	Rafiee et al. (2020)
5	6.364	Protocatechuic aldehyde	C ₇ H ₆ O ₃	197.04	138.12	5.28	Jiang et al. (2019)
6	5.914	Paeonol	C ₉ H ₁₀ O ₃	165.05	166.17	2.53	Ding et al. (2016)
7	6.447	Hesperetin	C ₁₆ H ₁₄ O ₆	347.07	302.27	6.71	
8	7.063	Mellein	C ₁₀ H ₁₀ O ₃	237.07	178.18	0.83	
9	6.214	Scopoletin	C ₁₀ H ₈ O ₄	237.04	192.16	4.86	
10	0.636	2-Hydroxyxanthone	C ₁₃ H ₈ O ₃	257.04	212.20	-3.27	
11	6.663	Herniarin	C ₁₀ H ₈ O ₃	235.06	176.16	3.61	
12	6.397	Sinapic acid	C ₁₁ H ₁₂ O ₅	223.06	224.21	1.95	Bin Jardan et al. (2020)
13	6.43	Naringenin	C ₁₅ H ₁₂ O ₅	317.06	272.26	5.75	

TABLE 2 | QTOF-ESI-MS data of identified plant metabolites from hydroalcoholic extract of DP in positive mode [M+H] + with possible molecular formula.

Peak no.	Retention time	Name	Molecular formula	Mean measured mass (Da) m/z	Mass (Da)	Diff (Tgt, ppm)	
1	21.107	Coumaric acid	C ₉ H ₈ O ₃	165.05	192.17	1.45	
2	0.995	Cinnamic acid	C ₉ H ₈ O ₂	149.05	148.16	2.38	
3	5.857	Herniarin	C ₁₀ H ₈ O ₃	177.05	176.16	-2.91	
4	16.279	Umbelliferone	C ₉ H ₆ O ₃	163.03	162.12	2.49	Luo et al. (2018)

TABLE 3 | QTOF-ESI-MS data of identified plant metabolites from fraction F1 in negative mode [M-H] with a possible molecular formula.

S. NO.	Retention time	Name	Molecular formula	Mean measured mass (Da) m/z	Mass (Da)	Diff (Tgt, ppm)
1	6.958	Benzoic acid	C ₇ H ₆ O ₂	167.03	122.12	4.43
2	1.047	Gallic acid	C ₇ H ₆ O ₅	169.01	170.12	3.23
3	7.308	Ellagic acid	C ₁₄ H ₆ O ₈	301.00	302.0077	4.83
4	7.008	Syringic acid	C ₉ H ₁₀ O ₅	197.04	198.21	4.31
5	3.046	Protocatechuic aldehyde	C ₇ H ₆ O ₃	137.18	138.12	3.18
6	6.709	Coumaric acid	C ₉ H ₈ O ₃	163.04	164.0481	4.4
7	8.241	Dihydroquercetin	C ₁₅ H ₁₂ O ₇	303.05	304.25	4.74
8	7.358	Epi-catechin-3-gallate (ECG)	C ₂₂ H ₁₈ O ₁₀	441.08	442.40	4.76
9	10.672	Hispidulin	C ₁₆ H ₁₂ O ₆	299.05	462.40	5.29
10	0.831	2-Hydroxyxanthone	C ₁₃ H ₈ O ₃	257.04	212.20	-4.78
11	1.83	2,3-Dihydroxybenzoic acid	C ₇ H ₆ O ₄	153.01	154.12	3.73
12	10.838	Cirsilineol	C ₁₈ H ₁₆ O ₇	343.08	344.30	3.56
13	1.813	Catechol	C ₆ H ₆ O ₂	109.03	110.10	3.98
14	11.721	Formononetin	C ₁₆ H ₁₂ O ₄	327.08	268.26	5.16
15	6.909	Hydroxycaffeic acid	C ₉ H ₂₈ O ₅	241.03	196.16	2.96
16	10.072	Cirsimaritin	C ₁₇ H ₁₄ O ₆	359.07	314.29	5.34
17	10.072	Rosmarinic acid	C ₁₈ H ₁₆ O ₈	359.07	360.31	4.66
18	6.942	Umbelliferone	C ₉ H ₆ O ₃	207.03	162.14	5.62
19	0.648	5,6-Dihydroxy-7,8,3',4'-tetramethoxyflavone	C ₁₉ H ₁₈ O ₈	419.09	406.34	2.27
20	6.692	Eriodictyol 7-O-glucoside	C ₂₁ H ₂₂ O ₁₁	509.13	450.39	5.96
21	10.672	Dihydroxyflavone	C ₁₅ H ₁₀ O ₄	299.05	254.24	5.83
22	12.387	Glycyrin	C ₂₂ H ₂₂ O ₆	427.14	382.40	3.03
23	6.709	Citropten	C ₁₁ H ₁₀ O ₄	265.07	206.19	3.97
24	7.341	Caffeic acid	C ₉ H ₈ O ₄	225.04	180.16	3.42
25	7.441	Sinapic acid	C ₁₁ H ₁₂ O ₅	223.06	224.06	4
26	7.441	Mellein	C ₁₀ H ₁₀ O ₃	223.06	178.18	5.03

TABLE 4 | QTOF-ESI-MS data of identified plant metabolites from fraction F1 in positive mode [M+H]* with the possible molecular formula.

Peak no.	Retention time	Name	Molecular formula	Mean measured mass (Da) m/z	Mass (Da)	Diff (Tgt, ppm)
1	21.107	Coumaric acid	C ₉ H ₈ O ₃	165.05	192.17	1.45
2	5.857	Herniarin	C ₁₀ H ₈ O ₃	177.05	176.16	-2.91
3	16.279	Umbelliferone	C ₉ H ₆ O ₃	163.03	162.12	2.49

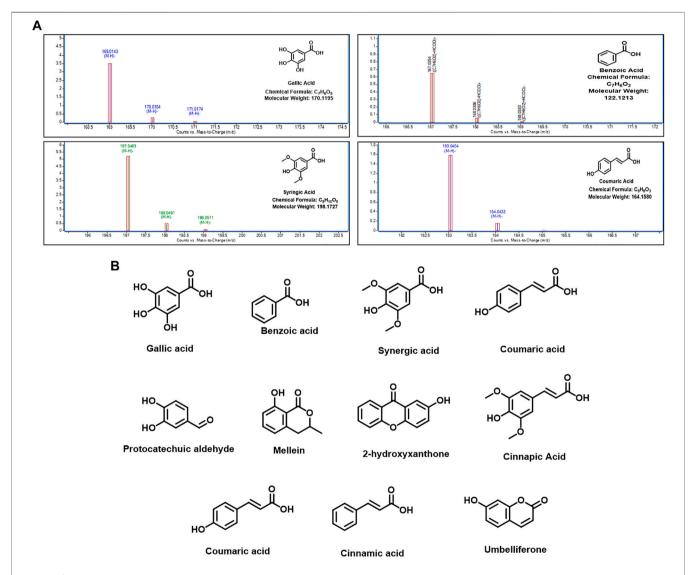


FIGURE 6 | Identified metabolite hits in the hydroalcoholic extract and its fraction F1 in the LC-QTOF-ESI-MS analysis. (A) Major metabolites present in both DP and F1. (B) Chemical compound structures present in both positive and negative mode in the LC-QTOF-ESI-MS.

Doxorubicin (Dox) is a widely known chemotherapeutic drug, which induces oxidative stress, leading to free radicals, subsequently causing oxidative damage to the cardiomyocytes (Pugazhendhi et al., 2018). Dox-induced cardiotoxicity model has been successfully demonstrated in various cultured cell lines (Chan et al., 1996), isolated heart cultures, whole animal models, and humans (Singal

et al., 1987). Identification and evaluation of safer bioactive molecules/ fractions, which help alleviate the existing chemotherapeutic drugs' cardiotoxic effect, would benefit cancer patients.

Dillenia pentagyna Roxb. is a nutritionally and medicinally valued plant distributed widely in South Asian countries. The fruits and bark of the plant were used for the treatment of various

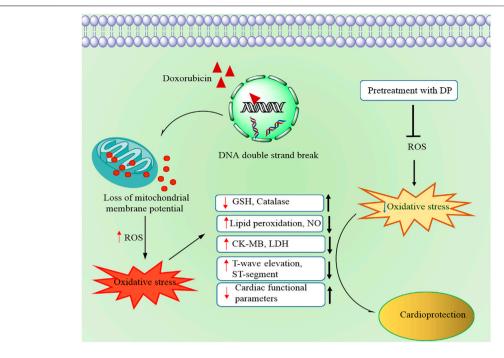


FIGURE 7 | Schematic representation of the proposed cardioprotective mechanism by the hydroalcoholic extract of DP

ailments. In the current study, we intend to evaluate the antioxidant role in alleviating the Dox-induced cardiotoxicity both *in-vitro* and *in-vivo*. The preliminary anti-oxidant tests suggested that the *Dillenia* pentagyna Roxb's hydroalcoholic extract had high anti-oxidant chemical compounds. Therefore, the bioactive DP was further subjected to fractionation to obtain a purified bioactive fraction (Fraction-1).

However, anti-oxidant chemical tests indicated that both the DP and Fraction-1 have an equivalent amount of anti-oxidant compounds, and fraction F1 has high phenolic content than the crude DP. The pretreatment with DP and F1 has shown the increased cell viability in H9c2 cells indicating the protective activity. Multiple pieces of evidence revealed that the reactive oxygen species (ROS) has a direct implication in the pathogenesis of Dox-induced cardiotoxicity (Hwang et al., 2008; Sun et al., 2015). In-vitro DCFDA and Mitosox staining revealed that the Dox treated cardiomyocytes (H9c2) have high levels of reactive oxygen species, which is evident by the fluorescence signal in both the flow cytometric and microscopic analysis. Simultaneously, the cells treated with the bioactive DP have shown a less amount of fluorescence, indicating the reduced ROS. The previous reports suggest that anti-oxidants can modulate the anticancer drug efficacy in cancer treatment (Conklin, 2004). However, the treatment with DP and F1 and Dox on the cancer cell line did not compromise the anticancer activity of Dox in the cancer cell line.

When evaluated by the ECG, the cardioprotective activity of the bioactive DP evidenced normalization of ECG changes, most notably ST height and T-wave elevation. An altered ECG was due to the propagation of lipid peroxidation in the Dox treated mice group as the bioactive fractions reduced lipid peroxidation, which could be responsible for the normalized T-wave elevation and ST-

height. Electrocardiographic (ECG) imaging is a non-invasive method to study the various cardiac parameters. In the current study, we have used the electrocardiography-based imaging technique to study the bioactive DP's cardioprotective effect in Dox-induced cardiotoxicity models. The application of such techniques provides reliable information about the cardiac profile. Dox causes a decrease in left ventricular wall thickness (Prathumsap et al., 2020), cardiac functional parameters ejection fraction, fractional shortening, stroke volume, cardiac output, and heart rate. Our findings of increased cardiac functional parameters indicated that DP had reduced the toxic effects of Dox-induced cardiotoxicity. In our study, in vivo anti-oxidant markers like GSH and catalase were also elevated, indicating the endogenous anti-oxidant defense system. Cardiac tissue biomarkers like Creatine kinase isoenzyme-MB (CKMB), Lactate dehydrogenase (LDH) were released when damage to the cardiomyocytes. We found that the Dox treatment has increased their levels in the Dox group, whereas the pretreatment significantly decreased the levels with bioactive DP, indicating the attenuation of the cardiac damage by Dox. The same was further supported by estimating tissue-based lipid peroxidation end product MDA and the nitrite levels. We found that the levels were significantly decreased, indicating that treatment with DP inhibited lipid peroxidation.

Nuclear factor (erythroid-derived 2)-like 2 (Nrf-2), a redox-sensitive transcription factor regulating various cellular responses to electrophilic/oxidative stress. It has previously been revealed the role of Nrf-2 in the detoxification process in cardiac cells (Howden, 2013). Therefore, growing evidence suggested that Nrf-2 may target Dox-induced cardiotoxicity treatment (Tomlinson et al., 2019; Zhang et al., 2020). Our study results indicated that treatment

with the bioactive DP increased the expression of Nfr-2 a critical anti-oxidant regulator of oxidative stress, by decreasing its negative regulator Keap-1 expression. The downstream proteins expression like SOD-2 and HO-1 were elevated, indicating the rise of anti-oxidant enzyme expression that counteracts the produced ROS in H9c2 cell line and *in vivo* anti-oxidant enzyme expression that neutralizes the produced ROS in H9c2 cell line and *in-vivo* evident from the western blot analysis. This proves that the bioactive DP ameliorated Dox-induced oxidative stress.

It is evident from this study that identified metabolite hits gallic acid, benzoic acid, syringic acid, coumaric acid, protocatechuic aldehyde, mellein, 2-hydroxy xanthone, sinapic acid, coumaric acid, cinnamic acid, and umbelliferone are phenolic containing chemical constituents present in hydroalcoholic extract DP and its F1 fraction in the LC-QTOF-ESI-MS. Therefore, it may be concluded that hydroalcoholic extract and its fraction F1 are enriched with polyphenols and have shown good cardioprotective activity in the preclinical screening model.

Taken together, our data showed convincing evidence that pre-treatment with DP and F1 alleviated the cardiotoxicity *invitro*. *In-vivo* mice model also indicated that the DP caused no significant effect to the body weights, meanwhile restoring the cardiac parameters nearly equal to the normal control group. Pretreatment with DP attenuated the Dox-induced cardiotoxicity by reducing the oxidative stress, and the Nrf-2 pathway mediated the cardioprotection. Further *in-vivo* studies are required to understand the role of fraction F1, and extensive studies have to be performed to know the exact molecules involved in the protective effect of the DP against Dox-induced cardiotoxicity.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding authors.

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ETHICS STATEMENT

The animal study was reviewed and approved by the Institutional Animal Ethics Committee (IAEC), Guwahati, India (NIPS/ NIPER/18/029).

AUTHOR CONTRIBUTIONS

VN, RG: Design and guidance for the whole experiment. KT, KK, and JK performed experiments. BG, EP: operation of the animal experiment: KT, DP: Interpretation of data and drafted, edited the manuscript. PK provided phytochemical analysis. UM, VN: acquired funding.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.624706/full#supplementary-material

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Turbina oblongata Protects Against Oxidative Cardiotoxicity by Suppressing Lipid Dysmetabolism and Modulating Cardiometabolic Activities Linked to Cardiac Dysfunctions

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Erukainure OL, Chukwuma Cl, Matsabisa MG, Javu MT, Salau VF, Koorbanally NA and Islam MS (2021) Turbina oblongata Protects Against Oxidative Cardiotoxicity by Suppressing Lipid Dysmetabolism and Modulating Cardiometabolic Activities Linked to Cardiac Dysfunctions. Front. Pharmacol. 12:610835. doi: 10.3389/fphar.2021.610835 Cardiotoxicity leading to cardiovascular dysfunction and ultimately cardiac failure remains a major global health issue irrespective of race, age and country. Several factors including lipotoxicity, oxidative imbalance, exacerbated angiotensin-converting enzyme (ACE) activity and altered bioenergetics have been implicated in the pathophysiology of cardiovascular diseases. Turbina oblongata (E. Mey. ex Choisy) A. Meeuse is among the medicinal plants commonly used traditionally in the treatment and management of various ailments including cardiovascular dysfunctions in South Africa. In the present study, T. oblongata was investigated for its cardioprotective mechanism on oxidativemediated cardiotoxicity by determining its effect on redox imbalance, purinergic and cholinergic dysfunction, and ACE activity as well as lipid dysmetabolism and pathways in iron-induced oxidative cardiac injury. Oxidative injury was induced ex vivo in freshly isolated heart by incubating with 0.1 mM FeSO₄. Treatment was done by co-incubating with T. oblongata extract or gallic acid which served as the standard antioxidant. Induction of oxidative cardiac injury led to significant depleted levels of glutathione, triglyceride, HDLcholesterol, superoxide, catalase and ENTPDase activities, with concomitant elevated levels of malondialdehyde, cholesterol, LDL-cholesterol, ACE, acetylcholinesterase, ATPase and lipase activities. These levels and activities were significantly reversed following treatment with T. oblongata. Induction of oxidative injury also caused alterations in lipid metabolites, with concomitant activation of beta oxidation of very long chain fatty acids, plasmalogen synthesis and mitochondrial beta-oxidation of long chain saturated fatty acids pathways. Some of the altered metabolites were restored following treatment with T. oblongata, with concomitant inactivation of beta oxidation of very long chain fatty acid pathway. These results indicate the cardioprotective effect of T. oblongata against oxidative-mediated cardiotoxicity. This is evidenced by its ability to mitigate lipotoxicity and modulate dysregulated cardiometabolic activities as portrayed by

its antioxidative activity and suppressive effects on ACE, acetylcholinesterase and lipase activities, while modulating cardiac lipid dysmetabolism.

Keywords: cardiotoxicity, lipid dysmetabolism, metabolomics, turbina oblongata, cardiometabolism

INTRODUCTION

Cardiovascular dysfunctions leading to cardiovascular failure has been linked to global early mortalities, with oxidative stress arising from disordered cardiac bioenergetics playing a triggering role (Poulter, 2003; Wold et al., 2005; Li et al., 2019). This is often depicted by cardiac lipid dysmetabolism which is characterized by hyperlipidemia as well as defects in beta-oxidation pathway and mitochondrial oxidative phosphorylation (Antozzi and Zeviani, 1997). Fatty acids (FAs) have been reported as a major energy source for the heart, as they are estimated to meet over 70% of the heart's energy needs (Drosatos and Schulze, 2013). Alteration in cardiac FAs and their metabolism leading to lipotoxicity has been implicated among the pathomechanism of cardiovascular dysfunctions (Erukainure et al., 2020b; Salau et al., 2020b). Exacerbated activities of cardiac lipase and angiotensinconverting enzyme (ACE), as well as altered cardiac supply of triglycerides from the liver and accumulation of cholesterol in the heart are major contributing factors of lipotoxicity. Lipotoxicity has been linked to increased production and accumulation of free radicals leading to oxidative stress, when the latter overwhelms the cardiac endogenous antioxidant system (Jiménez-González et al., 2020). This crosstalk between lipotoxicity and oxidative stress presents pathogenic mechanisms and progression of cardiotoxicity and other cardiovascular dysfunctions, ultimately leading to heart failure.

Turbina oblongata is among the medicinal plants commonly used traditionally in the treatment and management of various ailments in South Africa. It is a perennial herb belonging to the Convolvulaceae family and widely distributed in Botswana, Swaziland, Malawi, Tanzania, Zimbabwe and South Africa (Srivastava and Rauniyar, 2020). In South Africa, the plant is commonly found in all provinces except the Western Cape and it is locally referred to as ubhogo (Semenya et al., 2018; Srivastava and Rauniyar, 2020). Its other synonyms are Ipomoea atherstonei, Ipomoea lambtoniana, oblongata and Ipomoea randii (Foden and Potter, 2005). The plant leaves have been reported for their wound healing properties and anticancer activities (Hutchings et al., 1996; Kose et al., 2015). The plant is also traditionally used in the treatment of diarrhea, respiratory infections, hypertension, impotency, renal disease, and sexually transmitted infections (Srivastava and Rauniyar, 2020). These properties can be attributed to its phytochemical constituents which have been reported to consist of flavonoids, terpenoids, glycosides, steroids, anthocyanins, and alkaloids.

The present study investigated the cardioprotective mechanism of *T. oblongata* on oxidative-mediated cardiotoxicity by reporting its effect on redox imbalance,

purinergic and cholinergic dysfunction, ACE activity and lipid dysmetabolism in iron-induced oxidative cardiac injury.

MATERIALS AND METHODS

Plant Material and Extraction

Turbina oblongata was collected from Eastern Cape Province, South Africa (GPS coordinates: 32°44′20.1″S 26°54′58.3″E). The plant sample was identified and authenticated at the Geo Potts herbarium (BLFU), University of the Free State (specimen voucher number: BLFU MGM0019).

The plant sample was air-dried after washing and was blended to fine powder. The powdered sample (100 g in a 1:5 mass:solvent ratio in ml) was subjected to sequential extraction using solvents of increasing polarity vis-à-vis hexane, dichloromethane (DCM), methanol and dichloromethane (MeOH:DCM; 1:1, v/v) and methanol (MeOH). Each extraction was carried out at ambient room temperature for 24 h. After extraction, each extract was filtered and subsequently concentrated *in vacuo* with an R–215 rotary evaporator (Buchi, Switzerland). Concentrated samples were collected into glass vials and stored at 4 C.

Enzyme Inhibitory Activity

The concentrated extract samples were investigated for their antihypertensive activities by determining their ability to inhibit the activity of ACE *in vitro* (Shalaby et al., 2006). Based on the ACE inhibitory activities, the DCM extract was selected for further evaluation for its anti-hypertensive potential by determining its ability to inhibit the activity of renin using modified standard method (Udenigwe et al., 2009). The DCM extract, based on its activity on ACE and Renin, was chosen for further *ex vivo* studies.

Induction of Oxidative Cardiac Injury Ex Vivo

Hearts harvested from Sprague Dawley rats were homogenized in 50 mM sodium phosphate buffer (pH 7.5; with 1% Triton X-100). The homogenates were then centrifuged at 15,000 rpm at 4 $^{\circ}$ C for 10 min to obtain the tissue supernatants.

A 100 μ l of the cardiac tissue supernatant was incubated with 0.1 mM FeSO4 (pro-oxidant) and different concentrations (30, 60, 120 and 240 $\mu g/ml)$ of the DCM extract of $\it T.~oblongata$ at 37°C for 30 min according to previously published methods (Erukainure et al., 2020a; Salau et al., 2020b). Reaction samples without the extract served as the negative control (untreated), while reaction sample without the pro-oxidant and extract served as the normal control. Gallic acid was used as the standard antioxidative drug.

The study was conducted under the approved guidelines of the Animal Ethics Committee of the University of KwaZulu-Natal, Durban, South Africa (Protocol approval number: AREC/020/017D).

Determination of Oxidative Stress Parameters

Reduced Glutathione Level

This was determined according to Ellman's method (Ellman, 1959). Briefly, $100~\mu l$ of the reaction samples was deproteinized with $300~\mu l$ of 10% TCA and centrifuged at 3,500 rpm for 5 min. $200~\mu l$ of the mixture was added to $50~\mu l$ of Ellman's reagent in a 96-well plate and incubated for 5 min. Absorbance was measured at 415 nm and GSH level was extrapolated from a GSH standard curve.

Superoxide Dismutase Enzyme Activity

This was determined with slight modification of a previously established method (Kakkar et al., 1984). Briefly, 15 μ l of the reaction samples was mixed with 170 μ l of 0.1 mM diethylenetriaminepentaacetic acid (DETAPAC) in a 96-well plate. Then 15 μ l of 1.6 mM 6-hydroxydopamine (6-HD) was added to the mixture and swirled. Absorbance was immediately read at 492 nm for 3 min at 1 min interval.

Catalase Activity

Catalase activity was determined using a previously established protocol (Aebi, 1984). Briefly, 100 μ l of the reaction samples was mixed with 340 μ l of 50 mM phosphate buffer (pH 7.0). Thereafter, 150 μ l of 2 M hydrogen peroxide was added to the mixture and incubated for 5 min. Absorbance was measured at 240 nm at 1 min interval for 3 min.

Lipid Peroxidation

Lipid peroxidation was carried out by measuring the malondial dehyde (MDA) level of the reaction samples using a previously established method (Chowdhury and Souls by, 2002). In brief, a reaction mixture made up of equal volumes (100 μ l) of the reaction samples and 8.1% SDS solution, 1 ml of 0.25% thiobarbituric acid (TBA) and 375 μ l of 20% acetic acid was boiled for 1 h. Absorbance was measured at 532 nm and MDA levels were extrapolated from a MDA standard curve.

Determination of ACE Activity

ACE activity was determined spectrophotometrically by a slight modification of Holmquist's method (Holmquist et al., 1979), using N-[3-(2-Furyl) acryloyl]-L-phenylalanyl-glycyl-glycine (FAPGG) as substrate. Briefly, 200 μ l of the reaction samples were incubated with 1 ml of 0.5 mM FAPGG for 10 min at 37°C. Absorbance was measured at 345 nm at 2 min intervals. ACE activity was measured as the rate of reaction (Δ A/min) as expressed below:

$$ACE \ activity = \frac{(AI - AF)Sample - (AI - AF)Blank}{Time \ interval \ (min)}$$

Where AI = initial absorbance; AF = final absorbance.

Determination of Cholinergic Enzymes Activity

Cholinergic enzyme activity was determined by analyzing the acetylcholinesterase activity of the reaction samples using the

Ellman's procedure (Ellman et al., 1961). A reaction containing 20 μ l of the reaction samples, 10 μ l of Ellman's reagent (3.3 mM, pH 7.0) and 50 μ l of phosphate buffer (0.1 M, pH 8) was incubated for 20 min at 25°C. Then 10 μ l of 0.05 M acetylcholine iodide was added to the reaction samples and absorbance was measured at 412 nm at 3 min intervals.

Determination of Purinergic Enzymes Activities

The purinergic enzyme activities of the reaction samples were determined by analyzing the activities of adenylpyrophosphatase (ATPase) (Adewoye et al., 2000; Erukainure et al., 2017) and ectonucleoside triphosphate diphosphohydroase (ENTPDase) (Akomolafe et al., 2017) respectively.

ATPase Activity

Briefly, a reaction mixture containing 100 μ l of the reaction samples, 100 μ l of 5 mM KCl, 650 μ l of 0.1 M Tris-HCl buffer, and 20 μ l of 50 mM ATP was incubated in a shaker for 30 min at 37°C. Then 1.25% ammonium molybdate and 500 μ l of a distilled water were added to terminate the reaction. Thereafter, a 500 μ l of a freshly prepared 9% ascorbic acid was added to the mixture and allowed to stand for 30 min. Absorbance was measured at 660 nm.

ENTPDase Activity

Briefly, $20~\mu$ l of the reaction samples was incubated with a mixture containing $200~\mu$ l of the reaction buffer (1.5 mM CaCl₂, 5 mM KCl, 0.1 mM EDTA, 10~mM glucose, 225~mM sucrose and 45~mM Tris-HCl) for 10~min at 37° C. $20~\mu$ l of 50~mM ATP was then added to the reaction mixture and further incubated in a shaker for 20~min at 37° C. Reaction was halted by adding $200~\mu$ l of 10%~TCA, followed by $200~\mu$ l of 1.25%~ammonium molybdate and a freshly prepared 9%~ascorbic acid. The mixture was allowed to stand on ice for 10~min. Absorbance was read at 600~nm.

Determination of Lipase Activity

The lipase activity of the reaction samples was determined by a little modification of a previously established method (Kim et al., 2010). A 100 μ l of the reaction samples was incubated with 169 μ l of Tris buffer (100 mM Tris–HC1 and 5 mM CaCl₂, pH 7.0) at 37°C for 15 min 5 μ l of 10 mM p-NPB (p-nitrophenyl butyrate in dimethyl formamide) was added to the mixture and further incubated for 15 min at 37°C. Absorbance was measured at 405 nm at 1 min interval. Lipase activity was expressed as the rate of reaction (Δ A/min).

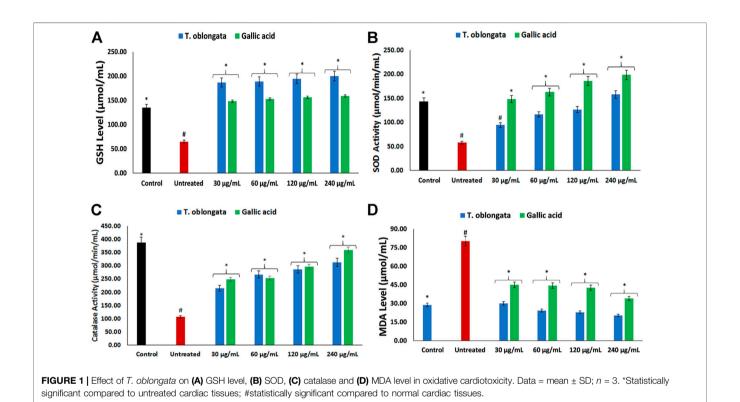
Determination of Cardiac Lipid Profile

Cardiac tissue supernatants were incubated overnight (12 h) with 0.1 mM $FeSO_4$ and 240 µg/ml of $\it{T.~oblongata}$ DCM extract or gallic acid as described above. The samples were centrifuged at 15,000 rpm for 10 min at 4°C. The supernatants were immediately assayed for lipid profile levels including, total cholesterol, triglycerides, and HDL-cholesterol using an Automated Chemistry Analyzer (Labmax Plenno, Labtest Co. Ltd., Lagoa Santa, Brazil) with commercial assay kits according to manufacturer's manual.

TABLE 1 | IC50 values for ACE and renin inhibitory activities of T. oblongata extracts.

Activities	HEX	МЕОН	DCM:MEOH (1:1)	DCM	Aqueous	Captopril	Aliskiren
				(µg/ml)			
ACE inhibition Renin inhibition	ND ND	364 ND	167 ND	81.1 127	ND ND	1.31 ND	ND 13.4

HEX, hexane extract; MEOH, methanol extract; DCM:MEOH, dichloromethane and methanol extract; DCM, dichloromethane extract. ND = not determined.



Metabolite Extraction and Profiling

As described above, the reaction mixture was prepared and incubated overnight (12 h). Lipid metabolites were then extracted from the samples and subjected to GC-MS metabolic profiling (Ralston-Hooper et al., 2011) with slight modification. Briefly, cold chloroform was mixed with the reaction samples in a ratio of 5:1 and vortexed for 1 min. The mixture was incubated on ice for 20 min and centrifuged at 15,000 rpm for 10 min at 4°C to yield two liquid phases. The lower phase (chloroform) layer containing the lipid metabolites and other non-polar metabolites was collected and subsequently profiled with GC-MS.

GC-MS Analysis of Lipid Metabolites

The chloroform layer which contains the lipid and other non-polar metabolites were analyzed with GC-MS (Agilent technologies 6,890 series GC coupled with (an Agilent) 5,973 Mass Selective Detector and driven by Agilent Chemstation software). The operating parameters include: Column: HP-5MS capillary column (30 m \times 0.25 mm ID, 0.25 μ m film

thickness, 5% phenylmethylsiloxane); Carrier gas: ultra-pure helium; Flow rate: 1.0 ml min⁻¹ and a linear velocity of 37 cm s⁻¹; Injector temperature: set at 250°C. Initial oven temperature: 60°C, programmed to 280°C at the rate of 10°C min⁻¹. Injection: 1 µl made in split mode at a split ratio of 20:1; Electron ionization mode: 70 eV; Electron multiplier voltage: at 1859 V; Ion source temperature: 230°C; Quadrupole temperature: 150°C; Solvent delay: 4 min; Scan range: 50–70 amu. Lipid metabolites were identified using an inbuilt NIST library.

Metabolic Pathway Analysis

To identify the relevant pathways involved in lipid metabolism in the protective role of *T. oblongata* on oxidative cardiotoxicity, the identified lipid metabolites were subjected to pathway enrichment analysis using the MetaboAnalyst 4.0 online server (Chong et al., 2018).

High-Performance Liquid Chromatography

HPLC-diode array detection analysis was performed on the DCM extract using an Agilent 1,100 series (Agilent, Waldbronn,

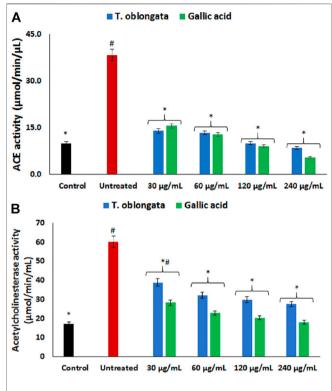


FIGURE 2 | Effect of *T. oblongata* on **(A)** ACE and **(B)** acetylcholinesterase activities in oxidative cardiotoxicity. Data = mean \pm SD; n=3. *Statistically significant compared to untreated cardiac tissues; #statistically significant compared to the control (normal cardiac tissue).

Germany) instrument equipped with photo diode array, autosampler, column thermostat and degasser. A Phenomenex: Luna 5 μm C_{18} (2) (150 × 4.6 mm; 5 μm particle size) column was used as the stationary phase. Water containing 0.1% of formic acid (A) and acetonitrile (B) served as mobile phases at a flow rate of 1 ml/min. Gradient elution was applied as follows: Initial ratio 95% A: 5% B, keeping for 10 min, changed to 90% A: 10% B in 10 min, changed to 70% A: 30% B in 10 min, to 50% A: 50% B in 10 min, maintaining for 0.5 min and back to initial ratio in 0.5 min. Temperature was set to 30°C. Extract or standards were dissolved in HPLC grade methanol (2 mg/ml) and the injection volume was 20.0 μl. Chromatograms were recorded at 254 nm.

Statistical Analysis

One-way analysis of variance (ANOVA) was used in analyzing the data and presented as mean \pm SD. Significant differences between means at p < 0.05 were obtained with the Tukey's HSD-multiple range post-hoc test. Statistical analyses were done using IBM Statistical Package for the Social Sciences (SPSS) for Windows, version 23.0 (IBM Corp., Armonk, NY, United States). The GC-MS identified metabolites were subjected to statistical analysis (distinct changes and distribution) using the MetaboAnalyst 4.0 online server (Chong et al., 2018). Graphs were prepared using Microsoft Excel Spreadsheet and MetaboAnalyst 4.0 online server.

RESULTS

Except for MEOH:DCM and DCM extracts, the extracts had no inhibitory effect on ACE activity as shown in **Supplementary Figure S1A**. The MEOH:DCM and DCM extracts significantly (p < 0.05) inhibited the enzyme activity in a dose dependent manner. This is further depicted by their IC₅₀ values of 167 and 81.1 µg/ml, respectively (**Table 1**) and compared favourably with that of the standard ACE-inhibitor captopril oil (**Supplementary Figure S1B**).

The DCM extract having displayed the best ACE inhibitory activity, and was recommended for further investigated for its renin inhibitory activity. The extract significantly (p < 0.05) inhibited the ACE activity dose dependently (**Supplementary Figure S2A**), with an IC₅₀ value of 127 µg/ml (**Table 1**). This activity compared favorably with that of Aliskiren (**Supplementary Figure S2B** and **Table 1**).

Induction of oxidative cardiac injury led to significant (p < 0.05) decreased levels of GSH, SOD and catalase activity, with concomitant elevated level of MDA as depicted in **Figures 1A–D**. Following treatment with the DCM extract, these levels and activities were significantly (p < 0.05) reversed to near normal. Except for GSH level, these reversals were dose-dependent and compared favourably with gallic acid.

ACE activity was significantly (p < 0.05) elevated in cardiac tissues following the induction of oxidative cardiac injury as shown in **Figure 2A**. Treatment with the DCM extract led to

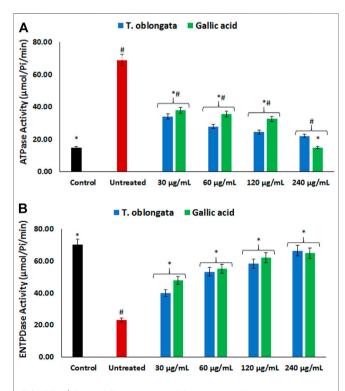
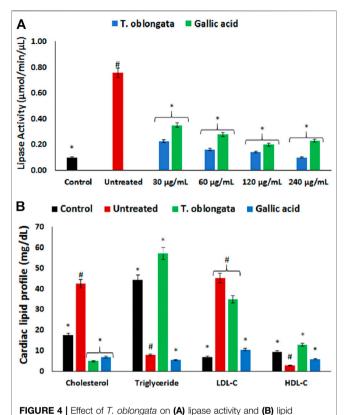


FIGURE 3 | Effect of *T. oblongata* on **(A)** atpase and **(B)** entpdase activities in oxidative cardiotoxicity. Data = mean \pm SD; n=3. *Statistically significant compared to untreated cardiac tissues; #statistically significant compared to the control (normal cardiac tissues).



profile in oxidative cardiomyopathy. Data = mean \pm SD; n=3. *Statistically significant compared to untreated cardiac tissues; #statistically significant compared to the control (normal cardiac tissues).

significant (p < 0.05) depletion in the activity dose-dependently, depicting an inhibitory effect.

As shown in **Figure 2B**, induction of oxidative cardiac injury led to significant (p < 0.05) elevation of cardiac acetylcholinesterase activity. The activity was significantly (p < 0.05) reversed dosedependently to near noel following treatment with the DCM extract. The reversed activity compared favorably with that of gallic acid.

As depicted in **Figures 3A,B**, there was a significant (p < 0.05) elevation in cardiac ATPase activity, with concomitant decreased ENTPDase activity following the induction of oxidative cardiac injury. Treatment with the DCM extract led to significant (p < 0.05) reversion of these activities to near normal dosedependently and compared favorably with gallic acid.

There was a significant (p < 0.05) elevation in cardiac lipase activity following the induction of oxidative cardiac injury as shown in **Figure 4A**. The activity was significantly (p < 0.05) inhibited dose-dependently after treatment with the DCM extract, and compared favorably with gallic acid.

Induction of oxidative cardiac injury led to significant (p < 0.05) elevation of cardiac levels of cholesterol and LDL-C, with concomitant decreased levels of triglycerides and HDL-C as shown in **Figure 4B**. Following treatment with the DCM extract, there was a significant depletion in cardiac level of cholesterol with concomitant elevation of triglyceride and HDL-C levels. Although the level of LDL-C was reduced in the treated tissues, it was however not statistically significant.

GC-MS analysis of the extracted lipid metabolites revealed the presence of unsaturated fatty acid, saturated fatty acid, fatty ester, fatty alcohol, fatty amide, glycerol and steroids in the cardiac tissue as shown in Table 1. Induction of cardiac tissue led to the complete depletion of octadecadienoic acid (Z,Z)-; cis-10-heptadecenoic acid; eicosanoic acid; n-heptadecanol-1 and retinal; with concomitant generation of 14-pentadecenoic acid; octadecanoic acid; tetracosanoic acid; cis-11,14-eicosadienoic acid, methyl ester; n-tetracosanol-1 and glycerol 1-palmitate. Treatment with the DCM extract led to the depletion of oxidative generated 14-pentadecenoic acid; tetracosanoic acid; cis-11,14-eicosadienoic acid, methyl ester; n-tetracosanol-1 and glycerol 1-palmitate, with concomitant generation of 9,12-Octadecadienoic acid (Z,Z)-; cis-11-eicosenoic acid; malonic acid, 2-hexyl tetradecyl ester; lpentanoic acid 2.6-dihexadecanoate: (+)-Ascorbic heptadecyl ester; 13-tetradecen-1-ol acetate; oleamide and pseduosarsasapogenin-5,20-dien methyl ether. Non lipid metabolites consisting of ursane-3,12-diol; betulin and 28hydroxylup-20(29)-ene-3,21-dione were also identified in cardiac tissues treated with the DCM extract.

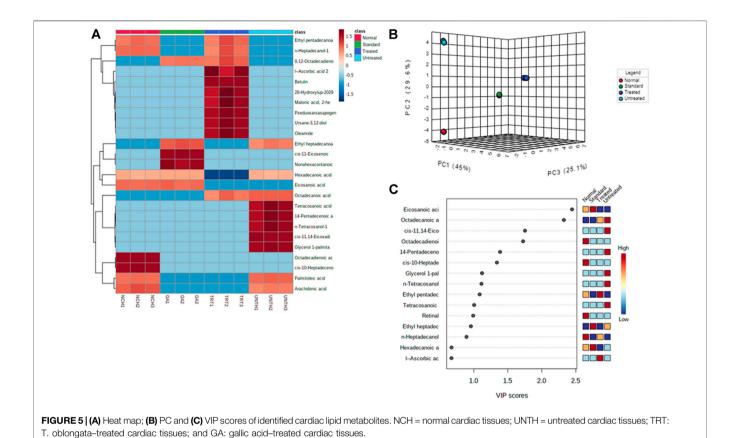
Distinct changes and distribution of the cardiac metabolites were observed for all the experimental groups as portrayed by the negative values and heat intensity of the heat map following clustering analysis (**Figure 5A**). This is also supported by the distinctive changes between the pair wise score plots between the selected principal components (PCs) of metabolites from the treated tissues and that of the untreated (**Figure 5B**). This is further corroborated by the distribution of the important identified features (metabolites) and their respective concentrations in each experimental group by Partial Least Squares - Discriminant Analysis (PLS-DA) as shown in **Figure 5C**.

Pathway enrichment of the identified cardiac lipid metabolites revealed an inactivation of retinol metabolism pathway, with concomitant activation of beta oxidation of very long chain fatty acids, plasmalogen synthesis and mitochondrial beta-oxidation of long chain saturated fatty acids pathways as depicted in **Figure 6** and **Table 2**. Treatment with the DCM extract did not reactivate the retinol metabolism pathway but inactivated oxidative-activated beta oxidation of very long chain fatty acids. It further inactivated arachidonic acid metabolism, glycerolipid metabolism, fatty acid elongation in mitochondria, fatty acid biosynthesis, fatty acid metabolism and steroidogenesis pathways. The oxidative-activated pathways were inactivated in cardiac tissues treated with gallic acid.

To determine the bioactive compound that may be responsible for the studied biological activity of the DCM extract, the extract was subjected to HPLC analysis. As depicted in **Figure 7**, quercetin was identified as the active compound in the extract.

DISCUSSION

Cardiotoxicity is a major global health issue as it has been implicated in the pathogenesis of cardiovascular dysfunction which may lead to cardiac failure if not well treated and managed (Poulter, 2003; Wold et al., 2005; Li et al., 2019).



Several factors including lipotoxicity, oxidative imbalance, exacerbated ACE activity and altered bioenergetics have been implicated in the pathophysiology of cardiovascular diseases. The high cost associated with its treatment coupled with the side effect of synthesized drugs are of major concerns to health practitioners. This have led to an increased paradigm shift to natural products for cheap and affordable drugs with little or no side effects. The present study reports the cardioprotective effect of *T. oblongata* and the possible mechanism and pathways by which it brings about its effect.

Oxidative stress has been implicated as a major mechanism in the pathogenesis and progression of cardiotoxicity and other cardiological dysfunctions (Fearon and Faux, 2009; Angsutararux et al., 2015). This has been attributed to suppressed endogenous antioxidant activity owing to increased free radical productions in the cardiac tissues. In the present study, the depleted GSH level, SOD and catalase activities (Figures 1A-C) depicts an onset of oxidative stress following induction of oxidative cardiac injury. This is further evidenced by the elevated cardiac MDA level (Figure 1D) which indicates a peroxidative effect on the cardiac lipids following the induction of oxidative cardiac injury. These altered activities and levels correspond with previous reports on the occurrence of oxidative stress after induction of oxidative injury in isolated hearts (Erukainure et al., 2020a; Salau et al., 2020b). The onset of oxidative stress can be attributed to ironcatalyzed Fenton's and Haber-Weiss reactions following the incubation of heart tissues with Fe2+. The exacerbated GSH

level, SOD and catalase activities, with concomitant suppressed MDA level in cardiac tissues treated with the DCM extract of *T. oblongata* indicate an antioxidative and anti-peroxidative effect of the extract. This corroborates previous reports on the antioxidant cardioprotective effect of plants (Wattanapitayakul et al., 2005; Adegbola et al., 2017). The antioxidative activity of the extract may be attributed to the identified flavonoid, quercetin (**Figure 7**). Quercetin is among the common flavonoids found in most fruits, herbs and vegetables, and has been reported for its potent antioxidant and cardioprotective properties (Zhang et al., 2011; Chen et al., 2013).

Increased ACE activity has been implicated in the pathophysiology of cardiotoxicity and other cardiovascular dysfunctions (Ferrario and Strawn, 2006; Salau et al., 2020b). The enzyme catalyzes the hydrolysis of angiotensin I to angiotensin II, with the latter possessing a vasoconstrictive effect leading to hypertension, myocyte death and hypertrophy (Fiordaliso et al., 2000; Agunloye et al., 2019). The increased ACE activity following the induction of oxidative cardiac injury (Figure 2A), therefore suggests an exacerbated cardiac level angiotensin II. The depleted ACE activity following treatment with the DCM extract of T. oblongata indicates an ACEinhibitory effect of the extract, thus depicting reduced cardiac levels of angiotensin II. This corroborates the ability of the extract to inhibit ACE activity in vitro (Table 1 and Supplementary Figure S1). ACE-inhibitors have been reported as potent therapies in the treatment and management of

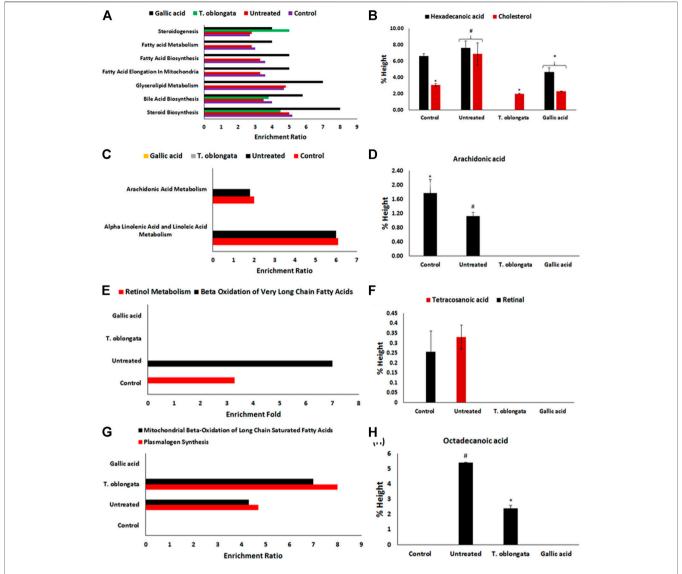


FIGURE 6 | (A) Fold enrichment for steroid biosynthesis, bile acid biosynthesis, glycerolipid metabolism, fatty acid elongation in mitochondria, fatty acid biosynthesis, fatty acid metabolism and steroidogenesis pathways and their (B) metabolites concentrations; (C) fold enrichment for alpha linolenic acid and linoleic acid metabolism, and arachidonic acid metabolism pathways and their (D) metabolites; (E) fold enrichment for beta oxidation of very long chain fatty acids and retinol metabolism pathways and their (F) metabolites; (G) fold enrichment for plasmalogen synthesis and mitochondrial beta-oxidation of long chain saturated fatty acids and their (H) metabolites.

cardiovascular diseases, which may be part of the possible mechanism by which the extract protect against oxidative-mediated cardiotoxicity. This corroborates previous reports on the use medicinal plants as ACE inhibitors (Khan and Kumar, 2019; Le et al., 2020). The ACE inhibitory activity of the extract may be attributed to the presence of quercetin, which has also been reported for its ACE inhibitory activity (Huang et al., 2017; Luo et al., 2017).

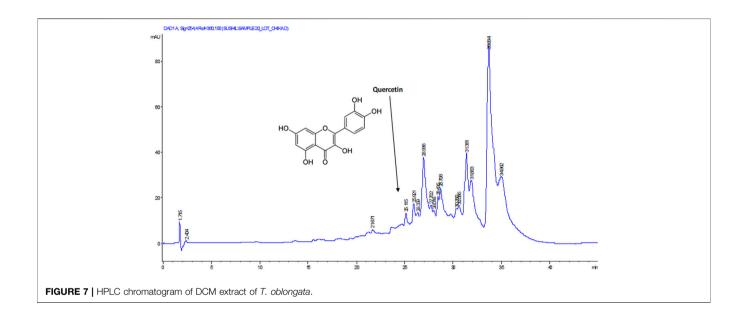
The elevated acetylcholinesterase activity following the induction of oxidative cardiac injury (**Figure 2B**) suggests a decreased cardiac level of acetylcholine, thus depicting a cholinergic dysfunction. This can be attributed to the fact the enzyme catalyzes the hydrolysis of acetylcholine to acetate and

choline. Acetylcholine is important in muscular contraction and also facilitates vasodilation via the muscarinic receptors (Kellogg et al., 2005; Agunloye et al., 2019), thus indicating that decreased concentrations could have detrimental effect on the normal physiological function of the heart. Several studies have reported acetylcholinesterase inhibition as a therapeutic mechanism in the treatment and management of cardiotoxicity and other cardiovascular dysfunctions (Gavioli et al., 2014; Roy et al., 2014; Wu et al., 2017). The decreased acetylcholinesterase in the treated cardiac tissues therefore suggests a therapeutic effect against oxidative-mediated cardiotoxicity. This corresponds with several reports on the ability of medicinal plants inhibit cardiac

TABLE 2 | Identified pathways in experimental cardiac tissues.

Pathways	Normal	Untreated	T. Oblongata	Gallic acid
Steroid biosynthesis	X	X	X	X
Bile acid biosynthesis	Χ	Χ	X	X
Alpha linolenic acid and linoleic acid metabolism	Χ	Χ	_	_
Glycerolipid metabolism	Χ	Χ	_	X
Fatty acid elongation in mitochondria	Χ	Χ	_	X
Fatty acid biosynthesis	Χ	Χ	_	X
Retinol metabolism	Χ	_	_	_
Fatty acid metabolism	Χ	Χ	_	X
Steroidogenesis	Χ	Χ	Χ	X
Arachidonic acid metabolism	Χ	Χ	_	_
Beta oxidation of very long chain fatty acids	_	Χ	_	_
Plasmalogen synthesis	_	Χ	Χ	_
Mitochondrial beta-oxidation of long chain saturated fatty acids	_	Χ	Χ	_

X = detected; - = not detected.



acetylcholinesterase activities (Agunloye et al., 2019; Salau et al., 2020b).

Purinergic enzyme activities have been reported to play an important role in the normal physiological activities of the heart. These enzymes phospho-hydrolyze adenosine triphosphate (ATP) and adenosine monophosphate (AMP) to produce the endogenous signaling nucleotide, adenosine which has been reported as a potent dilator and an important factor in bioenergetics (Das and Maulik, 1996; Burnstock, 2017). The increased ATPase and decreased ENTPDase activities following the induction of oxidative cardiac injury (Figures 3A,B) indicate a decreased cardiac level of ATP and adenosine. These levels in the untreated cardiac tissues corresponds with previous reports on altered purinergic activities in oxidative injuries (Salau et al., 2020a; Erukainure et al., 2020b). The increased ATPase activity suggests a diminished cardiac level of ATP and depicts an altered bioenergetic activity as ATP is an important energy-signaling molecule. Altered cardiac bioenergetics have been implicated in the pathophysiology of oxidative stress, cardiotoxicity and other cardiovascular dysfunctions (Das and Maulik, 1996). Both ATP and adenosine have been reported for their vasodilatory activities in coronary vessels (Kirby et al., 2010). The decreased ATPase and elevated ENTPDase activities following treatment with *T. oblongata* DCM extract therefore indicates an improved purinergic activity which may suggest improved bioenergetics.

The normal heart function depends on lipids as its energy fuel for its physiological functions *via* hydrolysis of cardiac triglyceride by lipase to fatty acids (Ritterhoff and Tian, 2017). The heart does not produce triglyceride and thus depends on its supply from the liver. The elevated lipase activity following the induction of oxidative cardiac injury (**Figure 4A**) therefore suggests an incessant breakdown of cardiac triglyceride, which corroborates with the depleted cardiac level of triglyceride (**Figure 4B**). The elevated lipase activity and reduced triglyceride level in the untreated cardiac tissues suggests

TABLE 3 | GC-MS identified lipid metabolites in experimental cardiac tissues.

Classes	Compounds	Control	Untreated	T. oblongata	Gallic acid
Unsaturated fatty acid	Palmitoleic acid	1.84 ± 0.18	2.62 ± 0.16	ND	ND
•	Octadecadienoic acid (Z,Z)-	3.56 ± 0.12	ND	ND	ND
	cis-10-Heptadecenoic acid	0.87 ± 0.10	ND	ND	ND
	Eicosanoic acid	5.19 ± 0.10	ND	ND	3.49 ± 0.29
	Arachidonic acid	1.78 ± 0.38	1.12 ± 0.10	ND	ND
	14-Pentadecenoic acid	ND	1.34 ± 0.29	ND	ND
	Octadecanoic acid		5.42 ± 0.01	2.38 ± 0.21	ND
	9,12-Octadecadienoic acid (Z,Z)-	ND	ND	1.48 ± 0.15	0.73 ± 0.11
	cis-11-Eicosenoic acid	ND	ND	ND	1.01 ± 0.10
Saturated fatty acid	Hexadecanoic acid	6.60 ± 0.33	7.60 ± 087	ND	4.68 ± 0.50
	Tetracosanoic acid	ND	0.33 ± 0.06	ND	ND
Fatty ester	Ethyl hexadecanoate	1.28 ± 0.24	1.11 ± 0.21	1.39 ± 0.27	1.68 ± 0.27
	Ethyl pentadecanoate	2.78 ± 0.61	2.44 ± 0.50	2.84 ± 0.57	2.72 ± 0.52
	cis-11,14-Eicosadienoic acid, methyl ester	ND	5.06 ± 0.40	ND	ND
	Ethyl heptadecanoate	ND	ND	ND	ND
	Malonic acid, 2-hexyl tetradecyl ester	ND	ND	0.15 ± 0.01	ND
	I-(+)-Ascorbic acid 2,6-dihexadecanoate	ND	ND	11.96 ± 9.16	ND
	Pentanoic acid, heptadecyl ester	ND	ND	0.17 ± 0.01	ND
Fatty alcohol	Pentadecanol	0.37 ± 0.03	1.59 ± 0.30	0.32 ± 0.02	0.85 ± 0.10
	n-Heptadecanol-1	0.86 ± 0.07	ND	0.72 ± 0.09	ND
	n-Tetracosanol-1	ND	0.49 ± 0.09	ND	ND
	13-Tetradecen-1-ol acetate	ND	ND	0.20 ± 0.03	ND
Fatty amide	Oleamide	ND	ND	0.26 ± 0.03	ND
Glycerol	Glycerol 1-palmitate	ND	0.50 ± 0.03	ND	ND
Steroids	Retinal	0.26 ± 0.11	ND	ND	ND
	Cholesterol	3.08 ± 0.18	6.87 ± 1.36	1.99 ± 0.04	2.29 ± 0.02
	Pseduosarsasapogenin-5,20-dien methyl ether	ND	ND	0.34 ± 0.06	
Non-lipid	Ursane-3,12-diol	ND	ND	0.35 ± 0.04	ND
•	Betulin	ND	ND	0.38 ± 0.13	ND
	28-Hydroxylup-20(29)-ene-3,21-dione	ND	ND	0.40 ± 0.01	ND
	Nonahexacontanoic acid	ND	ND	ND	0.32 ± 0.02

 $Values = mean \pm SD$; n = 3. ND = not detected.

abnormality in FA supply and utilization. This may further indicate a suppressed ATP level which also corroborates the increased ATPase activity (**Figure 3A**). This may therefore portray a metabolic dependence on aerobic glycolysis for cardiac energy (ATP) supply (Stanley, 2001; Salau et al., 2020b). The depleted lipase activity and elevated triglyceride level in cardiac tissues treated with *T. oblongata* extract therefore indicate an arrest of incessant lipolysis of triglyceride and improved lipid utilization, which also suggests an improved cardiac bioenergetic.

The elevated cholesterol and LDL-C, with concomitant depleted HDL-C following the induction of oxidative cardiac injury (**Figure 4B**) indicates a disrupted cardiac lipid spectrum and insinuate a cardiac lipotoxic effect which has been linked to the pathophysiology of cardiotoxicity (Poulter, 2003). High concentrations of cholesterol and LDL-C have also been implicated in vasoconstriction and linked to most cardiovascular dysfunctions (Lamping et al., 1994; Pfister and Campbell, 1996; Kopkan et al., 2009). The decreased cholesterol and LDL-C levels as well as elevated HDL-C level on treatment with *T. oblongata* therefore indicates an antilipemic effect of the extract against oxidative-disrupted cardiac lipid profile. This correlates with previous reports on the ability of medicinal plants to maintain cardiac lipid spectrum in oxidative-mediated cardiotoxicity (Erukainure et al., 2020a).

An occurrence of cardiac lipotoxicity on induction of oxidative cardiac injury was further depicted by dysregulated lipid metabolic pathways and altered lipid metabolites (Tables 2, 3 and Figures 5, 6). Dysregulated lipid metabolism in the heart leading to free fatty acids (FFAs) have been implicated among the pathophysiology of cardiotoxicity and other cardiovascular dysfunctions (Antozzi and Zeviani, 1997; Ventura-Clapier et al., 2004). The elevated cardiac level of cholesterol in the untreated tissues corroborates that of the cardiac lipid spectrum (Figure 4A) and the major metabolites for steroid biosynthesis, bile acid biosynthesis and steroidogenesis pathways (Figures 6A,B). The inactivation of retinol metabolism in the untreated cardiac tissue can be attributed to the complete depletion of retinal (Figures 6E,F) and corroborates previous reports linking the downregulation of the pathway to impaired cardiac lipid metabolism and heart failure (Osorio et al., 2002; Lee et al., 2014). The activation of beta oxidation of very long chain fatty acids and mitochondrial beta-oxidation of long chain saturated fatty acids pathways can be attributed to the metabolites octadecanoic acid and tetracosanoic acid (Figures 6E-H). The incessant activation of these pathways has been implicated in increased production of NADH, FADH2 and acetyl-CoA (Marín-García and Goldenthal, 2002). Acetyl-CoA is further broken down in the tricarboxylic acid (TCA) cycle to generate NADH, FADH2 and ATP. High concentrations of these

electron carriers have been reported to cause a high mitochondrial membrane potential leading to the inhibition of the electron transport (Brownlee, 2001; Du et al., 2001). This automatically reduces oxygen (O_2) to superoxide (O_2^-). Thus, it can be insinuated that the continuous production of O_2^- and concomitant low SOD activity (**Figure 1B**) in the untreated tissues may be an oxidative mechanism on induction of oxidative cardiac injury.

Inactivation of beta oxidation of very long chain fatty acids in tissues treated with T. oblongata DCM extract therefore suggests a decreased production of the electron carriers which depicts a suppressed production of ${\rm O_2}^-$. This corroborates the absence of tetracosanoic acid and the high SOD activity. The inactivation of alpha linolenic acid and linoleic acid metabolism, glycerolipid metabolism, fatty acid elongation in mitochondria, fatty acid biosynthesis, and fatty acid metabolism suggests a possible hypolipidemic mechanism by which the extract mitigates oxidative-mediated lipid dysmetabolism in oxidative-mediated cardiotoxicity.

As depicted in **Figure 7**, quercetin was identified as an active component of the DCM fraction of *T. oblongata*. Quercetin ranks among the most popular phenolics as it is commonly found in fruits, vegetables, and herbs (Zhang et al., 2011). Its potent antioxidant properties have been reported and has been exploited in the treatment and management of various oxidative-mediated ailments such as diabetes, cardiovascular diseases, and cancer (Zhang et al., 2011; Georgiev et al., 2014; Patel et al., 2018). The studied activities of *T. oblongata* in the present study may therefore be attributed to the presence of quercetin, which may also work in synergy with other unidentified phytochemicals.

CONCLUSION

These results indicate the cardioprotective effect of *T. oblongata* against oxidative-mediated cardiotoxicity. This is evidenced by the ability of its DCM extract to mitigate lipotoxicity and modulate dysregulated cardiometabolic activities as shown by its antioxidative activity and suppressive effects on ACE, acetylcholinesterase and lipase activities, while modulating cardiac lipid dysmetabolism. The presence of quercetin in the extract may contribute to these activities. However, further *in vivo* studies are recommended to identify the molecular mechanism

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DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding author.

ETHICS STATEMENT

The animal study was reviewed and approved by the animal ethical committee of the University of KwaZulu-Natal, Durban, South Africa.

AUTHOR CONTRIBUTIONS

Conceptualization: MM, MJ, CC and OLE; Plant material and Indigenous Usage: MJ and MM; Experiments: OE; CC; VS; and MI. Metabolomics: OE and NK; Original manuscript draft: OE; CC and VS; Manuscript editing: all authors; Funding and Supervision: MM.

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SUPPLEMENTARY MATERIAL

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A Critical Review and Scientific Prospective on Contraceptive Therapeutics from Ayurveda and Allied Ancient Knowledge

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Commonly used synthetic or prescribed hormonal drugs are known to interfere with the endocrine system and may have adverse reproductive, neurological, developmental, and metabolic effects in the body. These may also produce adverse effects such as polycystic ovarian disorder, endometriosis, early puberty, infertility or toxicity to gonads, testicular germ cell cancer, breast or prostate cancer, brain developmental problems, and even birth defects. Globally, the emergence of renewed interest in natural products for reproductive health is on the rise, which offers opportunities for new contraceptive developments. The search for alternate, safer contraceptive products or agents of natural origin is of scientific interest. Ayurvedic classical texts offer knowledge and information about the reproductive function and therapeutics including those for enhancement and limiting male and female fertility. Review of ancient, medieval, and recent - including texts on erotica that provide information on approaches and large numbers of formulations and drugs of plant, mineral or animal origin—claimed to have sterilizing, contraceptive, abortifacient, and related properties is presented. Few among these are known to be toxic and few are not so common. However, most of the formulations, ingredients, or modes of administration have remained unattended to, due to issues related to consumer compliance and limitations of standardization and lack of appropriate validation modalities. Several of these ingredients have been studied for their phytoconstituents and for the variety of pharmacological activities. Efforts to standardize several classical dosage forms and attempts to adapt to modern technologies have been made. List of formulations, ingredients, and their properties linked with known constituents, pharmacological, biological, and toxicity studies have been provided in a series of tables. The possible effectiveness and safety of selected formulations and ingredients have been examined. Suggestions based on new drug delivery systems integrated with advances in biotechnology, to provide prospects for new therapeutics for contraception, have been considered. Ayurveda is built on a holistic paradigm of biological entity rather than limited gonadal functions. Graphic presentation of a few carefully chosen possibilities has been depicted. New approaches to standardization and ethnopharmacological validation of natural contraceptive therapeutics may offer novel mechanisms and modalities and therapeutic opportunities to satisfy unmet needs of contraception.

Keywords: natural contraceptive, herbal contraceptive, ayurved contraceptive, reproductive health and traditional medicine, contraceptive traditions

INTRODUCTION

The world population is expected to reach more than 11 billion by 2050 (Census of India, 2011). Population in the world is currently (2020) growing at a rate of around 1.05% per year. The current average population increase is estimated at 81 million people per year and current world population is 7.9 billion as of March 2021 (World Population Clock, 2021). This burgeoning population particularly in developing countries is a matter of concern for social, economic, and environmental reasons in terms of providing food, shelter, and life. The challenge of dealing with an ever-increasing population has been dealt with largely by conventional medicine using different methods of contraception such as oral contraceptive pills, intrauterine contraceptive devices, and barrier devices. These devices, techniques, and drugs seem to have been efficiently practiced for contraception but with many reported adverse effects as well as failure resulting in unwanted pregnancy. (Dutta, 2013).

BIRTH CONTROL HISTORY

Technically, birth control can be defined as the methods, procedures, or practices that are implemented to prevent conception leading to pregnancy in women. The term can be associated with contraception and family planning where knowledge about birth control is equally important.

The Egyptian Ebers Papyrus from 1550 BCE and the Kahun Papyrus from 1850 BCE have some of the earliest documented descriptions of birth control: the use of honey, acacia leaves, and lint to be placed in the vagina to block sperm. (Lipsey et al., 2005; Cuomo, 2010).

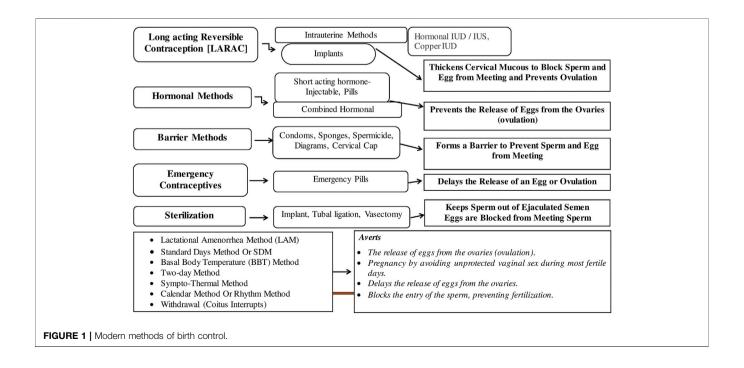
In medieval Europe, any effort to halt pregnancy was deemed immoral by the Catholic Church, (Cuomo, 2010), although it is believed that women of the time still used a number of birth control measures such as coitus interrupts and inserting lily root and rue into the vagina. Women in the middle ages were also persuaded to tie weasel—a small wild animal—testicles around their thighs during sex to prevent pregnancy. The oldest condoms discovered to date were recovered in the ruins of Dudley Castle in England and date back to 1640. They were made of animal gut and were most likely used to prevent the spread of sexually transmitted diseases during the English Civil War (Jon, 2012). Casanova, living in 18th-century Italy, described the use of a lambskin covering to prevent pregnancy; however, condoms only became widely available in the 20th century (Cuomo, 2010).

Modern Methods to Control Fertility (World Health Organization, 2020)

Several methods currently used to curb for contraception are presented (Figure 1).

ADVERSE EFFECTS

Commonly used synthetic or prescribed hormonal drugs are known to interfere with the endocrine system and may have adverse reproductive, neurological, developmental, and metabolic effects in the body. These may cause polycystic ovarian disorder, endometriosis, early puberty, infertility, toxicity to gonads, testicular germ cell cancer, breast or prostate cancer, brain developmental problems, and even birth defects. The search for alternate and safer means/drugs to prevent



birth is an open-ended area of scientific research. It is always an appealing idea to further research to develop contraceptive drugs of natural origin that have high efficacy without any adverse effects on the reproductive system.

UNMET NEEDS

According to a recent report from the Guttmacher Institute, 214 million women of reproductive age in the developing world who want to avoid pregnancy are not using a modern contraceptive method. These women are considered to have an "unmet need" for modern contraception, with 59 million relying on traditional methods such as abstinence and withdrawal and 155 million simply using no contraception at all. (Elizabeth et al., 2020).

India's total fertility rate (TFR) may have declined significantly over the years, but there remain significant challenges in family planning according to new research. In an Economic and Political Weekly article, Purushottam M. Kulkarni of Jawaharlal Nehru University suggested that there is a significant unmet need for contraception in India. Data from National Family Health Surveys (NFHS) have shown that while there was a decline in the unmet need for contraceptive services from 1992-93 (NFHS-1) through to 2005-06 (NFHS-3), and between 2005-06 and 2015-16 (NFHS-4), there has not been any significant improvement in access to contraception. (Mint, 2020).

SIGNIFICANCE OF REVIEW

Despite obvious success, the rise in population continues to remain a medical challenge due to reasons of social, economic, personal, and biological consequences. Though well-established contraceptive drugs and measures have been utilized, the long term and excessive use of hormonal contraceptives are of serious concerns due to their probable adverse effects. There is need to explore the alternative or new possibilities.

The search for an effective and safe contraceptive agent remains a challenge. Contraceptive drugs of natural origin are of all-time research interests. Traditional systems of medicine like Ayurveda address all issues related to health and illnesses based on the principle of equilibrium between the biosphere and cosmosphere, which include reproductive phenomenon. Ayurvedic pharmacopoeia has formulations and ingredients that are attributed to affect coitus, spermatogenesis, and ovulation, uterine, fetal, and placental activities. These include emmenagogues, ecbolic drugs, contraceptives, uterine sedatives for females, and depurate or drugs that hamper male sexual and reproductive capabilities, affect fluidity or motility of the seminal fluid, destroy sperms, or impede libido.

A large number of drugs are known to have sterilizing, contraceptive, and abortifacients properties. However, these indigenous means and drugs were extensively used even in rural or tribal cultures until the 20th century, when there has been no noteworthy systematic or scientific efforts to study these aspects except for a few intermittent studies. While the list of such ingredients is quite big, unusually small scientific data are

available about the nature of their active components and about their mechanisms of action.

As biotechnology-based advances open up new vistas in biomedical research, it will be of interest to examine the subject of contraception once again, as in Ayurveda, in the light of present-day pharmacology for future possibilities.

A thoughtful attempt has been made here to explore Ayurvedic and scientific aspects of formulations and ingredients as described in multiplicity of classical texts covering different facets of contraception.

METHODOLOGY

Ancient classical texts, medieval compendia, and other pertinent texts were assessed for enlisting different methods used for contraception and to enlist formulations and ingredients used for a variety of activities that could be pharmacologically linked to contraception. Specific search was undertaken for any existing review that could add to information on the subject. A systematic review of published articles on the subjects related to contraception was undertaken. The description of methods used in the experimental animal models, and the antifertility effect of active ingredients, their doses, safety, and toxicity were examined. Ninety-four plants and six minerals are reported in this review having a variety of contraceptive activities.

Flowchart of the systematic review process to search for contraceptive plants is presented. (Figure 2).

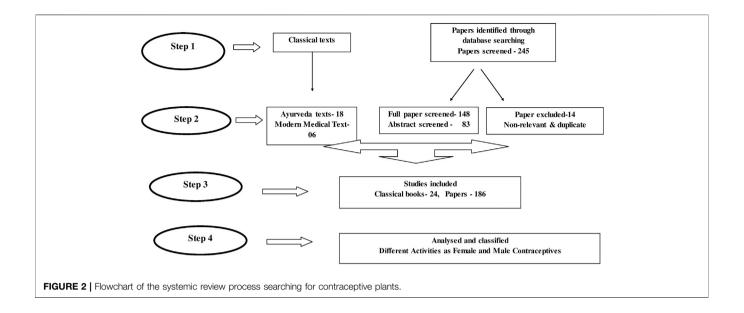
CONTRACEPTIVES IN AYURVEDA AND MEDIEVAL SANSKRIT LITERATURE

Ayurvedic literature is rife with thousands of formulations and has about 1100 ingredients attributed with well-defined therapeutic approaches including reproduction. There are references to temporary or permanent sterilization. Search for contraception from traditional knowledge of Ayurveda has been of interest to the Central Drug Research Institute, Council of Scientific and Industrial Research under Ministry of Science and Technology, and the Central Council for Research in Ayurvedic Sciences under Ministry of Health (now Ministry of AYUSH), bodies under the Government of India. Several other private and industry organizations had undertaken studies in the past. However, there is a need to revive research interest in Ayurveda in reproductive biology for safe, low-cost, user-friendly, and reliable therapeutic solutions to satisfy different contraception requirements.

Vedic Period (1500-500 BCE)

Regulated sexual life or abstinence from sex was considered the ideal method of contraception in *Vedic* times. The emphasis was more on propensity of the right, healthy progeny. Indirect references to contraception can be found in the *Atharva Veda*.

The use of drugs leading to impotence as punishment meted out to a person committing social sins or to an enemy or infliction



of injury to two cords situated near the scrotum or the scrotum itself, to put an end to one's desire for progeny were in practice. These can be considered as references for use of drugs to prevent conception, vasectomy, and castration, respectively (Satvalekar, 1958a).

A mechanical device made of stone to obstruct multiple channels of *Yoni*—the vaginal cavity to prevent conception has been mentioned. This could be considered as the earliest form of an intrauterine contraceptive device. Similarly, artificially induced changes to make the vaginal cavity rough or dry, besides its mechanical obstruction for futile coitus have been mentioned (Satvalekar, 1958b). This reference reflects some chemical changes to be produced artificially, probably in the cervical mucus obstructing the entry of sperms, or in the endometrium influencing the implantation of the zygote and a mechanical barrier in the vaginal canal. (Tewari and Chaturvedi, 1981). In *Brhadaranyaka Upanishad*, a breath exercise is advised during coitus to avoid conception (Dash and Basu, 1968).

Samhita Period: (300-500 BCE)

Though Charak Samhita, Sushrut Samhita, and Ashtang Sangraha-Bruhatryee, the three ancient most Ayurveda treatises, have elaborated the subject of reproduction extensively, there are no direct references to contraception.

Kshetra—the female reproductive system as the field, ambu—the nutrient fluids, bija—the sperm or ovum as the seed, rutukal—the ideal ovulatory period, marga—the female canal, Vayu—the neural system, and hrid—the psychological status are considered the essential factors for conception. Any or more of these factors if influenced artificially can lead to a failure of conception. The shukravaha srotas and aartavavaha srotas representing seminal and menstrual flows, respectively, are among the 13th intrinsic and interdependent biological pathways or channels (that could be explained based on now prevalent means of system biology). This early knowledge could pave the way for the development of different kinds of contraceptive

methods prevailing in the present scenario, and all of them influence one or the other factors that have been explained in the ancient classics (Vagbhatt, 2000; Sushrut, 2002).

Contraceptive activities in the context of Ayurvedic principle of fertility are explained in **Figure 3**.

Medieval Period (1000 AD to 1900 AD)

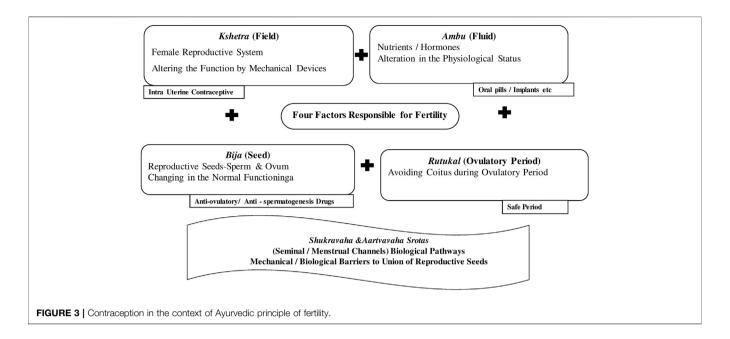
Rajamartanda written in the 11th century is probably one of the earliest texts to mention a specific prescription for contraceptives. Compendia texts like *Bhava Prakash*, *Yoga Ratnakara*, *Bhaishajya Ratnavali*, *Gadanigrah*, and several others prescribe many herbal and herbo-mineral contraceptive preparations for local and oral use by men and women.

By the 11th century, the oriental connectivity that had sociocultural effects also brought in practices to prevent conception or induce abortion. References to oral and local contraceptives are found in Bruhad Yoga Tarangini and RatiRahasya [AD800], RasaPrakashSudhakar Panchasayaka, Smaradeepika and RasaRatnaSamuccchay [AD1400], RatiManjiri [AD1500], Kandarpchudamani [AD1577], AnnangaRang, Bhavprakash and YogaRatnakar [AD1600], YogaRatnaSamucchaya [AD 1800], and Brihan Nighantu Ratnakar and BhaishjyaRatnaval i[AD 1900].

The subject of contraceptives in ancient times dealt not only with medieval medicine but also with art and the literary works of poets, playwrights, and philosophers. Like *Kama Sutra*, the famous text on erotica, a large number of books in the 19th century contain various recipes for contraception and for inducing abortions and diverse birth control practices.

Some of the most prescribed practices and recipes for preventing conception are as follows.

1. Local Contraceptives for Females
Vaginal fumigation or application before coitus with (1)
moistened *Saindhava lavana* (*Rock salt*) with *Til* (*Sesame*)
oil. (Jugnu and Sharma, 2011), (2) wood of *Neem* (*Azadirachta*



indica A. Juss.) before coitus (Tripathi, 1969), and (3) powdered root of *Dhattura (Datura metel L.)* plucked on the 14th°day (dark night) of the lunar month[Indradev, 1998] or tying the waist with roots (Lakmipatishashtri, 1983).

2. Oral Contraceptives

- Powder of Pippali (Piper longum L.) and Vidanga (Embelia ribes Burm.f.) with Tankana (Borax) taken in equal quantity in fertile phase with milk (Lakmipatishashtri, 1983).
- Flowers of *Japa (Hibiscus rosa-sinensis* L.): immediately after the delivery of a child (Bhavamisra, 1961; Lakmipatishashtri, 1983) or with *Kanji (fermented drink)* along with 48 grams of old jaggery to be taken for 3°days in the fertile phase. (Lakmipatishashtri, 1983).
- Root of *Tanduliyaka (Amaranthus spinosus* L.) with *Tandulodaka (rice water)* to be taken after menstruation for 3°days. (Lakmipatishashtri, 1983).
- Powders of *Talisa patra* (*Abies spectabilis* (D.Don) Mirb.) and *Gairika* (*Red Ochre*, Fe_2O_3) in equal parts to be consumed on the 4th day of menstruation with water. (Lakmipatishashtri, 1983).
- Aqueous extract of Rasanjana (Extract of Berberis aristata DC.), Hemavati (Sweta Vacha) (Iris × germanica L.), and Vayastha (Terminalia chebula Retz.) with cold water. (Rajeshwaradatta, 2001).
- Powders of *Amla* (*Phyllanthus emblica* L.), *Arjuna* (Terminalia arjuna (Roxb. ex DC)), and *Abhaya* (*Terminalia chebula Retz.*) with water. (Rajeshwaradatta, 2001).
- Paste made of the root of *Chitraka (Plumbago zeylanica* L.) mixed with *Nirgundi (Vitex negundo* L.) juice given orally in the dose of one 12°gm with honey. (Lakmipatishashtri, 1983).
- Powder of seeds of Sarshapa (Brassica rapa L.) with Tanduliyam (Amaranthus spinosus L.) and Sarkara

- (Sugar candy) pounded with Tandulodaka (rice water) given with milk. (Jugnu and Sharma, 2011).
- Ashes of Sehund stem (Euphorbia neriifolia L.), 12°g daily. (Kuchimara, 2007).
- Rhizome of Haridra (Curcuma longa L.) daily during the 3°days of menstruation followed by an additional 3°days (Kuchimara, 2007).
- Powders of Krishna Jeeraka (Carum carvi L.), Karchooram (Hedychium spicatum Sm.), Nagakesara (Mesua ferrea L.), Haritaki (Terminalia chebula Retz.), Kalonji (Nigella sativa L.), and Kayaphala (Myrica nagi Thunb.) made into pills in the size of ziziphus fruit for 7°days. (Kuchimara, 2007).

3. Abortifacient

- Root of Sweta Aparajita (Clitoria ternatea L.), Kakadani (Sarngesta)(Cardiospermum halicacabum L.) or Punarnava (Boerhavia diffusa L.) with oil of Eranda (Ricinus communis L.)—Patradanda (stem of leaf) to be inserted in the vagina (Rajamartanda), 1966; Tripathi, 1969; Lakmipatishashtri, 1983
- Devalaya Churna (scrapped lime powder from the wall of temple) 12°g with water. (Lakmipatishashtri, 1983; Indradev, 1998).
- Seeds of Grnjana (Carrot) (*Daucus carota* L) with roots of Tuvari (*Cajanus cajan* (L.) Huth) and Sindura (lead oxide).
- Ghotipurisa (feces of mare) mixed with Kanji, filtered, and mixed with rock salt, Ugra (*Apium graveolens* L.), and AsuriTaila (Oil of *Brassica juncea* (L.) Czern.) with Visha (*Aconitum chasmanthum* Stapf ex Holmes) (Lakmipatishashtri, 1983).

Plant and mineral drugs mentioned as contraceptives in the Ayurvedic classical texts are given in **Table 1**.

It is observed that 79 plant drugs and six mineral drugs are used as abortifacients, oral contraceptives, or as local applications

TABLE 1 List of plant and metal drugs as contraceptives in Ayurveda classics. Vertical column numbers indicate *AaartavJanan*—Emmenagogue (1), *Aparapatan*—placental expulsion (2), *Garbhanuloman/Garbhapatkar*—Abortifacient or *Garbhastravakar*—expel Fetus (3), *Garbhanirodhak Contraceptives* (4), *Garbhashayasancochak*—Ecbolic (5), *Shandhyakar/Pumstvopadhatin*— drugs that hamper male sexual or reproductive capability (6), and *Shukrashodhan*—Depurates (7).

Sanskrit name	Botanical name	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Aguru	Aquilaria malaccensis Lam.		.1					
Ahiphen	Papaver somniferum L.		\checkmark				./	
Amalaki	Phyllanthus emblica L				1		\checkmark	
Ashok	Saraca asoca (Roxb.) J.J.de Wilde	/			\checkmark	/		
Asuri		\checkmark		,		٧		
	Brassica juncea (L.) Czern			\checkmark	/			
Arjuna Rhanga	Terminalia arjuna (Roxb. ex DC.) Wight &Arn. Cannabis sativa L.				\checkmark		,	,
Bhanga Bhurianatra	Betula utilis D. Don		,	,			\checkmark	√
Bhurjapatra Chandan	Santalum album L.		\checkmark	\checkmark			,	
Chandan			,				\checkmark	
Chavya Chirbilva	Piper retrofractum Vahl Holoptelea integrifolia (Roxb.) Planch.		V	,				
Chitraka	,	,	,	√ ,	/			
	Plumbago zeylanica L.	\checkmark	\checkmark	\checkmark	\checkmark		,	
Chuka	Rumex acetosa L.	,	,				\checkmark	
Devdaru	Cedrus deodara (Roxb. ex D. Don) G. Don	\checkmark	\checkmark				,	
Dhanyak	Coriandrum sativum L.				,		√,	
Dhattura	Datura metel L.		,	,	$\sqrt{}$		\checkmark	
Ela -	Elettaria cardamomum (L.) Maton		\checkmark	√				
Eranda	Ricinus communis L.			√,				
Eshvari	Aristolochia indica L.			√,		\checkmark		
Grnjana	Daucus carota L.			\checkmark				
Haridra	Curcuma longa L.				\checkmark			
Haritaki	Terminalia chebula Retz.				\checkmark			
Harmal	Peganum harmala L.					\checkmark		
Hemavati	Iris germanica L.				\checkmark			
Hingu	Ferula assa-foetida L.			\checkmark				
Hirabol	Commiphora myrrha (Nees) Engl.					\checkmark		
Japa	Hibiscus rosa-sinensis L.				$\sqrt{}$			
Karchuram	Hedychium spicatum Sm.				$\sqrt{}$			
Kadamb	Neolamarckia cadamba (Roxb.) Bosser							\checkmark
Kakadani (Sarngesta)	Cardiospermum halicacabum L.			$\sqrt{}$				
Kakamachi	Solanum nigrum L.						\checkmark	
Karpas	Gossypium herbaceum L.	$\sqrt{}$				\checkmark		
Karpur	Cinnamomum camphora (L.) J. Presl						$\sqrt{}$	
Kasani	Cichorium intybus L.						\checkmark	
Kayaphala	Myrica nagi Thunb.				\checkmark			\checkmark
Ketaki	Pandanus tectorius Parkinson ex Du Roi			$\sqrt{}$				
Krishna Jeeraka	Carum carvi L.			$\sqrt{}$	$\sqrt{}$			
Kulattha	Vigna unguiculata (L.) Walp.	$\sqrt{}$	\checkmark				$\sqrt{}$	
Kushtha	Aucklandia costus Falc	$\sqrt{}$	\checkmark	$\sqrt{}$				
Langali	Gloriosa superba L			$\sqrt{}$		\checkmark		
Lodhra	Symplocos racemosa Roxb.					\checkmark		
Mandukparni	Centella asiatica (L.) Urb.		\checkmark					
Mocharas	Bombax ceiba L.					$\sqrt{}$		
Nagakesara	Mesua ferrea L.				$\sqrt{}$			
Nagdamani	Artemisia nilagirica (C. B. Clarke) Pamp.			$\sqrt{}$				
Neem	Azadirachta indica A. Juss.					\checkmark		
Nimbu	Citrus × aurantium L.				·	•	\checkmark	
Nilophar	Nymphaea alba L.						· √	
Nirgundi	Vitex negundo L.			\checkmark	\checkmark		V	
Pippali	Piper longum L.		\checkmark	,	, √		,	
Punarnava	Boerhavia diffusa L		•	$\sqrt{}$	•			
Rasanjana	Berberis aristata DC.			٧	$\sqrt{}$			
Rason	Allium cepa L.				•		\checkmark	
Sarshapa	Brassica rapa L.					\checkmark	٧	
Sehund	Euphorbia neriifolia L.					V √		
Shal-sarjarasa	Shorea robusta Gaertn.	\checkmark				٧		
Shallaki	Boswellia serrata Roxb.	٧				\checkmark		
Shan	Dioscorea polystachya Turcz.	$\sqrt{}$				٧		
Shigru	Moringa oleifera Lam.	V		./				
Shinshapa	Dalbergia sissoo Roxb. ex DC.			√ •/				
'	-			\checkmark		. /		
Shyonak	Oroxylum indicum (L.) Kurz					√		ollowing p

TABLE 1 | (Continued) List of plant and metal drugs as contraceptives in Ayurveda classics. Vertical column numbers indicate AaartavJanan—Emmenagogue (1), Aparapatan—placental expulsion (2), Garbhanuloman/Garbhapatkar—Abortifacient or Garbhastravakar—expel Fetus (3), Garbhanirodhak Contraceptives (4), Garbhashayasancochak—Ecbolic (5), Shandhyakar/Pumstvopadhatin—drugs that hamper male sexual or reproductive capability (6), and Shukrashodhan—Depurates (7).

Sr. No.	Sanskrit name	Botanical name	(1)	(2)	(3)	(4)	(5)	(6)	(7)
	Sitab	Ruta graveolens L.					√	√	√
	Sitaphal	Annona squamosa L.			1/	$\sqrt{}$	V	V	v
	Sunthi	Zingiber officinale Roscoe		1/	•	•			
	Sweta Aparajita	Clitoria ternatea L.		•	v /				
	Talisa patra	Abies spectabilis (D. Don) Mirb.	√	$\sqrt{}$	•	√			
	Tanduliyaka	Amaranthus spinosus L.	,	•		v			
	Tintidika	Tamarindus indica L.				•			
	Tilataila	Sesame oil						•	
	Tuvari	Cajanus cajan (L.) Huth				,			
	Ugra	Apium graveolens L.			v				
	Ulatakambal	Abroma augusta (L.) L.f.	$\sqrt{}$				$\sqrt{}$		
	Unnab	Ziziphus jujuba Mill.							
	Upakunchika	Nigella sativa L.		$\sqrt{}$			$\sqrt{}$		
	Ushir	Chrysopogon zizanioides (L.) Roberty							$\sqrt{}$
	Vacha	Acorus calamus L.			$\sqrt{}$				
	Vansha	Bambusa bambos (L.) Voss	\checkmark					\checkmark	
	Vidanga	Embelia ribes Burm.f.		\checkmark					
	Visha	Aconitum chasmanthum Stapf ex Holmes			$\sqrt{}$				
Minerals	s/Metals								
	Devalaya Churna	Scrapped lime powder from the wall of temple				$\sqrt{}$			
	Gairika	Red Ochre, Fe ₂ O ₃				$\sqrt{}$			
	Nausagar	NH ₄ Cl						\checkmark	
	Saindhava lavana	Rock salt				$\sqrt{}$			
	Sindura	Lead oxide			$\sqrt{}$	$\sqrt{}$			
	Tankana	Borax							

along with *Kanji* (fermented drink), *Tandulodaka* (rice water), *Sarkara* (sugar candy), milk, and honey.

POTENTIAL INGREDIENTS HAVING ANTIFERTILITY OR CONTRACEPTIVE PROPERTIES

This literature survey revealed that there are about more than 94 indigenous medicinal plants having scientific evidence of acting as contraceptives. Some of the remarkable plant drugs with parts used, their chemical constituents, and pharmacological activities are described in **Table 2**. This compiled information will provide useful reference for new drug designing models, acting either as male or female contraceptives.

Pharmacologically, there are about 67 medicinal plants which possess antifertility activity in females and 56 medicinal plants in males. Several plants have shown to help contraception from the female and male perspectives.

In various experimental animal models, these herbal extracts have shown minimal side effects in comparison to the chemically synthesized contraceptives, which usually contain various combinations of hormones. These plant extracts have active phytoconstituents, which are responsible for the antifertility effects such as antiovulation, anti-implantation, and others.

CLINICAL STUDIES

Some of the plants that have demonstrated interesting antifertility activity in clinical trials are as follows.

Embelia ribes Burm.f.

Single drug was administered in a dose of 2°g for 5°days followed by 1°g daily for another 10°days. After observing the effect on 2051 cycles in 45 women over 4°years, it was reported that the plant protected 95% of women from pregnancy (Tewari et al., 1976).

Hibiscus rosa-sinensis L.

Red petals of the plant *Rudrapushpaka* collected between October and December. The extract was administered to 30 sexually active women at a dose of 750°mg/day from day 7 to day 22 of the reproductive cycle. It was observed that no one had become pregnant (Tewari, 1974).

Neem oil

A study was conducted on neem seed oil as local application for the reproductive female [246 women in the fertile age-group, 4 dropped out] as a method of family planning for a period of 12–36 cycles. In nine cases, there was conception due to drug failure and in four cases, there was conception due to drug omission. Neem seed oil may be used as an external barrier as

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TABLE 2 | Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
A Anti-implantation activity					
1.	Abies spectabilis (D. Don) Mirb. Pinaceae Talisa Patra, leaf	Flavonoids, bioflavonoids, glycosides, phytosterols	Benzene, alcoholic	Anti-implantation activity	Anonymous (1996)
2.	Abroma augusta (L.) L.f. Malvaceae Pishach karpas, roots	L-rhamnose, L-arabinose, D-xylose, D- mannose, D-galactose, D-glucose, D- galacturonic acid, and D-glucuronic acid	Alcoholic	Anti-implantation	Maurya et al. (2004), Pokharkar e al. (2010), Kalita et al. (2011)
3.	Adhatoda vasica Nees synonym of Justicia adhatoda L. Acanthaceae Vasa, leaves	Alkaloids, tannins, saponins, and phenolics flavonoids	Aqueous	Anti-implantation	Pokharkar et al. (2010); Kaur et a (2011); Raj et al. (2011)
4.	Ailanthus excelsa Roxb Simaroubaceae Maharukha, leaves	Sitosterol, quassinoids, and ailantic acid	Ethanolic	Anti-implantation decreased of implant sites	Priya et al. (2012); Tamboli and Konadawar (2013)
5.	Allium cepa L. Amaryllidaceae Palandu, onion, bulb	Kampferol, $\beta\text{-sitosterol},$ ferulic acid, and myritic acid	Ethanolic	Anti-implantation inhibition of implant sites	Thakare et al. (2009); Ola- Mudathir et al. (2008)
6.	Aloe barbadensis Mill. Synonym of aloe vera (L.) Burm.f. Asphodelaceae Kumari, leaves	Water, polysaccharides, pectin, cellulose, hemicellulose, and glucomannan	Ethanolic and aqueous	Anti-implantation	Shah et al. (2017), Shah et al. (2016)
7.	Areca catechu L. Arecaceae Poogaphala, Nuts	Alkaloids—pilocarpine, arecaidine, and arecoline	Petroleum ether, alcoholic, and aqueous	Anti-implantation	Garg and Garg (1970); Garg and Garg (1971)
8.	Cassia fistula L. Fabaceae Aragvadha, fruits, bark	Alkaloid	Aqueous	Anti-implantation, decreased glycogen content in uterus, and antifertility	Yadav and Jain (2009)
9.	Carica papaya L. Caricaceae, Papaya unripe fruit pulp, seeds, latex	Papain, caricacin, carpasemine, and oleanolic glycoside	Pet ether, alcohol, and aqueous ethanol	60 % anti-implantation activity, abortifacient in albino rats	Garg and Garg (1970); Garg and Garg (1971); Das (1980); Sinha and Nathawat (1989); Changamma and Lakshman (2013)
10.	Centratherum anthelminticum (L.) Gamble Asteraceae Vanya Jeeraka, seeds	Glycosides, carbohydrates, phenolic compounds, tannins, flavonoids, proteins, saponins, and sterols	Ethanol	Postcoital anti-implantation activity	Sharma et al. (1994)
11.	Citrus × aurantium L Rutaceae Bijaura, seeds	Citroflavanoids, glucosides, and triterpenoids	Petroleum ether	Anti-implantation, antiovulatory, abortifacients increased ovarian weight, decreased Graafian follicles, and irregular estrous cycle	Patil and Patil (2013)
12.	Embelia ribes Burm.f. Primulaceae Vidang, berries	Embelin, volatile oil, and fixed oil	Isolated embelin	Anti-implantation and postcoital antifertility activity	Prakash (1981); Nand (1981); Dixi and Joshi (1983)
					(Continued on following page

TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
13.	<i>Gloriosa superba</i> L. Colchicaceae Langli Root	Colchicine (superbine)	Hydroalcoholic extract at two different doses	Antifertility, anti-implantation activity in postcoital study, abortifacient activity	Latha et al. (2013)
14.	Grewia asiatica L. Malvaceae, seeds	Potassium, calcium, phosphorus, copper, zinc, and magnesium	Aqueous	Anti-implantation and abortification activity	Kamboj and Dhawan (1982)
15.	Hibiscus rosa-sinensis L. Malvaceae Japa Flowers	Cyclopeptide alkaloid	Ethanol and benzene extract	Anti-implantation, antiovulatory, increased uterine weight, secretion of estrogenic by atretic follicles, postcoital antifertility	Neeru and Sharma (2008); Vasudeva and Sharma (2008); Hadimur et al. (2014), Pal et al. (1985)
16.	Mesua ferrea L. Calophyllaceae Nagakeshara, flowers	Mesuol, mammegin, mesuaferronea, and mammeuisin	Aqueous	Anti-implantation activity	Seshadri and Pillai (1981); Munshi et al. (1977)
17.	Michelia champaca L. Magnoliaceae Champaka, Anthers	Essential oil	Benzene and hydroalcholic extract	Postcoital anti-implantation activity	Sharma et al. (1994); Taprial et al. (2013)
18.	Momordica charantia L. Cucurbitaceae Karwellaka roots, leaves	Glycosides, saponins, alkaloids, fixed oils, triterpenes, proteins, and steroids	Aqueous	Uterine stimulant activity, Antifertility, estrogenic activity	Jamwal and Anand (1962); Saksena (1971)
19.	Plumbago zeylanica L. Plumbaginaceae Chitrak, root	Plumbagin	Plumbagin-free alcohol	Anti-implantation and abortifacient activity	Gupta et al. (2011)
20.	Ricinus communis L. Euphorbiaceae Erand, castor bean Seed	Ricinine and isoquinoline	Aqueous	Anti-implantation, increase in diameter of the uterus, and decrease in uterine hormones	Makonnen et al. (1999)
21.	Rubia cordifolia L. Rubiaceae Manjishtha Root	Munjistin, purpurin, and pseudopurpurin	Ethanolic extract	Anti-implantation	Maurya et al. (2004)
22.	Sapindus trifoliatus L. Sapindaceae Arishtak Fruits, pulp, and seeds	Essential oil	Butanol	Antizygotic, blastocytotoxic, or anti- implantation activity	Pal et al. (2013); Bodhankar et al. (1974)
23.	Sesbania sesban (L.) Merr. Fabaceae Sesban Leaves	Alkaloids, flavonoids, glycosides, tannin, anthraquinone, steroid, pholobatannins, and terpenoids	Extract and powder	Inhibit the ovarian function, change the uterine structure, and prevent the implantation	Singh (1990a); Samajdar and Ghosh (2017)
B Abortification					
activity 1.	Abroma augusta (L.) L.f. Malvaceae Pishach karpas, roots	L-rhamnose, L-arabinose, D-xylose, D-mannose, D-galactose, D-glucose, D-galacturonic acid, and D-glucuronic acid	Alcoholic	Abortification activity	Pokharkar et al. (2010); Kalita et al. (2011)
		5			(Continued on following page)

TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
2.	Abrus precatorius L. Papilionaceae Gunja, Seeds	Abrin, abrasine, precasine, and precol	Aqueous	Abortifacient activity or antifertility agent with a risk of DNA damage	Sarwat et al. (2009); Kaur et al. (2011); Shrivastava et al. (2007); Azmeera et al. (2012); Priya et al. (2012)
3.	Achyranthes aspera L. Amaranthaceae ApamargaWhole plant, Stem bark, Root	Fatty acids, oleonic acid, bisdesmosidic, triterpenoid alkaloids, D-glucuronic, betaine, and achyranthine	Benzene, ethanolic, and chloroform	Abortifacient activity in rabbits	Raj et al. (2011); Vasudeva and Sharma (2006)
4.	Adhatoda vasica Nees synonym of Justicia adhatoda L. Acanthaceae, Vasa, Leaves	Alkaloids, tannins, saponins, phenolics, and flavonoids	Aqueous	Abortification activity	Pokharkar et al. (2010); Kaur et al. (2011); Raj et al. (2011)
5.	Aegle marmelos (L.) Corrêa. Rutaceae Bilva, whole plant, leaves	Marmelosin, luvangetin, psoralen, tannins, and marmin	Aqueous extract	Abortifacient activity in albino rats	Gangadhar and Lalithakumari (1995); Sathiyaraj et al. (2010)
6.	Annona squamosa L. Annonaceae Custard apple Seeds, leaves, and bark	Atropine alkaloids, and anonaine	Ethyl acetate extract	Abortifacient induces early abortion	Jain and Dixit (1992)
7.	Areca catechu L. Arecaceae Poogaphala, nuts	Alkaloids — pilocarpine, arecaidine, and arecoline	Petroleum ether, alcoholic, and aqueous	Abortifacient activity in albino rats and antifertility activity	Garg and Garg (1970); Garg and Garg (1971); Shrestha et al. (2010)
8.	Barleria prionitis L. Acanthaceae Saireyak, Roots	Acbarlerin, barlerin, β-sitosterol, flavanol glycoside, and iridoids	Methanol extract	Abortifacient	Gupta et al. (2000)
9.	Carica papaya L. Caricaceae Papaya unripe fruit pulp, seeds, and latex	Papain, caricacin, carpasemine, and oleanolic glycoside,	Pet ether, alcohol, and aqueous ethanol	Abortifacient in albino rats and antifertility	Garg and Garg (1970), Garg and Garg (1971); Das (1980); Sinha and Nathawat (1989); Changamma and Lakshman (2013)
10.	Citrus × aurantium L Rutaceae Bijaura, Seeds	Citroflavanoids, glucosides, and triterpenoids	Petroleum ether	Abortifacient, increased ovarian weight, decreased Graafian follicles, and irregular estrous cycle	Patil and Patil (2013)
11.	Daucus carota L. Apiaceae <i>Grinjanak</i> , seed	Essential oil	Petroleum, ether, benzene, alcohol, and water	Abortifacient activity	Garg (1975); Jansen and Wolhimuth (2014); Shah and Varute (1980)
12.	<i>Gloriosa superba</i> L. Colchicaceae <i>Langli</i> Root	Carbohydrates, flavonoids, steroids, alkaloids, tannins, and glycosides	Ether, chloroform, and ethyl alcohol extracts	Abortifacient activity and significant reduction in number of implants and number of pups born	Malpani and Mahurkar (2018)
13.	Grewia asiatica L. Malvaceae, seeds	Potassium, calcium, phosphorus, copper, zinc, and magnesium	Aqueous	Abortification activity	Kamboj and Dhawan (1982)
14.	Lepidium sativum L. Brassicaceae <i>Chandrasur</i> Mature explants	Lepidine	Methanolic	Abortifacient and antiovulatory	Pande et al. (2002)
	mature explaints				(Continued on following page)

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TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
15.	Ricinus communis L. Euphorbiaceae Erand, Castor bean Seed	Ricinine and isoquinoline	Aqueous extract	Abortifacient	Makonnen et al. (1999), Sandhyakumary et al. (2003)
16.	Woodfordia fruticosa (L.) Kurz Lythraceae Dhataki, flowers	Tannins, flavonoids, anthraquinone glycosides, and polyphenols	Aqueous and ethanol	Abortifacient	Pathak et al. (2005)
C Antifertility activity					
1.	Abrus precatorius L. Papilionaceae Gunja, Seeds	Abrin, abrasine, precasine, and precol	Aqueous	Antifertility agent with a risk of DNA damage	Sarwat et al. (2009); Kaur et al. (2011); Shrivastava et al. (2007); Azmeera et al. (2012); Priya et al (2012)
2.	Acacia leucophloea (Roxb.) Willd. Leguminosae—Fabaceae Shwet babul, roots	N-hexacosanol, beta-amyrin, beta-sitosterol, and tannin	Alcoholic	Antifertility activity	Dheeraj (2011)
3.	Annona squamosa L. Annonaceae Custard apple Seeds, leaves, and bark	Atropine alkaloids and anonaine	Ethyl acetate extract	Abortifacient — induces early abortion	Jain and Dixit (1992)
4.	Areca catechu L. Arecaceae Poogaphala, Nuts	Alkaloids—pilocarpine, arecaidine, and arecoline	Nut oil Ethanolic extract	Antifertility activity in female albino rats, antiovulatory, and ovarian weight decreased due to imbalance in gonadotrophins	Garg et al. (1974); Shrestha et al. (2010)
5.	Azadirachta indica A. Juss Meliaceae Nimba Leaves, flower, and seed	Azadirachtin, nimbolinin, nimbin, nimbidin, nimbidol, sodium nimbinate, and gedunin	Female albino rabbits Seed oil	Antifertility and functional sterility	Vyas and Purohit (2018)
6.	Carica papaya L. Caricaceae Papaya unripe fruit pulp, seeds, and latex	Papain, caricacin, carpasemine, and oleanolic glycoside	Pet ether, alcohol, aqueous, and ethanol	Antifertility	Garg and Garg (1970); Garg and Garg (1971); Das (1980); Sinha and Nathawat (1989); Changamma and Lakshman (2013)
7.	Cissampelos pareira L. Menispermaceae, Patha Leaves and stem	Berberine	Leaf extract	Altered the estrous cycle pattern in female mice, Antifertility	Ganguly et al. (2007); Samatha et al. (2011)
8.	Cuminum cyminum L Apiaceae Jeerak, seeds	Cuminal and cuminic alcohol	Extract	Antifertility effect in female albino rat	Priya et al. (2012); Sharma J et al. (2001)
9.	Crateva nurvala Buch-Ham. Capparaceae Varuna Dried stem bark	Alkaloids, triterpene, tannins, saponins, flavonoids, sterols, glucosylinate, lupeol, and diosgenin	Ethanol, aqueous	Antifertility effects estrogenic activity	Bhaskar et al. (2009)
10.	Curcuma longa L. Zingiberaceae Haldi, rhizome	Curcumin and flavanoids	Ethanol, aqueous	Propylene glycol solution, antifertility, antiovulatory—suppression of GnRH	Ghosh et al. (2011); Bhagat and Purohit (1986)
					(Continued on following page)

TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
11.	Daucus carota L. Apiaceae <i>Grinjanak,</i> Seed	Essential oil	Petroleum, ether, benzene, alcohol, and water	Antifertility activity	Garg (1975); Jansen and Wolhlmuth (2014); Shah and Varute (1980)
2.	Desmodium gangeticum (L.) DC. Fabaceae Shalipami, Root	Lavonoid glycosides, pterocarpanoids, lipids, glycolipids, and alkaloids	Gangeticum	Antifertility effect	Pillai et al. (1982)
3.	Embelia ribes Burm.f. Primulaceae <i>Vidang,</i> Berries	Embelin, volatile oil, fixed oil, resin, tannin, christembine (alkaloid), and phenolic acids	Isolated embelin	Anti-implantation and postcoital antifertility activity	Prakash (1981b)
4.	Ferula jaeschkeana Vatke Apiaceae Heengupatri, Dried leaves	Flavonoids, alkaloids, terpenoids, cardiac glycosides, saponins, and phenolics	Hexane	Duration-dependent luteolytic changes in the corpora lutea	Pathak et al. (1995)
5.	<i>Gloriosa superba</i> L. Colchicaceae <i>Langli</i> , Root	Colchicine (superbine)	Hydroalcoholic extract at two different doses 30 and 60°mg/kg	Antifertility, anti-implantation activity in postcoital study	Latha et al. (2013)
6.	<i>Hibiscus rosa-sinensis</i> L. Malvaceae <i>Japa</i> Flowers	Cyclopeptide alkaloid	Ethanol and benzene extract	Anti-implantation, antiovulatory, secretion of estrogenic by atretic follicles, and postcoital antifertility	Neeru and Sharma (2008)
7.	<i>Lawsonia inermi</i> s L. Lythraceae <i>Madayantika</i> Leaves	Lawsone, esculetin, fraxetin, isoplumbagin, scopoletin, betulin, betulinic acid, hennadiol, lupeol, lacoumarin, quinone, and napthaquinone	Powder	Preventing pregnancy in 60% of the animals tested	Munshi et al. (1977)
8.	Lepidium sativum L. Brassicaceae Chandrasur Mature explants	Lepidine	Methanolic	Abortifacient and antiovulatory	Pande et al. (2002)
9.	Melia azedarach L. Meliaceae, MalaïVembu seed and leaves	Triterpenoids	Seed extract	Antifertility effect, increased preimplantation, postimplantation, and total prenatal mortalities	Mandal and Dhariwal (2007)
0.	<i>Momordica charantia</i> L. Cucurbitaceae <i>Karwellaka</i> Roots and leaves	Glycosides, saponins, alkaloids, fixed oils, triterpenes, proteins, and steroids	Aqueous	Uterine stimulant activity, antifertility, and estrogenic activity	Jamwal and Anand (1962); Saksena (1971)
1.	<i>Nigella sativa</i> L. Ranunculaceae <i>Krishna jeerak,</i> Seeds	Fixed oil, volatile oil, and alkaloids	Hexane	Antifertility activity in rats, postcoital contraceptive	Keshri et al. (1995)
2.	<i>Piper betle</i> L. Piperaceae <i>Betel leaf, Pan</i> Petiol	Eugenol, eugenol acetate, piper betol, piperol, and methyl eugenol phytol	Alcoholic	Antifertility, antiestrogenic effects in female rats	Sharma et al. (2007)
3.	Piper longum L. Piperaceae Pippali Root and ruits	Piperine	Powder, hexane fraction, and benzene	Antifertility activity—prolonged the length of the extort cycle, drastic reduction in the number of implantation sites, marked suppression in the ovarian cytokines and siting solid length.	Laxmi et al. (2006); Kholkute e (1979)
				nitric acid level	(Continued on following pa

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TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
24.	Trichosanthes cucumerina L. Cucurbitaceae Snake gourd, Fruit	Cucurbitacin B, cucurbitacin E, isocucurbitacin B, E, sterols 2 β -sitosterol stigmasterol	Aqueous	Affected the normal estrous cycle, significantly reduced the number of healthy follicles, corpora lutea, and increased the number of regressing follicles. Reduced serum FSH and LH levels	Devendra et al. (2009)
25.	Zingiber officinale Roscoe Zingiberaceae Sunthi Rhizome	Monocyclic, phenols, sesquiterpenees sential oil, oleoresins, and proteolytic enzymes	Aqueous, ethanol extracts	Antifertility activity	Pathak et al. (2005)
D Antiovulatory activity					
1.	Achyranthes aspera L. Amaranthaceae ApamargaWhole plant, Stem bark, Root	Fatty acids, oleonic acid, bisdesmosidic, triterpenoid alkaloids, D-glucuronic, betaine, and achyranthine	Benzene, ethanolic, chloroform	Antiadulatory, anti-implantation, hormonal disturbance in uterus, and expulsion of ovary	Shibeshi et al. (2006); Vasudeva and Sharma (2006)
2.	Areca catechu L. Arecaceae Poogaphala, Nuts	Alkaloids—pilocarpine, arecaidine, and arecoline	Ethanolic extract	Antiovulatory, ovarian weight decreased due to imbalance in gonadotrophins	Shrestha et al. (2010)
3.	Azadirachta indica A. Juss. Meliaceae Nimba Leaves, flower, and seed	Azadirachtin, nimbolinin, nimbin, nimbidin, nimbidol, sodium nimbinate, and gedunin	Alcoholic extract flower in Sprague–Dawley rats	Disrupted the estrous cycle and caused a partial block in ovulation	Gbotolorun et al. (2003); Vyas and Purohit (2018)
4.	Butea monosperma (Lam.) Kuntze Fabaceae Palash, bark, and flowers	Kino-tannic acid, gallic acid, and pyrocatechin	Aqueous extract	Inhibit ovulation	Shrivastava et al. (2007), Sinha and Nathawat (1989)
5.	Calotropis procera (Aiton) W.T. Aiton Apocynaceae Arka, Root	Steroidal alkaloid	Calotropin, aqueous ethanol	Antiovulatory prolonged di-estrous stage with temporary inhibition of ovulation	Gupta et al. (1990); Abdelgader and Elsheikh (2018); Sharma and Jacob (2001a); Pokharkar et al. (2010)
5.	Catunaregam spinosa (Thunb.) Tirveng. Rubiaceae Madanphal, Fruits, seeds, and pulp	Saponins, valeric acid resin, wax, and coloring matter	Ethanolic extract, isolated oleic acid	Antiovulatory effect in rabbits, antiimplantation activity in albino rats	Malhi and Trivedi (1972); Pillai et al. (1977)
7.	Citrus × aurantium L Rutaceae Bijaura, Seeds	Citroflavanoids, glucosides, and triterpenoids	Petroleum ether	Anti-implantation, antiovulatory, abortifacient, increased ovarian weight, decreased Graafian follicles, irregular estrous cycle	Patil and Patil (2013)
3.	Curcuma longa L. Zingiberaceae Haldi, rhizome	Curcumin and flavanoids	Ethanol, aqueous	Propylene glycol solution antifertility, antiovulatory, decreased ovarian weight, suppression of GnRH	Ghosh et al. (2011)
9.	Hibiscus rosa-sinensis L. Malvaceae Japa, Flowers	Cyclopeptide alkaloid	Ethanol, benzene extract	Anti-implantation, antiovulatory, increased uterine weight, secretion of estrogenic by atretic follicles, postcoital antifertility	Neeru and Sharma (2008)
	•			,	(Continued on following page)

TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
0.	<i>Musa paradisiaca</i> L. Musaceae, <i>Banana</i> , stem	Alkaloids and flavonoids	Ethanolic	Antiovulatory suppressed ovulation due to inhibition in secretion of GnRH	Soni et al. (2013)
1.	Papaver somniferum L. Papaveraceae Ahiphen, Latex	Noscapine alkaloid	Alcoholic extract	Antiovulatory decreased production of gonadotrophin	Kumar and Sachin (2013)
2.	Plumbago rosea L. Plumbaginaceae Raktachitrak, Leaves	Plumbagin, sitosterol glycoside, tannins, and fatty alcohol	Acetone, ethanolic	Antiovulatory inhibition of ovulation with irregular estrous cycle	Sheeja et al. (2011)
3.	Semecarpus anacardium L.f. Anacardiaceae Bhallatak Fruits	Alkaloids	Aqueous and ethanolic	Reversible antiovulatory activity	Sushma et al. (2016)
4.	Taxus baccata L. Taxaceae Talishpatra Common Yew Leaves	Pseudo alkaloids	Leaf extract	Antiovulatory, inhibited secretion of ovarian hormones	Priya et al. (2012); Kaur et al. (2011)
5.	Vitex negundo L. Lamiaceae Nirgundi, roots, and seeds	Casticin, isoorientin, chrysophenol D, luteolin, p-hydroxybenzoic acid, and D-fructose	Aqueous	Antiovulatory activity	Lal et al. (1992)
Antiestrogenic					
ctivity	Allium sativum L. Amaryllidaceae Rason, Bulb	Sulfur-containing compounds	Alcohol	Ecobolic in mice and rats, estrogenic activity in female albino rats	Tewari et al. (1971); Ola-Mudatl et al. (2008)
	Cyperus rotundus L. Cyperaceae Musta, Rhizome	Cyperene, humulen, selinene, zierone, campholenicopaene, and limonene	Aqueous	Antiestrogenic property	Gediya et al. (2011)
	Glycyrrhiza glabra L. Fabaceae Yashtimadhu, Roots	Triterpene glycyrrhizin acid and glycoside	Water	Estrogenic activity	Ahmad et al. (2011)
	Guilandina bonduc L. sy. Caesalpinia bonduc (L.) Roxb. Leguminosae Karanja, seeds	Phytosterinin, β -sitosterol, flavonoids, bonducellin, aspartic acid, arginine, and citrulline β -carotene	Aqueous	Antiestrogenic activity	Salunke et al. (2011)
	Nelumbo nucifera Gaertn. Nelumbonaceae Kamala, Lotus Seeds	Hydrocarbons	Ethanolic extract	Antiestrogenic, decreased ovarian weight, estrogens inhibition	Mutreja et al. (2008)
	Sesamum indicum L. Pedaliaceae Tila, seeds	Oil, protein, and carbohydrate	Extract	Estrogenic effect in female albino rats	Priya et al. (2012)
	Vitex negundo L. Lamiaceae Nirgundi, roots and seeds	Casticin, isoorientin, chrysophenol D, luteolin, p-hydroxybenzoic acid, and D-fructose	Aqueous	Antiovulatory activity	Lal et al. (1992)

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TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
F Antispermatogeni activity	С				
1.	Abru sprecatorius L. Papilionaceae Gunja, seeds	Abrin, abrasine, precasine, and precol	Aqueous	Reduced sperm motility, density, antispermatogenic effect, reduced activity of testicular enzyme, post-testicular antifertility effect	Bajaj et al. (1981); Dixit et al. (1987); Kulshreshtha and Mathur (1990); Sinha (1990)
2.	Aegle marmelos (L.) Corrêa. Rutaceae Bilva, whole plant and leaves	Marmelosin, luvangetin, psoralen, tannins, and marmin	Aqueous extract	Inhibit spermatogenesis and sperm motility male rat reproduction, affecting the sexual behavior and epididymal sperm concentration	Sur et al. (1999); Sur et al. (2002)
3.	Albizia lebbeck (L.) Benth. Fabaceae Shirish, Pods	Melacacidin, D-catechin, β-sitosterol, albiziahexoside, betulnic acid, and echinocystic acid glycosides	Methanolic extract	Spermatogenic arrest in male albino rats	Gupta et al. (2004); (Gupta et al. 2005a)
4.	Andrographis paniculata (Burm.f.) Nees Acanthaceae Kirattikta, leaves	Andrographolide, Andrographidoids A, B, C, D, E, diterpenoid, and lactone	Water extract	Antispermatogenic	Akbarsha et al. (1990); Akbarsha and Murugaian (2000)
5.	Ananas comosus (L.) Merr. Bromeliaceae Custard apple, seeds	Atropine alkaloids and anonaine	Water	Antispermatogenic activity	Satyawati (1983)
6.	Annona squamosa L. Annonaceae Custard apple Seeds, leaves, and bark	Atropine alkaloids and anonaine	Ethyl acetate extract	Antispermatogenic activity	Jain and Dixit (1992)
7.	Areca catechu L. Arecaceae Poogaphala, Nuts	Alkaloids—pilocarpinearecaidine, arecoline	Water	No abnormality in Leydig cell and interstitium tissue	Ave Olivia et al. (2020)
8.	Aristolochia indica L. Aristolochiaceae Ishwari, roots	Aristolochic acid, ceryl alcohol, β-sitosterol, stigmast-4-en-3-one, friedelin, and cycloeucalenol	Aristolochic acid	Antispermatogenic	Gupta et al. (1996)
9.	Azadirachta indica A. Juss. Meliaceae Nimba Leaves, flower, and seed	Azadirachtin, nimbolinin, nimbin, nimbidin, nimbidol, sodium nimbinate, and gedunin	Aqueous, alcoholic	Decrease in the weight of seminal vesicles, ventral prostate, reduction in epithelial height, nuclear diameter, and the secretory materials in the lumen	Gediya et al. (2011)
10.	Bacopa monnieri (L.) Wettst. Plantaginaceae Brahmi, whole plant	Bacosides and saponins	Aqueous extract	Reversible suppression of spermatogenesis and fertility, without producing apparent toxic effects	Singh et al. (2013)
11.	Balanites roxburghii Planch. Zygophyllaceae Ingudi, Fruit pulp	Saponin, furanocoumarin, and flavonoid	Methanol, palmitine hydroxide	Antispermatogenic activity	Dixit et al. (1981), Agarwal and Dixit (1982)
12.	Berberis aristata DC. Berberidaceae Daruharidra, Roots	Berberine and berbamine	Palmitine hydroxide	Antispermatogenic action	Gupta and Dixit (1989)
	_ a a nana, a, . 10000				(Continued on following page)

TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
13.	Butea monosperma (Lam.) Kuntze Fabaceae Palash, bark, and flowers	Kino-tannic acid, gallic acid, and pyrocatechin	Aqueous extract	Antispermatogenic effect	Wati and Verute (1988)
14.	Calotropis procera (Aiton) W.T. Aiton Apocynaceae Arka, root	Steroidal alkaloid	Calotropin, aqueous ethanol	Antispermatogenic, antiandrogenic activities, and/or endocrine disrupting effects, functional alteration in genital organ	Gupta et al. (1990); Abdelgader and Elsheikh (2018); Sharma and Jacob (2001b) Pokharkar et al. (2010)
15.	Carica papaya L. Caricaceae Papaya, unripe fruit pulp, seeds, latex	Papain, caricacin, carpasemine, oleanolic glycoside,	Pet ether, Alcohol, aqueous Ethanol	Antispermatogenic activity reduced spermatogenesis, inhibition in steroidal hormones	Changamma and Lakshman (2013)
16.	Celastrus paniculatus Willd. Celastraceae Jyotishmati, seeds	Alkaloids, tannins, saponins, steroid, terpenoid, flavonoids, phlobatannin, cardiac, and glycoside	Seed	Antispermatogenic activity	Bidwai et al. (1990)
17.	Cichorium intybus L. Asteraceae, Chicory Whole plant	Inulin, sesquiterpene lactones, vitamins, minerals, fat, and mannitol,	Aqueous	Antispermatogenic activity	Roy and Venkatakrishna (1983)
18.	Cinnamomum camphora (L.) J.Presl Lauraceae Karpur Camphor, leaves and resin	Essential oil—camphor, linalool, and cineole	Leaf	Inhibition of spermatogenesis	Singh (1990b)
19.	Cuminum cyminum L Apiaceae Jeerak, seeds	Cuminal and cuminic alcohol	Extract	Antispermatogenic effect	Priya et al. (2012); Sharma J et al (2001)
20.	Embelia ribes Burm.f. Primulaceae <i>Vidang</i> , berries	Embelin, volatile oil, and fixed oil	Isolated embelin	Inhibition of spermatozoa motility	Prakash (1981); Nand (1981); Dixi et al. (1983); Gupta et al. (1989)
21.	Euphorbia neriifolia L. Milk brush Euphorbiaceae Latex, Whole plant	$\beta\text{-amyrin}$ acetate, lupenone, 3-acetoxy-20-lupanol, cycloart-25-en-3 β , 24 ζ -diol, and cycloart	Ethanol	Antispermatogenic effect	Mali (1999)
22.	<i>Hibiscus rosa-sinensis</i> L. Malvaceae <i>Japa</i> Flowers	Cyclopeptide alkaloid	Ethanol, benzene extract	Spermatogenic elements of testis and epididymal sperm count., androgenic activity	Reddy et al. (1997); Gupta et al. (1985)
23.	<i>Momordica charantia</i> L. Cucurbitaceae <i>Karwellaka</i> Roots and leaves	Glycosides, saponins, alkaloids, fixed oils, triterpenes, proteins, and steroids	Aqueous	Antispermatogenic, antisteroidogenic activity	Naseem et al. (1998)
24.	Ocimum sanctum L. Lamiaceae, Tulsi, leaves	Carvacrol, sesquiterpene, hydrocarbon, and caryophyllene	Benzene extract	Decreased sperm count, weight of testis, and sperm motility	Pandey and Madhuri (2010) (Continued on following page)

TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
25.	Piper betle L Piperaceae Betel leaf, Pan Petiole	Eugenol, eugenol acetate, piper betol, piperol, methyl eugenol, and phytol	Alcoholic extract	Reduced sperm motility	Adhikary et al. (1989); Sarkar et al (2000)
26.	Piper nigrum L. Piperaceae Marich, Black pepper Fruit	Piperine	Fruit powder—suspended in sterile distilled water containing milk powder	Alterations in the male reproductive organs, reversible after cessation of treatment	Mishra and Singh (2009), Malini e al. (1999)
27.	Plumbago zeylanica L. Plumbaginaceae Chitrak, Root	Plumbagin	Ethnol	Antispermatogenic	Purohit et al. (2008)
28.	Pterocarpus santalinus L.f. Fabaceae Raktachandan Stem bark	Santalin A, B, savinin, calocedrin, pterolinus K, L, and pterostilbenes	Water	Semen coagulating activity	Dhawan et al. (1980)
29.	Pueraria tuberosa (Willd.) DC. Fabaceae, Varahikand, rhizome	Puerarin, genistein, and daidzein	Methanol	Inhibition of spermatogenesis	Gupta et al. (2004), Gupta et al. (2005b)
30.	Semecarpus anacardium L.f. Anacardiaceae Bhallatak, Marking nut, Seeds	Bhilwanols, phenolic compounds, biflavonoids, and sterols glycosides	Ethanolic	Reduction in the number of primary spermatocytes, secondary spermatocytes, and spermatids	Gupta et al. (2013); Sharma et al. (2003)
31.	Terminalia arjuna (Roxb. ex DC.) Wight &Arn. Combretaceae Arjuna, Bark	Tannins, triterpenoid saponins, flavonoids, gallic acid, ellagic acid, and phytosterols	Crude form	Inhibition of spermatogenesis	Jha and Dixit (1986), Lal and Udupa (1993)
32.	Tylophora asthmatica (L. f.) Wight &Arn. Apocynaceae Khadki Rasna Leaf and stem	Aempferol, quercetin, tyloindane, cetyl-alcohol, Pure alkaloid Antispermatogenic activity tannins, glucose, calcium salts, and potassium chloride		Antispermatogenic activity	Dikshith et al. (1990)
G Spermicidal					
activity 1.	Acacia concinna (Willd.) DC. Leguminosae-Mimosoideae Shikekai, stem bark	Hexacosanol, spinasterone, oxalic, tartaric, citric, succinic, ascorbic acid, alkaloids calyctomine, and nicotine	Alcoholic	Spermicidal and semen coagulating activity	Kamboj and Dhawan (1982)
2.	Achyranthes aspera L. Amaranthaceae ApamargaWhole plant, Stem bark, Root	Fatty acids, oleonic acid, bisdesmosidic, triterpenoid alkaloids, D-glucuronic, betaine, and achyranthine	Benzene, ethanolic, and chloroform	Spermicidal	Raj et al. (2011); Shibeshi et al. (2006); Vasudeva and Sharma (2006)
3.	Alstonia scholaris (L.) R.Br. Apocynaceae Saptaparna, stem bark	Erythrodiol, uvaol, betulin, oleanolic acid ursolic acid, and $\beta\text{-amyrin}$	Water extract	Decline germ cell population	Gupta et al. (2003), 2004)
4.	Azadirachta indica A. Juss. Meliaceae Nimba Leaves, flower, and seed	Azadirachtin, nimbolinin, nimbin, nimbidin, nimbidol, sodium nimbinate, and gedunin	Aqueous and Alcoholic	Spermicidal effect on number of spermatozoa and level of fructose	Gediya et al. (2011), Kasturi et al. (1997)
5.	Bambusa bambos (L.) Voss Poaceae, Vansha Tender stem	Balarenone, barlerin, barlerinosideverbascoside, acetylbarlerin, and lupulinoside	Ethanolic	Reduced sperm motility	Vanithakumar et al. (1989)
					(Continued on following page)

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TABLE 2 | (Continued) Medicinal plants and their phyotoconstituents validated for various female/male contraceptive activities. Different contraceptive activities studied on medicinal plants could be categorized as follows. Female contraceptive activities: (2A) anti-implantation activity, (2B) abortification, (2C) antifertility, (2D) antiovulatory, and (2E) antiestrogenic activity. Male contraceptive activities: (2F) antispermatogenic, (2G) spermicidal, and (2H) antiandrogenic activity.

Cannabaceace Cann	Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference
7. Counting contents (1,1 Schrad Carbohystate, protein, amino acid, sarnis, Counting appoints, prepared and plaid (1997) Counting appoints, pagents, phenoics, and cardogycoloids Indivivantial Bitter appoint, fulls 8. Datus carofe L. Essential of Essential Office Essential Offic	6.	Cannabaceae	Cannabinoids, terpenes, and sesquiterpenes	Butin	Testicular lesions	Dixit and Joshi (1982)
Aguing Secretary Aguing Secr	7.	Citrullus colocynthis (L.) Schrad. Cucurbitaceae Indrawaruni		Ethanol	Impairment of sperm	Chaturvedi and Dixit (1997)
Privalecace Mortifica arrayeans Mortificace	3.	Daucus carota L. Apiaceae	Essential oil		Spermicidal activity	Wolhlmuth (2014); Shah and
Lamilaceae Pudina, leaves 11. Myristica fragrans Houtt Myristicin, elemicin, myristic acid, alpha-pinene, and trimyristin 12. Strychnors potatorum L.f. Strychnine Seeds Nimal, Seeds 13. Terminalis belinica (Saertn) Pennolic acids, saponins, lignans, triterpenoids, resveratrol glycosides, arjungenin, β-sitosterol, and stigmasterol Babhitak 14. Tinospora cordilolia (Willd.) Berberine, palmatine D, choline D, diterpene, Aqueous Spermicidal Reduced weight of testis, sperm count 15. Tinoson Menispermaceae 16. Minitalis Seeds 17. Tingonela foenum-graecum L., Fabaceae 18. Multina, Seeds 18. Tinoson Menispermaceae 18. Aminta Gible 18. Stem 19. Water, carbohydrates, protein, fat, and calcium Aqueous 19. Stem, ethanolic 19. Stem, ethanolic 19. Withanosomillera (L.) Dunal Seeds 19.	9.	Primulaceae	Embelin			Nand (1981); Dixit and Bhagava (1983)
Myristicaceae terpenes, beta-pinene, and trimyristin Nutriney, Jatiphals, seeds Strychnine potatorum Lr. Strychnine Seed extract Suppressive effects on male fertility Gupta et al. (2006) Cuganiaceae Nirmals, Seeds Nirmals,	10.	Lamiaceae	Alkaloids, steroids, and glycosides	Petroleum ether		Sharma and Jacob (2001a)
12. Strychnos potatorum L.f. Loganiaceae Nimal, Seeds 13. Farminalia bellifica (Gaertn.) Phenolic acids, saponins, lignans, triterpenoids, Pooth Row Row Row Row Row Row Row Row Row Row	11.	Myristicaceae		Ethanol	Premature ejaculation	Mishra and Shukla (1980)
13. Terminalía bellirica (Gaertn.) Phenolic acids, saponins, lignans, triterpenoids, Roxb. resveratrol glycosides, arjungenin, β-sitosterol, Combretaceae Bibhitak Fruits Fruits Trinospora cordifolia (Willd.) Berberine, palmatine D, choline D, diterpene, Hook.f. 4. Thomson Amispermaceae Amita Giloe Stem Amita Giloe Amita Gi	12.	Strychnos potatorum L.f. Loganiaceae	Strychnine	Seed extract	suppressive effects on male fertility	Gupta et al. (2006)
Hook.f. terpenoids alkaloids, and steroids sperm count & Thomson Menispermaceae Amrita Giloe Stem 15. Trigonella foenum-graecum L., Fabaceae Methika, Seeds 16. Withania somnifera (L.) Dunal Solanaceae Ashwagandha Stem and root H Antiandrogenic activity 1. Aloe barbadensis Mill. Synonym of Aloe vera (L.) Burm.f. Asphodelaceae Kumari, leaves Hook.f. Erpenoids alkaloids, and steroids Sperm count	13.	Terminalia bellirica (Gaertn.) Roxb. Combretaceae Bibhitak	resveratrol glycosides, arjungenin, β -sitosterol,	Aqueous		Kaur et al. (2011)
Fabaceae Methika, Seeds 16. Withania somnifera (L.) Dunal Solanaceae Ashwagandha Stem and root H Antiandrogenic activity 1. Aloe barbadensis Mill. Synonym of Aloe vera (L.) Burm.f. Asphodelaceae Kumari, leaves Fabaceae Methika, Seeds Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (198) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (198) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (198) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (198) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (198) Stem and root H Antiandrogenic activity on monkeys Dixit et al. (1983)	14.	Hook.f. & Thomson Menispermaceae <i>Amrita Gil</i> oe		Aqueous		Gupta and Sharma (2003)
Mithania somnifera (L.) Dunal Withanolides Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Solanaceae Ashwagandha Stem and root H Antiandrogenic activity 1. Aloe barbadensis Mill. Water, polysaccharides, pectin, cellulose, Synonym of Aloe vera (L.) Burm.f. Asphodelaceae Kumari, leaves Withanolides Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Alia (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Stem, ethanolic Reversible spermicidal and infertilizing effect Singh et al. (2013); Mali (1995) Stem et al. (2013); Mali (1995) St	15.	Trigonella foenum-graecum L., Fabaceae	Water, carbohydrates, protein, fat, and calcium	Aqueous	Spermicidal activity in human and rat semen	Priya et al. (2012)
activity 1. Aloe barbadensis Mill. Water, polysaccharides, pectin, cellulose, Extract Antiandrogenic activity on monkeys Dixit et al. (1983) Synonym of Aloe vera (L.) Burm.f. hemicellulose, and glucomannan Asphodelaceae Kumari, leaves	16.	Withania somnifera (L.) Dunal Solanaceae Ashwagandha	Withanolides	Stem, ethanolic	Reversible spermicidal and infertilizing effect	Singh et al. (2013); Mali (1999)
1. Aloe barbadensis Mill. Water, polysaccharides, pectin, cellulose, Extract Antiandrogenic activity on monkeys Dixit et al. (1983) Synonym of Aloe vera (L.) Burm.f. hemicellulose, and glucomannan Asphodelaceae Kumari, leaves						
		Synonym of Aloe vera (L.) Burm.f. Asphodelaceae		Extract	Antiandrogenic activity on monkeys	Dixit et al. (1983)
		Kumari, leaves				(Continued on following page

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Sr. No.	Botanical name, family, Sanskrit name, parts	Chemical composition	Extract	Mode of action in experimental studies	Reference	
2.	Aristolochia indica L. Aristolochiaceae Ishwari, roots	Aristolochic acid, ceryl alcohol, β-sitosterol, stigmast-4-en-3-one, friedelin, and cycloeucalenol	Aristolochic acid	Antiandrogenic effects on langur monkey	Gupta et al. (1996)	
3.	Andrographis paniculata (Burm.f.) Nees Acanthaceae Kirattikta, leaves	Andrographolide, andrographidoids A, B, C, D, E, diterpenoid, and lactone	Water extract	Antiandrogenic	Akbarsha et al. (1990); Akbarsha and Murugaian (2000)	
4.	Azadirachta indica A. Juss., Meliaceae Nimba Leaves, flower, and seed	Azadirachtin, nimbolinin, nimbin, nimbidin, nimbidol, sodium nimbinate, and gedunin	Seed oil	Antiandrogenic	Sharma et al. (1987); Sinha et al. (1984); Roop et al. (2005)	
5.	Cuscuta reflexa Roxb Convolvulaceae Amarwel, whole plants	Alkaloids	Methanolic	Antisteroidogenic	Gupta et al. (2003)	
6.	Curcuma longa L. Zingiberaceae Haldi, rhizome	Curcumin and flavanoids	Ethanol, aqueous	Antiandrogenic	Bhagat and Purohit (1986)	
7.	Foeniculum vulgare Mill Apiaceae Common fennel, seeds	Anethole, alpha pinene, beta myrcene—pinene, bitter fenchone, camphene, and estragole	Alcoholic	Antiandrogenic	Farooq et al. (1997)	
8.	Hibiscus rosa-sinensis L. Malvaceae Japa, Flowers	Cyclopeptide alkaloid	Ethanol and Benzene extract	Spermatogenic elements of testis and epididymal sperm count., androgenic activity	Reddy et al. (1997); Gupta et al. (1985)	
9.	Mucuna urens (L.) Medik. Fabaceae Horase been, Kapikacchu Seeds	L-DOPA, with trace amounts of serotonin, nicotine, and bufotenine	Water	Effect on gonads and sex accessory glands	Udoh and Ekpenyong (2001)	
10.	Nicotiana tabacum L Solanaceae Tobacco, leaves	Lipid constituents, free fatty acids, triglycerides, and sterol esters free sterols	Nicotine	Antiandrogenic	Londonkar et al. (1998)	
11.	Plumbago zeylanica L. Plumbaginaceae Chitrak, root	Plumbagin	Plumbagin-free alcohol	Antiandrogenic	Bhargava (1984)	
12.	Ruta graveolens L. Rutaceae, Rue, leaves	Volatile oil	Aqueous extracts	Adverse effects on territorial aggression and sexual behavior in male albino rats	Khouri and Akawi (2005)	
13.	Semecarpus anacardium L.f. Anacardiaceae Bhallatak, Marking nut, Seeds	Bhilwanols, phenolic compounds, biflavonoids, and sterols glycosides	Aqueous extracts	Antiandrogenic	Singh (1985)	

a cost-effective herbal contraceptive for its spermicidal property and is considered safe for regular use. (Achintya, 2018).

Ricinus communis L.

The seeds of *Ricinus communis Linn* RICOM-1013-J, administered as a single oral dose of $2.3-2.5^{\circ}g$ once/12°months acted as protection against pregnancy in 50 women volunteers. The study revealed very minimal side effects. The antifertility and contraceptive efficacy of RICOM-1013-J is due to hormonal mechanisms (Isichei et al., 2000). Goncim et al. (2010) stated that one seed of *Ricinus communis L*. taken orally can prevent ovulation in humans and the anticonceptive effect may be due in part to the prevention of ovulation.

Compound Formulation

A study was conducted on a combination of Ashoka (Saraca indica L.), Vidanga (Embelia ribes Burm.f.), Laksha (lac), and Kramuk (Areca nut) on 834 young, healthy patients in active reproductive age below 40°years. The drug was administered from the 5th°day of LMP for a period of 15°days in a daily dose schedule of 1°gm (2 tablets) at bedtime with milk. Results suggested that the failure rate of treatment 1.19/HWY is comparable to both steroidal oral contraceptive pills and intrauterine device. It does not affect the hypothalamopituitary axis and did not have any other adverse effects. It can be a good alternative for lactating women (Palep and Jukar, 2003).

Central Council for Research in Ayurveda and Siddha had taken up a number of studies to evaluate the efficacy of Ayurvedic formulations like *K Capsule, Ayush AC-IV, Pippalyadi yoga (in three different doses), Ayush AC II, Talisadi yoga, Vidangadi yoga*, etc., which were proved as safe and effective in different clinical studies. Besides this, the council also tried the efficacy of *neem oil*—as a local contraceptive and found encouraging results (Galib et al., 2008).

TERATOGENIC EFFECT

Ayurveda classical texts have references to congenital birth [anmabalapravrita] disorders as per the etiopathology and clinical presentation. Some congenital malformations in the fetus may occur but the mechanism is still not clear.

Teratogen is an agent or factor that causes malformation in the embryo. One of the causes of malformation may be toxic substances such as drugs and environmental toxins in pregnancy.

Herbal drugs with appropriate dose and duration may not cause teratogenic effect but in the case of excess dose with improper mode of administration, for a longer duration than therapeutically advised, teratogenic effect may be seen. Scientific validation of their safe use in pregnancy is hardly documented. Teratogenic effects of some of the medicinal plans have been mentioned in **Table 3**.

It is observed that drugs having contraceptive and abortifacient action have potent teratogenic effect in experimental models. There are several studies of teratogenicity on other herbal drugs which are not showing teratogenic effects in low doses and may cause

teratogenic effects in high doses, for example, Ashwagandha (Withania somnifera (L.) Dunal), Punarnava (Boerhavia diffusa L.), Narangi (Citrus aurantium L), Nimba (Azadirachta indica A. Juss.), Jatamansi (Nardostachys jatamansi (D.Don) DC.), (Bala Abutilon indicum L.) Sweet), and Yastimadhu (Glycyrrhiza glabra L.) (Jati, 2018).

Different contraceptive activities in the abovementioned 94 plant ingredients are categorized in **Table 4**.

DISCUSSION

Presently, scientifically established methods of contraception and contraceptive drugs are used extensively. The synthetic contraceptive drugs known to interfere with the endocrine system and natural hormones may produce reproductive, neurological, developmental, and metabolic adverse effects that are serious at times. Search for safer drugs and preference for natural origin contraceptive drugs and methods are of research interests. Necessarily, the objectives for research of novel contraceptives from nature would be the assurance regarding effectiveness, safety, and user compliance. There are many plants known to have antifertility activity both in male and female. Some of these plants had spermicidal and altered hormone levels.

The classical Ayurvedic texts offer substantial knowledge on reproductive biology for healthy progeny and medieval Ayurvedic and specific Sanskrit texts provide information about methods and a broad range of therapeutics and ingredients that are described for use in contraception. These include local and oral contraceptives, abortifacients, and other methods of antifertility and birth control. These formulations and ingredients are a valuable source for extended research in the field of contraception.

In this study, 94 indigenous medicinal plants have been reviewed. Chemotaxonomically, it is of interest to note that the maximal number of plants having abortifacient and contraceptives are from *Fabaceae*, *Acanthaceae*, *Euphorbiaceae*, and *Liliaceae* families.

Ingredients, Phytoconstituents, and Contraceptive Activities

Certain alkaloids, glycosides, saponins, tannins, terpenoids, and other phytoconstituents are known to disrupt ovarian functions and estrous cyclicity through interplay of ovarian and extra ovarian hormones. Alkaloids are a major group of secondary metabolites bitter in taste that stimulate the central nervous system or directly work on the human brain. These are antiparasitic, antiplasmodial, anticorrosive, antioxidative, antibacterial, anti-HIV, and have insecticidal activities. In a review, it has been suggested that maximum alkaloids containing plant drugs have been reported to have an antifertility, antiovulatory, anti-implantation, abortifacient effect on animals (Choudhury and Jadhav, 2013).

A majority of these medicinal ingredients used either in formulations or singly over centuries have also been studied for a variety of pharmacological, biological, and therapeutic activities.

Achyranthes aspera L.

A plant known to have antimicrobial, hypolipidemic, and has antifertility qualities is also used to treat asthma and cough.

Fruits of Annona squamosa L.

A known insecticidal, antiovulatory, and abortifacient plant that is hematinic, cooling, a sedative, stimulant, expectorant, and tonic. Its seeds are abortifacient and insecticidal and are used to destroy lice in the hair.

Calotropis gigantea L.

Calotropis gigantea L. having certain antifertility glycosides and cardenolides is used for colic pain, flatulence, asthma, cough, and whooping cough and has wound healing, anticancer, and hypoglycaemic effects. Calotropis Madar rootbark is used for

abortive purposes and in India is used as an antidote and in the treatment of elephantiasis, leprosy, and chronic eczema.

Camphor

Camphor, the well-known aromatic, has hormone-modulating, contraceptive, abortifacient, and lactation-inhibiting properties in women. It has a dose-dependent effect in human sperm motility and viability. Camphor can pass the placental barrier and affect embryo development. Camphor-containing compounds have shown uterotrophicantitussive, anticonvulsant, nicotinic receptor blocking, anti-implantation, antiestrogenic, as well as estrogenic activities and can reduce serum triglyceride and thyroid hormone.

Flowers of *Hibiscus rosa-sinensis* L containing quercetin-7-O-galactoside, polyphenolic compounds, and kaempferol, having antispermatogenic compounds, is prescribed for contraception

TABLE 3 List of drugs with teratogenic	TABLE 3	toaenic effect	
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Sr. No.	Name of plants	Phytoconstituent	Dose and duration	Teratogenic effect
1	Asparagus racemosus Willd.	Shatavarin, Racemosol	1000°mg/kg/body weight for 60-day Charles foster rat pups	Prenatal study—increased resorption of fetus, gross malformation i.e., swelling in legs, IUGR with small placental size.
	Root		Methanolic extract	Postnatal study—decreased number of pups per litter and increased mortality of pups and delayed developmental parameters Goel et al. (2006)
2	<i>Datura metel</i> L. Leaves	Atropine alkaloids	500°mg/body kg wt rats, ethanolic extract	Teratogenic in the late stage of pregnancy Azeez and Philip (2013)
3	Gloriosa superba L. Tuber	Colchicine	1-3 ppm and 4-5 ppm Hydroalcoholic extract	Antifertility activity scarcely produced abnormal embryos. Induce high percentage of abnormalities. Badwaik (2011)
4	Lawsonia inermis L.	Flavonoid and phenolic compounds	100°mg/kg body wt. BALB/c mice between 8- 12°wk hydroalcoholic extract	90% embryo, more extra ribs anencephaly, exencephaly, skeletal abnormalities, height and weight loss in embryos Lobat (2015)
5	Luffa operculata (L.) Cogn. Tea, decoction	Glycosides, saponins, resin, free sterols, aliphatic esters, quinones	After ingestion of a variable amount of tea made with dried fruit, decoction	Abortion, reduction in birth rate Barilli et al. (2005)
6	Plumbago zeylanica L.	Plumbagin	100°mg/body kg wt orally with 0.5°ml of distilled water in mice	Stunted growth, subcutaneous, and deep hemorrhage, kinking of tail, protrusion of back o head Srivastava (2017)
7	Ruta graveolens L.	Essential oil	5, 10, and 20% w/v or plain water (control) orally for 4 days	Changes in the blastocyst formation, reducing the number, and delaying the development of embryos Gutiérrez-Pajares et al. (2003) embryotoxic effect De Freitas et al. (2005)
8	Sena (Senna) alexandrina Mill- Fabaceae	Sennosides	Extract	Increase blood flow to the uterus and its attachments, increasing the risk of fetal loss, and may pass spasms in the infant Schulz et al. (2002)
9	Zingiber officinale Roscoe	Carbohydrates (50–70%), lipids (3–8%), terpenes, and phenolic compounds	Orally at 0, 250, 500, 1000, or 2000 °mg/kgbw/day—five groups	High dose significantly reduced the number of live fetuses, increased fatal death, and resorption. Reda et al. (2018)
10	Pipalyadi gutika	Piperine	5 times to one and five times to the other than the recommended dose for humans Rats	Fetus—LBW, smaller in length, developmental defects of soft tissues, skeletons, herniation of intestines into umbilical cord, Mother—less weight gain during gestation Chaudhury et al. (2001)
11	Vishamustivati [W] & Shuddha Tankana [ST]	-	175°mg/kg of aqueous solutions of VisamustiVati, 300°mg/kg aqueous solutions of SuddhaTankana, orally from day 1 to day 7 of post mating period	W and ST shows positive Teratological effect or new-borns, gross remarkable external morphological and skeletal defects Jati (2018)

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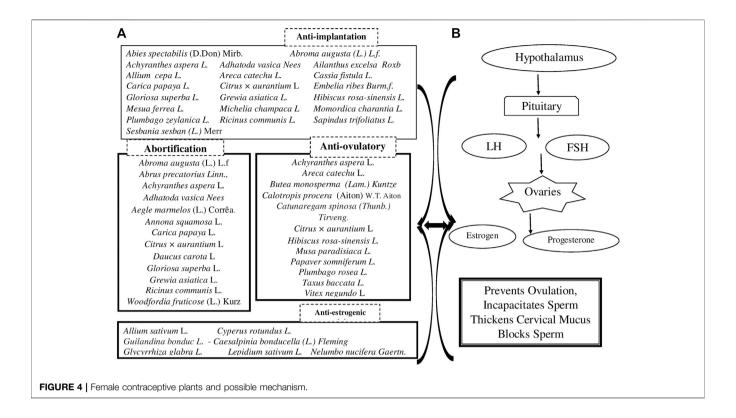
TABLE 4 | List of medicinal plants with one or more contraceptive activities.

Sr. No	Plant name	Anti- implantation	Abortification	Antifertility	Antiovulatory	Antiestrogenic activity	Antispermatogenic	Spermicidal	Antiandrogenic activity
1	Abies spectabilis (D.Don) Mirb.	√							
2	Abroma augusta (L.) L.f.	√	\checkmark						
3	Abrus precatorius L.		√ √	\checkmark			\checkmark		
1	Acacia concinna (Willd.) DC.							\checkmark	
5	Acacia leucophloea (Roxb.) Willd.			\checkmark					
3	Achyranthes aspera L.		\checkmark		\checkmark			\checkmark	
,	Adhatoda vasica Nees	\checkmark	\checkmark						
3	Aegle marmelos (L.) Corrêa.		\checkmark				\checkmark	\checkmark	
9	Ailanthus excelsa Roxb	\checkmark							
10	Albizia lebbeck (L.) Benth.						\checkmark		
11	Allium cepa L.	\checkmark							
12	Allium sativum L.					\checkmark			
13	Aloe barbadensis Mill.	\checkmark							\checkmark
	Synonym of Aloe vera (L.) Burm.f.								
14	Alstonia scholaris (L.) R.Br.						$\sqrt{}$		\checkmark
15	Andrographis paniculata (Burm.f.) Nees						$\sqrt{}$		\checkmark
16	Ananas comosus (L.) Mer							\checkmark	
7	Annona squamosa L.		\checkmark				\checkmark		
8	Areca catechu L.	\checkmark	\checkmark	\checkmark	\checkmark		\checkmark		
9	Aristolochia indica L.						$\sqrt{}$	\checkmark	
.0	Azadirachta indica A. Juss.			\checkmark	\checkmark		\checkmark	\checkmark	\checkmark
21	Bacopa monnieri (L.) Wettst.						\checkmark		
22	Balanites roxburghii Planch.						\checkmark		
23	Bambusa bambos (L.) Voss							\checkmark	
24	Barleria prionitis L.		\checkmark						
25	Berberis aristata DC						\checkmark		
26	Butea monosperma (Lam.) Kuntze				\checkmark				
27	Calotropis procera (Aiton) Dryand.						√		
28	Cannabis sativa L.							\checkmark	
29	Carica papaya L.	\checkmark	\checkmark	\checkmark			\checkmark		
30	Cassia fistula L.	\checkmark							
81	Catunaregam spinosa (Thunb.) Tirveng.								
32	Celastrus paniculatus Willd.						\checkmark		
33	Centratherum anthelminticum (L.) Gamble	\checkmark							
34	Cichorium intybus L.						\checkmark		
35	Cinnamomum camphora (L.) J. Presl						$\sqrt{}$		
36	Cissampelos pareira L.			\checkmark					
37	Citrullus colocynthis (L.) Schrad.							\checkmark	
88	Citrus × aurantium L	\checkmark	\checkmark		\checkmark				
9	Crateva nurvala BuchHam			\checkmark					
0	Cuminum cyminum L.			\checkmark			$\sqrt{}$		
1	Cuscuta reflexa Roxb								\checkmark
12	Curcuma longa L.			\checkmark					
13	Cyperus rotundus L.					\checkmark			
14	Daucus carota L		\checkmark	\checkmark				\checkmark	
15	Desmodium gangeticum (L.) DC.			√ √					
-6	Embelia ribes Burm.f.	\checkmark	$\sqrt{}$				$\sqrt{}$	\checkmark	
	Euphorbia neriifolia L.						√		

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TABLE 4 | (Continued) List of medicinal plants with one or more contraceptive activities.

Sr. No	Plant name	Anti- implantation	Abortification	Antifertility	Antiovulatory	Antiestrogenic activity	Antispermatogenic	Spermicidal	Antiandrogenic activity
48	Ferula jaeschkeana Vatke			√					
49	Foeniculum vulgare Mill								\checkmark
50	Gloriosa superba L.	\checkmark	\checkmark	$\sqrt{}$					
51	Glycyrrhiza glabra L	•	•	•		\checkmark			
52	Grewia asiatica L	$\sqrt{}$	\checkmark			·			
53	Guilandina bonduc L.					\checkmark			
	Sy. Caesalpinia bonducella (L.) Fleming								
54	Hibiscus rosa-sinensis L.	\checkmark		\checkmark	\checkmark		\checkmark		\checkmark
55	Lawsonia inermis L.			√					
56	Lepidium sativum L		\checkmark	√					
57	Melia azedarach L			√					
58	Mentha arevensis L			•				\checkmark	
59	Mesua ferrea L.	\checkmark						·	
60	Michelia champaca L.	V							
61	Momordica charantia L.	V		$\sqrt{}$			\checkmark		
62	Mucuna urens (L.) Medik	·		•			•		$\sqrt{}$
63	Musa paradisiaca L.				\checkmark				•
64	Myristica fragrans Houtt				•			\checkmark	
65	Nelumbo nucifera Gaertn.					\checkmark		•	
66	Nicotiana tabacum L.					*			$\sqrt{}$
67	Nigella sativa L.			$\sqrt{}$					•
68	Ocimum sanctum L.			•			\checkmark		
69	Papaver somniferum L.				\checkmark		•		
70	Piper betle L.			\checkmark	*		\checkmark		
71	Piper longum L.			√			v √		
72	Piper nigrum L.			v			√		
73	Plumbago rosea L.			*	$\sqrt{}$		•		
74	Plumbago zeylanica L.	\checkmark			v		\checkmark		\checkmark
75	Pterocarpus santalinus L.f.	v					√ √		v
76	Pueraria tuberosa (Willd.) DC						v √		
77	Ricinus communis L.	\checkmark	\checkmark				V		
78	Ruta graveolens L	V	V						2/
79	Sapindus trifoliatus L.	\checkmark							V
80	Semecarpus anacardium L.f.	V			$\sqrt{}$		$\sqrt{}$		2/
81	Sesbania sesban (L.) Merr	\checkmark			V		V		V
82	Sesamum indicum L	V				\checkmark			
83	Strychnospotatorum L.f.					v		\checkmark	
84	Taxus baccata L				\checkmark			v	
85	Terminalia arjuna (Roxb. ex DC.) Wight &Arn				٧		\checkmark		
86	Terminalia arjuna (Noxo: ex Bo.) Wight dami						V	$\sqrt{}$	
87	Tinospora cordifolia (Willd.) Hook.f.& Thomson							v 1/	
88	Trichosanthes cucumerina L.			$\sqrt{}$				v	
89	Trigonella foenum-graecum L.			v				$\sqrt{}$	
90	Tylophora asthmatica (L. f.) Wight & Arn						$\sqrt{}$	V	
91	Vitex negundo L.				\checkmark	\checkmark	V		
92	Withania somnifera (L.) Dunal				V	V		$\sqrt{}$	
93	Woodfordia fruticosa (L.) Kurz		\checkmark					V	
94	Zingiber officinale Roscoe		٧	,					



and is used to treat bacterial infection, hyperlipidemia, and depression and act as an antioxidant.

Two of the most bitter stimulant plants, *Momordica charantia* L. and *Azadirachta indica* A. Juss., produce an irregular pattern of estrous cycle with prolonged diestrus phase. Steroids, triterpenoids, reducing sugars, alkaloids, phenolic compounds, flavonoids, and tannins in the plant cause reduction in the number of normal follicles because of atresia which occur due to disruption of the process of follicle selection. *Azadirachta* arrests spermatogenesis and androgen depletion.

Roots of *Plumbago zeylanicum* L. have been used as an abortifacient, internally or as an irritant to the uterus. This acrid and stimulant root increases appetite helps indigestion and is used for dyspepsia, piles, and skin diseases. It induces sweating, its powder is occasionally taken as snuff to relieve headache, and it helps in the adhesion of tissues in the body and is antidiarrheal.

Tinospora cordifolia (Willd.) Hook.f. and Thomson, an immunomodulator plant used to treat tuberculosis, fever, and wounds, has antifertility qualities. It is used for antioxidant, hypoglycaemic, and cardioprotective activities.

Excessive use of substances having pungent, bitter, and astringent tastes is contraindicated for sexual functions. Excess consumption of bitter taste leads to loss of strength and energy, astringent taste affects the sperm count, and can even reduce the sex drive while strongly pungent ingredients like pepper exhibit spermicidal or abortifacients effects.

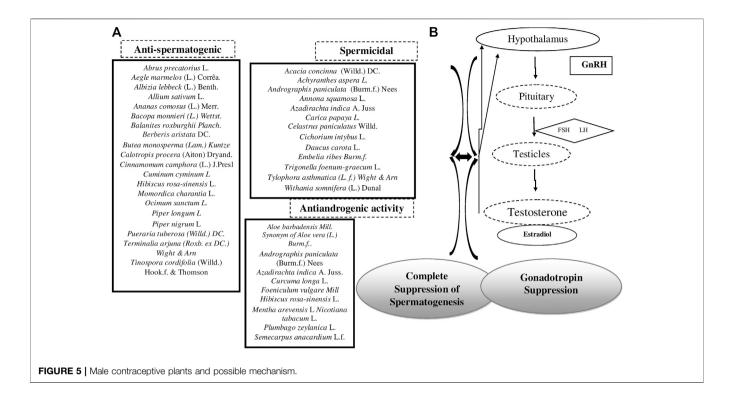
Prolonged consumption of these tastes may lead to emaciation of the body.

Mechanism of Action

Female Contraceptives

Medicinal plants may induce infertility in distinct ways. They may affect the ovarian, uterine, and hormone production functions and interfere with implantation or sperm production. These drugs are of natural origin, hydrophilic, and lipophilic; can traverse paracellularly through the vaginal mucosa; and exhibit its efficacy as contraceptive, by altering the vaginal pH. These drugs may variably act locally to bring changes in the cervical mucus and alter decidual embedding and thereby act as anti-implantation agents, or may inhibit propulsion of sperm in the fallopian tubes by altering tubal mechanism or may act on hormones as antiovulation agents. They may act through rapid expulsion of the fertilized ova from the fallopian tube or inhibit implantation due to disturbance of the estrogen progesterone balance or induce fetal abortion by inhibition of nutrition to the uterus and the embryo.

Moreover, plants with estrogenic property can directly influence pituitary action by peripheral modulation of luteinizing hormone (LH) and follicle stimulating hormone (FSH), decreasing their secretions and blocking ovulation (Brinker, 1997). Plants with antiestrogenic activities intercept in the process of development of ovum and endometrium and on the other hand, plants have abortifacient effects (Gark et al., 1978; Prakash et al., 1985).



The site of action of antifertility agents in females comprises the hypothalamus, the anterior pituitary, the ovary, the oviduct, the uterus, and the vagina. The mammalian uterus is the main site of antifertility effects (Williamson et al., 1996). Typical estrogenic compounds posses the ability to increase the uterine wet weight and induce cornification and opening of vagina in immature rats, which results in anti-implantation effects (Turner, 1971).

Antifertility plants prevent fertilization; these drugs obstruct the formation of gametes and interfere with the process of fertilization. Antiovulatory plants induce infertility by suppressing ovulation. Anti-implantation plants prevent the attachment or penetration of fertilized ovum into the uterus. Butea monosperma (Lam.) Kuntze, Ocimum sanctum L., Calotropis procera (Aiton) W.T. Aiton, Mentha arvensis, and Lawsonia inermis L-all have antiimplantation activity. Abortifacient plants cause early expulsion of the fetus. These act during the first five weeks of pregnancy as they block the action of progesterone so that the uterus sloughs off the embryo. Abrus precatorius L., Annona squamosa L., Calotropis procera (Aiton) W.T. Aiton, Carica papaya L., Dhatura metel L., Momordica charantia L., and Catunaregam spinosa (Thunb.) Tirveng are medicinal plant drugs which can be used as abortifacients. Stimulant, irritant, and bulk forming characteristics of these drugs facilitate abortion along with hormonal regulation and modulation of genital functioning. These ingredients are considered stimulants and are hot in nature and hence should be used for a short duration.

It observed that large numbers of antifertility plant extracts are known to exhibit estrogenic activity in rats (Dahanukar et al., 2000). Estrogenic substance may cause the expulsion of ova from the tube, disruption of luteotrophic activity of the blastocyst, and disrupt the functional equilibrium between the endogenous

estrogen and progesterone, which may result in failure in fertility. Increase in the wet weight of uterus of substance-treated ovariectomized immature rats may indicate that the substance has an estrogenic effect (Mukherjee, 2002).

The hypothalamus has threshold requirement for estrogen to cause a massive release of LH by the pituitary gland. This surge of LH is the trigger, which initiates the rupture of the follicle (ovulation) (Bullock et al., 1995). It is known that an increase in the serum progesterone level prevents pregnancy through inhibition of ovulation and alteration of cervical mucus.

Most of the plants possess inhibition of implantation or reduction of estrogen level and increment of progesterone level as the possible mechanism of antifertility effect.

The anti-implantation effect may be due to the disturbance of endocrine-endometrial synchrony that is dependent on estrogen and progesterone balance. Factors other than the hormones such as histamine, prostaglandins, proteolytic enzyme NOS, alkaline phosphatase, interleukins, and leukemia-inhibitory factors, which are important for implantation, may also be affected by the various plant extracts (Gupta, 1994; Garg et al., 1978; Novaro et al., 1997; Prakash et al., 1989; Dimitriadis et al., 2003; Yang et al., 1994)

Male Contraceptives

Male contraceptive drugs may inhibit spermatogenesis or act on male hormones when used orally or may be spermistatic or spermicidal when used intravaginally. Male contraceptives might work to suppress sperm production by antispermatogenic or prevent maturation of sperm or prevent the flow of sperm through the vas deferens or deposition of the sperm (Soni et al., 2015).

Plant extracts have also shown promising antifertility effects when administered to male rats. The various effects on male reproductive system to induce antifertility action shown by plants includes antispermatogenic effect, post-testicular antifertility effect, spermicidal effect, sperm-immobilizing effect, antiandrogenic effect, etc.

Antispermatogenic activity indicates interference in the steroidogenesis when the cholesterol level rises and sudanophilic lipid accumulates (Mandal et al., 2010). Some of the plant extracts kill the viability and work on Sertoli cells and have various effects on spermatogenesis, such as reducing the nuclear and cytoplasmic volume and vacuolizing Sertoli cells (Sharma RS et al., 2001) or acts through Leydig cells (Dufau et al., 1984). Some plant extracts act by unbalancing the hormones or through their antimotility activity (Verma and Yadav, 2021).

Spermicidals are contraceptive substances that destroy the sperm when inserted vaginally prior to intercourse. The spermicidal agents consist of a surfactant that destroys the sperm cell membrane. Lipid peroxidation may play an important role in disrupting the sperm membrane physiology that may or may not be accompanied with a detrimental effect on the defense system of the human spermatozoa against the ROS.

Antiandrogens, also known as androgen antagonists or testosterone blockers, prevent androgens like testosterone and dihydrotestosterone (DHT) from mediating their biological effects in the body. Andrographis paniculata (Burm.f.) Nees, Azadirachta indica A. Juss., Curcuma longa L., Hibiscus rosasinensis L., and Plumbago zeylanica L. act by blocking the androgen receptor (AR) and/or inhibiting or suppressing androgen production. They can be considered as the functional opposites of AR agonists, for instance, androgens and anabolic steroids (AAS) like testosterone, DHT, and nandrolone and selective androgen receptor modulators (SARMs) like enobosarm.

Figures 4, **5** provide group of these plants 3 (a) and 4 (a) with probable female and male contraceptive activities 3 (b) and 4 (b), respectively.

Limitations/Challenges

A major limitation is the contradictory reports or non-reproducibility of published data, which can provide useful leads. At times, failure of reproducibility of contraceptive activity of a plant or its constituent is observed. This could be due to the multiple factors at different levels that are known to affect the reproductive process. The other reason could be the variable effect of the herbal contraceptive/s in animals as against when used in humans.

The contraceptives of natural origin are not used much in practice, the main factor being the lack of standardization and reliable validation studies. The information has thus remained fragmented. Studies have consequently been scarce. Interest has weaned due to the complexity and enormity of the large and long-term study requirements covering multiple variables.

Analytical methods, information on phytoconstituents, availability of markers, and their activities have now provided

new standardization approaches to herbal products that assure higher safety and stability.

The solution to this is to investigate the efficacy of these herbs in humans themselves, after ascertaining their safety in animal models. There is also a need to record the conditions under which the plants are used by indigenous people, including the time and place of collection, proper botanical authentication, and schedule of administration. Advances in biology offer adaptable and promising experimental models to examine the effectiveness of natural products for altering reproductive functions and contraception

CONTRACEPTION AND NEW TECHNOLOGIES FOR NATURAL PRODUCTS

There is a need to use new contraceptive methods to minimize the side effects. The following technological advances are relevant in the context of this review for discovery and development of novel contraceptives of natural origin.

- o Ayurveda recommends fumigation as a method and as a therapeutic procedure to treat various diseases, including microbial infections. Ayurvedic methods of sterilization with fumigation can be alternated as a modern contraceptive with the help of nanotechnology. Natural novel bioactive compound drugs could be developed with novel drug-delivery systems.
- o A team in the University of Washington has developed an electrically spun cloth with nanometer-sized fibers that get dissolved to release drugs, thus providing a platform for cheap, discrete, and reversible protection ("Drug-Eluting Fibers for HIV-1 Inhibition and Contraception").
- o Pharmacy on a chip is one of the most exciting parts of the drug-delivery system. It is a chip implanted into the body which releases drugs at set intervals. It would release the hormones estrogen and progestogen over a specific period to stop the release of eggs from the ovaries and thus prevent pregnancy.
- o Nanotechnology-based condom systems have the potential to prevent the spread of HIV and STIs.
- o Transdermal drug delivery (TDD) is an alternative method of drug administration for drugs whose delivery by conventional oral, topical, intravenous, and intramuscular methods is of limited efficacy. Recent advances in TDD involve the use of nanoparticles (NPs), which exhibit great potential to enhance drug permeation across the skin.
- o Skin patches containing microneedles is a painless and minimally invasive method of TDD in which micron-sized pores are created in the epidermis to allow delivery of drugs to the blood vessels present in the dermal layer of the skin.
- o Researchers report on a technique for administering contraceptive hormones through special backings on jewelry such as earrings, wristwatches, rings, or necklaces. The contraceptive hormones are contained in patches applied to portions of the jewelry in contact with the skin, allowing the drugs to be absorbed into the body (Georgia Institute of Technology, 2019).

Possibilities for new means of drug development

- Developing newer biotechnology-based cellular or molecular models that could better replicate reproductive processes.
- Methods that act after ovulation and interfere with sperm delivery or function in the male or in the female genital tract or both ought to be adopted.
- Design of nonhormonal contraceptive agents—as an alternative option to hormonal formulations—with the help of herbals.
- New delivery mechanisms that can act both short and long term; the possibilities are to develop herbal pessary, jelly, patches, and condoms, or mechanical devices with natural ingredients to optimize the effects.
- Methods which limit the side effects associated with systemic exposure should be developed in lower dosage forms to ensure efficacy.
- Technologies that markedly improve the cost, acceptability, and deliverability of contraceptives.
- Personalized contraception-human genome could minimize the side effects while maximizing health benefits at the individual level.

CONCLUSION

Fertility and contraception are continued subjects of biomedical research and innovation. Alternatives to unmet needs for safer contraception methods and drugs are searched for. Many Ayurvedic medicinal ingredients and compound formulations are claimed to inhibit male and female fertility as mentioned in the classical literature. Several of these validated drugs possess

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spermicidal, antispermatogenic, antiovulatory, anti-implantation, antiestrogenic, and abortifacient activity. The Indian system of medicine, Ayurveda, offers highly promising opportunities when analytical, biological, technological, and clinical advances are collectively integrated with therapeutic rationale based on Ayurvedic principles. A plethora of available data, information, and knowledge on these ingredients could be the subject of newer research interests.

These medicinal ingredients need further reexamination and critical evaluation to explore their lesser known or unknown pharmacological and biological activity/activities and effects. Present-day biotechnological methods could be usefully utilized to evaluate their contraceptive efficacies. There is a need to revive and stimulate new research programs and projects that will not only benefit the need of contraception but will also throw new light on reproductive biology.

AUTHOR CONTRIBUTIONS

The corresponding author Dr. NB contributed to the concept, initial compilation, structure of the review, and final editing of the text and figures. Co-author Dr. MD contributed to compiling and comparing pharmacological data and the preparation of tables and figures.

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Yeast-Host Interactions: Anadenanthera colubrina Modulates Virulence Factors of C. albicans and Inflammatory Response In Vitro

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Oral candidiasis is one of the most common fungal infections in humans. Its incidence has increased widely, as well as the antifungal resistance, demanding for the search for novel antifungal therapeutic agents. Anadenanthera colubrina (Vell.) Brenan is a plant species that has been proven to possess pharmacological effects, including antifungal and antiinflammatory activities. This study evaluated in vitro the effects of standardized A. colubrina extract on virulence factors of Candida albicans and its regulation on immune response through C. albicans-host interaction. Antifungal activity was evaluated by Broth Microdilution Method against reference Candida strains (C. albicans, C. glabrata, C. tropicalis; C. dubliniensis). Anti-biofilm effect was performed on C. albicans mature biofilm and quantified by CFU/mL/q of biofilm dry weight. Proleotlytic enzymatic activities of proteinase and phospholipase were assessed by Azocasein and Phosphatidylcholine assays, respectively. Cytotoxicity effect was determined by Cell Titer Blue Viability Assay on Human Gingival Fibroblasts. Co-cultured model was used to analyze C. albicans coexisting with HGF by Scanning Electron Microscopy and fluorescence microscopies; gene expression was assessed by RT-PCR of C. albicans enzymes (SAP-1, PLB-1) and of host inflammatory cytokines (IL-6, IL-8, IL-1β, IL-10). Cytokines secretion was analysed by Luminex. The extract presented antifungal effect with MIC<15.62 µg/ml against Candida strains. Biofilm and proteolytic activity were significant reduced at 312.4 µg/ml (20 × 15.62 µg/ml) extract concentration. Cell viability was maintained higher than 70% in concentrations up to $250 \,\mu\text{g/ml}$ (LD₅₀ = $423.3 \,\mu\text{g/ml}$). Co-culture microscopies demonstrated a substantial decreased in C. albicans growth and minimal toxicity against host cells. Gene expressions of SAP-1/PLB-1 were significantly down-regulated and host immune response was modulated by a significant decreased on IL-6 and IL-8 cytokines secretion. A. colubrina had antifungal activity on Candida strains, antibiofilm, and anti-proteolytic enzyme effects against C. albicans. Presented low cytotoxicity to the host cells and modulatory effects on the host immune response.

Keywords: phytotherapy, antifungal agents, oral candidiasis, *Candida albicans*, biofilm, virulence factors, immune response

INTRODUCTION

Oral candidiasis is one of the most common fungal infections in humans (Hertel et al., 2016; Rosa-García et al., 2020) and is caused by yeasts from the genus *Candida* (Williams and Lewis, 2011), a polymorphic fungus and a commensal microorganism that colonizes the human oral cavity in healthy people (Nikou et al., 2019). However, under circumstances where host immunity is impaired, *Candida* spp. can switch its harmless phenotype to a pathogenic form capable of breaching mucosal barriers (Dantas et al., 2016), causing from superficial mucosal infection to deep seated invasive and life-threatening disseminated disease (Lewis and Williams, 2017; Nikou et al., 2019), which is related to a high mortality rate (58–81%) (Vaezi et al., 2017).

Candida albicans is the species most often associated to oral candidiasis (Prieto et al., 2016; Pappas et al., 2018), accounting for up to 95% of the cases (Vila et al., 2020). Its overgrowth and invasion of superficial tissues is dependent on the host's defenses and the virulence factors of the fungus (Tooyama et al., 2015; Millsop and Faze, 2016; Hellstein and Marek, 2019), such as, adherence to oral epithelial or medical devices surfaces; biofilm formation; destruction of host tissue through secretion of proteolytic enzymes; evasion of host defenses invasion mechanisms and development of drug resistance (Höfs et al., 2016; Vila et al., 2020).

Considering the continuing rise of resistant *Candida* spp. strains and the limited number of antifungal agents, novel therapeutic strategies have been directed toward the identification of bioactive compounds that target virulence factors and pathogenic mechanisms to prevent *C. albicans* transition from harmless commensal to pathogen (Francisconi et al., 2020; Vila et al., 2020).

In this regard, natural products from plants are considered a potential source for the development of new antifungal therapies. Between the years of 1940 and 2014, 40% of all molecules accepted by FDA (US Food and Drug Administration) were natural products (Newman and Cragg, 2016). Anadenanthera colubrina (Vell.) Brenan, popularly known as Angico, is a plant species that can be found in Brazil, from the Northeastern to the Southeastern regions. It is a woody species typical of the Caatinga Brazilian biome (Silva et al., 2019) and its use by the traditional communities of Brazilian semiarid as a medicinal plant is common, which includes the treatment of inflammation in general (Araújo et al., 2014; Araújo et al., 2015). Recent researches have shown that A. colubrina has promising therapeutic properties, such as antifungal (Lima et al., 2014; Silva et al., 2019), anti-proliferative (Lima et al., 2014), antiinflammatory (Guarneire et al., 2019; Cardoso-Junior et al., 2020), antioxidant (Araújo et al., 2019; Cardoso-Junior et al., 2020), and anti-HIV (Maia et al., 2021).

Some studies regarding the antifungal effects of *A. colubrina* have suggested an inhibitory activity among *Candida* species, mainly on *C. albicans* biofilms. (Lima et al., 2014; Silva et al., 2019). Lima et al. (2014) demonstrated *in vitro* the strong antifungal activity of *A. colubrina* extract against *C. albicans* in planktonic culture and also its potential in inhibit the formation of *C. albicans* biofilm. Therefore, *A. colubrina* extract toxicity and

therapeutic action were evaluated *in vivo* on *Galleria mellonella* model, having not affected the viability of the larvae at doses below 100 mg/kg and high potential for the treatment of *C. albicans* infection (Silva et al., 2019). These recent findings suggest that *A. colubrina* extract is a strong *Candida*te for development of a new agent for the treatment of oral candidiasis.

Despite this therapeutic potential, there is little information available about how this plant species can regulate the expression of virulence factors of *Candida* co-cultured with humans cells and the host immune response during the fungal infection as well. Therefore, the present study aimed to evaluate *in vitro* the modulatory effects of *A. colubrina* extract on major virulence factors related to the pathogenicity of *C. albicans* infection through the interaction between host and pathogen.

MATERIAL AND METHODS

Plant Material and Standardized Extraction Procedures

The plant material was collected during the month of September in the semi-arid region of Paraíba state, Brazil (7° 22′ 25″ S, 35° 59' 32" W). Botanical specimens of Anadenanthera colubrina (Vell.) Brenan were deposited in the Manuel de Arruda Câmara Herbarium (ACAM) at the State University of Paraíba (UEPB), Campus I, Campina Grande, Paraíba, Brazil, under no 1936/ ACAM. This research was conducted under authorization number SisGen A289DF4. A hydroethanolic standardized extract was obtained according to the method described by Carvalho et al. (2011). Briefly, hydroethanolic extract (80%, v/v) of the plant bark was obtained by maceration for 48 h using the proportion of 10 mg of the plant for each 25 ml of 80% ethyl alcohol. Three filtrations of the material were performed, followed by vacuum concentration (Tecnal TE-211, Piracicaba, SP) and lyophilization (Martin Christ 1-2 LDplus, Germany). An extraction yield of 31.7% was obtained.

Considering the same standardized extract (same batch of plant material and same extraction process) used in this research and used by Lima et al. (2014), Rocha et al. (2017), Lima et al. (2018–data not published) and Silva et al. (2019), the presence of polyphenol, tannins and flavonoids, compounds with straight relationship with A. colubrina extract pharmacological activity, were also recently monitored by gas chromatograph (GC) coupled to mass spectrometer (MS) with electron impact ionization (EI) (model GCMS-QP2010 Ultra, Shimadzu) according to the method described by Maia et al. (2021), using the same standardized material.

Susceptibility Test

The antimicrobial activity of *A. colubrina* extract was assessed by Broth Microdilution Method against the following *Candida* spp: *C. albicans* ATCC 90028, *C. albicans* ATCC MYA-2876, *C. glabrata* ATCC MYA-275, *C. tropicalis* ATCC MYA-750; *C. dubliniensis* ATCC MYA-646, with the determination of the minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC), according to CLSI guidelines (M27-A2) (Clinical and Laboratory Standards Institute (CLSI),

2002). The assay was performed in 96 well-plates (Greiner Bio-One North America, Inc. Monroe, NC) containing 100 µL/well of RPMI-1640 culture medium (Lonza Bioscience, Walkersville, MD). One hundred microliters of the extract were added to the initial well (8,000 µg/ml), followed by serial microdilution, obtaining concentrations between 2,000 and 15.62 µg/ml. Inoculum concentration was standardized spectrophotomer (SpectraMax M3, Molecular Devices, Sunnyvale, CA), by first measuring the absorbance in the range of 0.08-0.1 at 625 nm, which yielded a yeast stock solution equivalent to 5×10^6 CFU/mL that was then diluted in RPMI-1640 medium to a final concentration of 5×10^3 CFU/ mL. Next, 100 µL of yeast suspension was added to each well, resulting in a final concentration of 2.5×10^3 CFU/ml. The plates were incubated for 24 h at 37°C in 5% CO₂ (VWR Symphony 5.3 A, Radnor, PA). Fluconazole (512 μg/ml) (Alfa Aesar , Tewksbury, MA) was used as positive control. The vehicle control used was Dimethyl Sulfoxide 1% (DMSO, BDH Solvents, Dawsonville, GA). The MIC was defined as the lowest concentration of the sample capable of inhibiting visible microbial growth, as confirmed by the change in the color of the RPMI-1640 medium. For the determination of the MFC, an aliquot of 10 µL from each well with concentrations equal to or higher than the MIC was sub-cultivated in Sabouraud Dextrose Agar medium (BD Difco, Franklin Lakes, NJ) and incubated at 37°C, in 5% CO₂, for 48 h. The MFC was defined as the smallest concentration that inhibited visible growth on the agar plates. All of the assays were performed in triplicates and repeated at least three different times for reproducibility (Seleem et al., 2016b).

Biofilm Assay

An inoculum of 1×10^6 CFU/mL of *C. albicans* (ATCC MYA-2876) was grown for 24 h in a sterile 24-well plate (Greiner Bio-One North America, Inc. Monroe, NC, United States) using Yeast Nitrogen Base Medium (YNB, Sigma Aldrich, San Luis, MO) with 50 mM of glucose (VWR Life Science, Radnor, PA) for 24 h at 37°C in 5% CO₂ to establish initial biofilm growth. Total volume of 1 ml of inoculum was pipetted in each well. After 24 h of incubation, the biofilms were treated once daily with 100 μ L of A. colubrina extract at concentrations equivalents to 156.2 µg/ml $(10 \times 15.62 \,\mu\text{g/ml})$ and $312.4 \,\mu\text{g/ml}$ $(20 \times 15.62 \,\mu\text{g/ml})$, which remained incubated with the biofilm suspended in medium overnight. The vehicle control used was 1% DMSO, while positive control was Fluconazole (10xMIC). Before each treatment, biofilms were washed with Phosphate Buffer Solution (PBS, Lonza Bioscience, Walkersville, MD) and replenished with 900 µL of fresh YNB medium in addition to 100 μL of the corresponding treatment, yielding a total volume of 1 ml in each well. After 72 h of treatments, adhered biofilms were collected by scraping the bottom of each well plate and suspending in PBS, which was then centrifuged at 10,000 rpm for 5 min. Biomass (dry weight) of each biofilm sample was obtained by discarding the supernatant and placing the samples in a speed vacuum to dry for 40 min. Colony formation unit (CFU) was determined by submitting the bioifilm suspension to serial dilutions (10⁻¹, 10⁻², 10⁻³, 10⁻⁴) and plating 10 µL of these dilutions on Sabouraud Dextrose Agar

plates, which were incubated at 37°C in 5% CO₂. After 24 h of incubation, the number of *C. albicans* colonies was counted and the data was normalized based on the CFU/ml/dry weight of biofilm sample (Santana et al., 2013; Seleem et al., 2016a; Seleem et al., 2016b; Chen et al., 2018).

Proteinase and Phospholipase Enzyme Secretion Assay

Proteinase and phospholipase enzyme secretion assays were conducted as previously performed by Santana et al. (2013), Chen et al. (2018). Biofilms of C. albicans were grown for 24 h in YNB Medium with 50 mM of glucose at 37°C in 5% CO2 and treated with A. colubrina extract (156.2 μ g/ml $-10 \times 15.62 \mu$ g/ml and 312.4 μ g/ml $-20 \times 15.62 \mu$ g/ml). Trypsin (Gibco, Invitrogen) was used as standard. The vehicle control used was 1% DMSO. After 72 h of biofilm maturation, the enzyme secretion assays were performed on biofilms suspended in PBS, which were sonicated for 15 s at 20% amplitude with pulses at 5 s and 10 s (FB120; Fischer Scientific, Pittsburgh, United States). The proteinase enzyme activity was determined by mixing the supernatant of the biofilm solution with 1% azocasein (Sigma Aldrich, San Luis, MO) at 9:1 (v/v) for 1 h at 37°C in 5% CO₂. Then, 500 μL of 10% trichloroacetic acid (VWR) was added to stop the reaction. The solution was centrifuged for 5 min at 10,000 rpm and 500 μL of the supernatant was combined with 500 µL of 0.5 M NaOH (Macron Fine Chemicals, Avantor VWR Life Science, Radnor, PA), which was incubated for 15 min at 37°C in 5% CO₂. Absorbance was read in a spectrophotometer at 440 nm (Pande et al., 2006; Gonçalves et al., 2012; Santana et al., 2013; Chen et al., 2018). The phospholipase enzyme activity was determined by mixing the supernatant of the biofilm solution (pH corrected to 7.5) with phosphatidylcholine substrate (Sigma Aldrich, San Luis, MO) at 9:1 (v/v) for 1 h at 37°C in 5% CO₂ and reading the absorbance in a spectrophotometer at 630 nm (Taniguchi et al., 2009). The rates of absorbance shifts (ΔOD) for the repetitions were adjusted by the blank. One enzyme unity was arbitrarily established as the absorbance shift, by minute of reaction, by biomass, multiplied by one thousand ($U = \Delta ODnm \times$ min $-1 \times 1,000$). The specific enzyme activity was defined as the amount of enzyme that elicited an increase of 0.001 units of absorbance/minute of digestion by biofilm dry weight (g) (Taniguchi et al., 2009; Santana et al., 2013; Chen et al., 2018).

Cytotoxicity Assay

The *in vitro* cytotoxic effect of *A. colubrina* extract was performed on oral fibroblasts cells (HGF-1 ATCC $^{\circ}$ CRL-2014) and determined by a resazurin fluorometric method (Cell Titer Blue Viability Assay, Promega Corp, Madison, WI). Oral fibroblast cells were cultured in Dulbecco's modifed Eagle's medium (DMEM, Lonza, Walkersville, MD) with 10% fetal bovine serum (FBS Gibco, Invitrogen, Waltham, MA) at 37°C in 5% CO $_2$. Fibroblast cells (1 \times 10 5 °cells/mL) were first seeded in each well of a 24-well plate in DMEM with 10% FBS, and the plates were incubated for 24 h at 37°C in 5% CO $_2$. The *A. colubrina* extract was diluted in DMSO 1%, with final concentration inside the wells of 0.1%, and then added to the

cultured cells wells (2,500–0.25 μ g/ml). The plates were incubated for 24 h at 37°C in 5% CO₂. Resazurin (30 μ L) was added to each well, and the cells were incubated for 3 h. The fluorescence of the supernatant was read in a microplate reader with excitation of 555 nm, emission of 585 and 570 nm *cut off* (O'Brien et al., 2000).

Co-Culture Model Fluorescence Microscopy

A co-culture model was conducted by culturing fibroblast cells and C. albicans together in a sterile 24-well plate, as adapted by Wong et al. (2014), Oliveira Silva et al. (2018). First, oral fibroblast cells were seeded in DMEM with 10% FBS at 37°C in 5% CO₂ for 24 h. The medium was then replaced with an inoculum of 5×10^3 to 2.5×10^3 CFU/mL C. albicans (MYA 2876) grown in DMEM without FBS. Fibroblast cells and C. albicans were treated with 33.28 µg/ml of A. colubrina extract. The plate was then incubated at 37°C in 5% CO2 for 24 h. The vehicle control tested was 0.1% DMSO and the positive control was Fluconazole (10 µg/ml). The distribution of dead and live fibroblast cells was examined using the viability/cytotoxicity Live/Dead Assay Kit for mammalian cell type (Molecular Devices, Sunnyvale, CA), which contains a mixture of Calcein AM and EthDIII (Ethidium Homodimer III). Calcofluor white (Sigma Aldrich, San Luis, MO) was used to stain C. albicans. Fluorescent images of the double staining were captured using fluorescence microscopy (Keyence All-in-One BZ-X810 Fluorescence Microscope, Itasca, IL).

Co-Culture Model Scanning Electron Microscopy

Co-culture model was conducted by culturing fibroblast cells and *C. albicans* together in a sterile petri dish (Greiner Bio-One North America, Inc. Monroe, NC), following the same protocol above described for co-culture plating and treatments. After the period of incubation, the samples were washed twice with PBS and fixed in glutaraldehyde 3% (v/v) at room temperature for 12 h. The dehydrated cells were submitted to sequential baths of ethanol at concentrations of 50, 70, 90% and absolute ethanol twice, then coated with gold/palladium alloy in a Metalizer (Desk V Denton Vacuum, Moorestown, NJ) and observed using a Scanning Electron Microscope (Zeiss EVO LS10 SEM, Oberkochen, Alemanha) (Bersan et al., 2014; Freires et al., 2014).

Co-Culture Model Quantitative Real-Time PCR

Following the same protocol above described for co-culture plating, RNA was isolated from fibroblast cells and *C. albicans* after 8 h of treatment with *A. colubrina* extract. The fibroblast cells RNA and *C. albicans* RNA were isolated and purified using RNeasy[®] Mini Kit (Qiagen, Hilden, Germany) and RiboPure[™]-Yeast Kit (Invitrogen, ThermoFischer Scientific, Rockford, IL) respectively. SpectraDrop Micro-Volume Starter Kit (Molecular Devices, Sunnyvale, CA) was used to quantify the total RNA extracted. Real-time PCR was conducted by using QuantiFast[®]

SYBR® Green RT-PCR One Step Kit (Qiagen, Hilden, Germany). The C. albicans primers for the genes: Secreted Aspartyl Proteinases-1 (SAP-1), Phospholipase B-1 (PLB-1), and ACT-1 (housekeeping) at 10 μM were used. ACT-1 was the gene used to normalize SAP-1 and PLB-1 genes expression. The following host inflammatory cytokines genes were selected: IL-6 (Qiagen Gene ID#: 3570), IL-8 (Qiagen Gene ID#: 3576); IL-10 (Qiagen Gene ID#: 3587); IL-1β (Qiagen Gene ID#: 3553) and GAPDH (housekeeping) (Qiagen Gene ID#: 2597). All data from cytokines genes expression were normalized using the housekeeping gene GAPDH. PCR amplification was performed by using 25 µl reaction mix per well in 0.2 ml 8-Strip PCR tubes. The reactions were conducted in thermocycler (QuantStudio 3 Real Time PCR System, ThermoFischer Scientific, Rockford, IL) at 50°C for 10 min (Reverse Transcription Step); 95°C for 5 min (PCR Initial Activation Step); followed by 40 cycles of 10 s at 95°C (Denaturation Step) and 30 s at 60°C (Annealing/Extension Step). Analysis of relative gene expression was achieved according to the $\Delta\Delta$ Ct method (Seleem et al., 2016a; Seleem et al., 2016b; Chen et al., 2018).

Host Inflammatory Cytokines Analysis Using Luminex

As previously described, co-culture models were performed using fibroblasts cells, *C. albicans* (MYA2876), and the tested groups of *A. colubrina* extract (33.28 μ g/ml), positive control (Fluconazole 10 μ g/ml) and 0.1% DMSO (vehicle control). After 8 h of incubation, the supernatants of the co-culture were collected, centrifuged for 10 min at 1,000 rpm, and assayed immediately using Human Magnetic Premixed Multi-Analyte Luminex Assay Kit (R&D Systems, Mienneapolis, MN) for secretion of proinflammatory cytokines IL-6, IL-8, IL-1 β , and anti-inflammatory IL-10. Culture supernatants and cytokine capture bead cocktails were incubated during the overnight period. The samples were then incubated for 1 h with biotin-labeled antibody and for 30 min in a dilution of streptavidin-PE. Data were obtained by Luminex 200 Milliplex System and analyzed with Milliplex Analyst software (Allin et al., 2016).

Statistical Analysis

Data were expressed as the mean \pm SEM using one-way analysis of variance (ANOVA) and Dunnett's multiple comparison tests in relation to the vehicle, using GraphPad Prism software (version 8.02). Results were considered significant if p-values were less than 0.05.

RESULTS

Phytochemical Analysis

Standardization of plant inputs for the pharmaceuticals industry plays an important role in product outcomes. The quality of the botanical material, as well as the adequate processing of the fresh material, including drying, transportation, storage, and the use of appropriate and reproducible extraction techniques have a straight outcome on health benefits and economic issues. Previous studies were conducted to determine the best

TABLE 1 | Phytochemical compounds identified in the hydroalcoholic bark extract of A. colubrina by GC-MS (Maia et al., 2021).

	Compound	RT	RI	Area (%)
1	2-Piperidinecarboxylic acid, 1TMS	8.404	1,267	0.06
2	Butanedioic acid, 2TMS	9.079	1,319	0.02
3	Glyceric acid, 3TMS	9.380	1,343	0.01
4	Isoeugenol, 1TMS	11.065	1,482	0.03
5	Malic acid, 3TMS	11.248	1,498	0.15
6	Erythritol, 4TMS	11.422	1,513	0.01
7	Erythronic acid, 4TMS	12.151	1,574	0.02
8	4-Hydroxybenzoic acid, 2TMS	12.918	1,636	0.02
9	D-Ribose, 2,3,4,5-tetrakis-O-(trimethylsilyl)-, O-methyloxime	13.285	1,664	0.01
10	Xylitol, 5TMS	14.295	1740	0.90
11	Xylitol, 5TMS	14.370	1745	0.1
12	β-D-Xylopyranose, 4TMS	14.510	1755	0.02
13	D-(+)-Galactopyranose, 5TMS	16.390	1884	0.02
14	D-Glucopyranose, 5TMS	16.930	1920	1.37
15	D-Glucopyranose, 5TMS	17.100	1930	0.04
16	D-Mannitol, 6TMS	17.560	1960	0.18
17	Gallic acid, 4TMS	17.800	1975	0.02
18	Palmitic acid, 1TMS	18.965	2047	0.07
19	Myo-inositol, 6TMS	20.220	2,125	0.27
20	Stearic acid, 1TMS	22.210	2,246	0.02
21	Sucrose, 8TMS	29.378	2,705	48.08
22	Catechin, 5TMS	32.458	2,920	0.52

TABLE 2 | Minimum Inhibitory Concentration (MIC) and Minimum Fungicidal Concentration (MFC) of A. colubrina extract against Candida strains.

		A. colubrina		Fluconazole			
Candida strain	MIC (μg/ml)	MFC (µg/ml)	MFC/MIC ratio	MIC (μg/ml)	MFC (µg/ml)	MFC/MIC ratio	
Candida albicans ATCC® 90028	<15.62	>2,000	>4	<1	64–128	>4	
Candida albicans ATCC® MYA-2876	<15.62	2,000	>4	<1	64-128	>4	
Candida glabrata ATCC® MYA-275	<15.62	>2,000	>4	8	>128	>4	
Candida tropicalis ATCC® MYA-750	<15.62	250	>4	4	>128	>4	
Candida dubliniensis ATCC® MYA-646	<15.62	>2,000	>4	<1	32-64	>4	

Note: MFC/MIC <4: fungicidal profile/MFC/MIC >4: fungistatic profile.

conditions for *A. colubrina* extract preparation (Lima et al., 2014; Rocha et al., 2017; Lima et al., 2018–*data not published*; Maia et al., 2021) The presence of polyphenol content of 53.1% (Lima et al., 2014) and 53.18% (Rocha et al., 2017) gallic acid equivalents; tannins (8.7% catechin equivalents) and flavonoids (0.3% quercetin equivalents) (Lima et al., 2014), compounds with straight relationship with *A. colubrina* extract activity were also recently monitored by GC-MS analysis (Maia et al., 2021). These results, presented in **Table 1**, suggest the maintenance of the same phytochemical profile of the standardized extract.

In Vitro Antifungal Activity

MIC and MFC values for *A. colubrina* extract and for the standard antifungal on *Candida* spp. are illustrated in **Table 2**. For the extract, the MIC were lower than 15.62 μg/ml and the MFC ranged from 250 μg/ml to higher than 2,000 μg/ml, while MIC and MFC of Fluconazole ranged from lower than 1 to 8 μg/ml and from 32 to higher than 128 μg/ml, respectively. The extract demonstrated strong antifungal activity against all *Candida* strains tested, based on the classification proposed by Holetz et al. (2002). According to the parameters stated by

Siddiqui et al. (2013), the ratio MFC/MIC found demonstrated a fungistatic effect of the extract against the species tested.

Biofilm Inhibition

Biofilm assay showed that the treatments with *A. colubrina* extract at 312.4 µg/ml, equivalent to 20×15.62 µg/ml for *C. albicans* MYA 2876, and with Fluconazole at 10 µg/ml (10MIC) had significant reduction (p < 0.05) in fungal load, expressed as CFU/ml/g of biofilm dry weight, in comparison to the vehicle control group (DMSO 0.1%) (**Figure 1**).

Proteinase and Phospholipase Enzymes Secretion

Phospholipase enzyme activity was significant reduced (p < 0.05) after the treatments with A. colubrina at $156.2~\mu g/ml$ ($10 \times 15.62~\mu g/ml$) and $312.4~\mu g/ml$ ($20 \times 15.62~\mu g/ml$), when compared to the vehicle (DMSO 0.1%). On the other hand, the proteinase enzyme activity was significant decreased (p < 0.05) by the extract only at $312.4~\mu g/ml$ ($20 \times 15.62~\mu g/ml$) in comparison to the vehicle control group (**Figures 2A,B**).

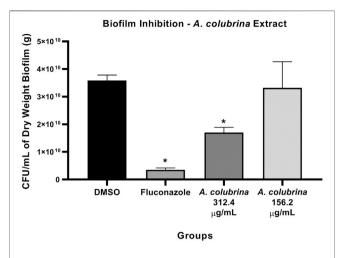


FIGURE 1 | Fungal viability of *C. albicans* MYA 2876 72-hours-biofilm expressed in CFU/ml/grams of dry weight after treatment with *A. colubrina* extract (312.5 μ g/ml-20 × 15.62 μ g/ml; 156.2 μ g/ml-10 × 15.62 μ g/ml). DMSO 0.1%: vehicle control; Fluconazole (10 μ g/ml): positive control. Values shown with asterisk (*) are statistically significant when compared to the vehicle control (ρ < 0.05).

Co-Culture Model of Fibroblasts and *C. albicans*

Cytotoxicity

The *A. colubrina* extract presented LD_{50} of 432.3 µg/ml and a non-toxic profile on gingival fibroblast cell culture up to a concentration of 250 µg/ml, with cell viability remaining higher than 70%, when compared to the vehicle and the cell control groups, as shown in **Figure 3**.

Proteolytic Enzymes Gene Expression

Similar to the profile obtained from the biofilm proteinase and phospholipase assays, the gene expression of SAP-1 and PLB-1 secreted by *C. albicans* MYA 2876, grown as immature biofilm in

a co-culture model, was significantly down-regulated (p < 0.05) after the exposure to *A. colubrina* extract at 33.28 µg/ml, when compared to the vehicle control group (**Figures 4A,B**).

Fluorescence Microscopy

In the co-culture model of fibroblasts coexisting with *C. albicans*, samples treated with *A. colubrina* extract showed a considerable decrease in *Candida* growth distribution in comparison with the vehicle control, as indicated by the sparse and less dense accumulation of *C. albicans* (blue color) among viable fibroblast cells (green color) in fluorescent images. In addition, fibroblasts viability was not significantly affected by the treatment with the extract, since there was no significant increase in the dead fibroblast population, indicated by the red fluorescent color, suggesting that *A. colubrina* was effective against *C. albicans* with minimal effects or toxicity on fibroblast cells (**Figures 5A–C**).

Scanning Electron Microscopy

As seen in **Figures 6A–C**, the pattern was similar to the arrangement observed on Fluorescence Microscopy. The SEM showed density reduction of *C. albicans* biofilm, and de-structuring of hyphae morphology, in comparison to the vehicle control group.

Pro and Anti-inflammatory Cytokines Gene Expression

The *A. colubrina* extract at 33.28 µg/ml presented a modulatory effect on the gene expression of host inflammatory cytokines in a co-culture model. The gene expression of IL-6, IL-1 β , and IL-10 were up-regulated after host cells exposure to the extract, while IL-8 gene expression was down-regulated. However, the *A. colubrina* concentration tested showed no statistical difference (p > 0.05) on the gene expression of the host cytokines in comparison to the vehicle control group (**Figures 7A–D**).

Pro and Anti-inflammatory Cytokines Secretion

Co-culture supernatants were assessed for expression of proinflammatory IL-6, IL-8, and IL-1β as well as anti-inflammatory

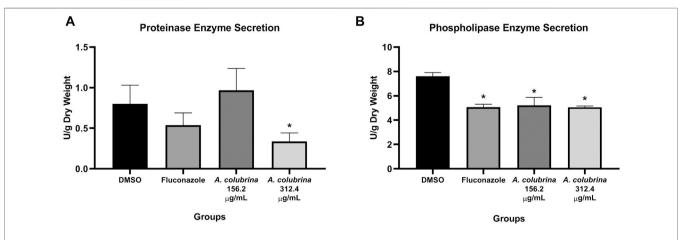


FIGURE 2 | C. albicans MYA 2876 72-hours-biofilm proteolytic enzymes secretion expressed in U/grams of dry weight after treatment with A. colubrina extract (312.5 μg/ml–20 × 15.62 μg/ml; 156.2 μg/ml–10 × 15.62 μg/ml). (A) Proteinase activity; (B) Phospholipase activity. DMSO 0.1%: vehicle control; Fluconazole (10 μg/ml): positive control. Values shown with asterisk (*) are statistically significant when compared to the vehicle control (p < 0.05).

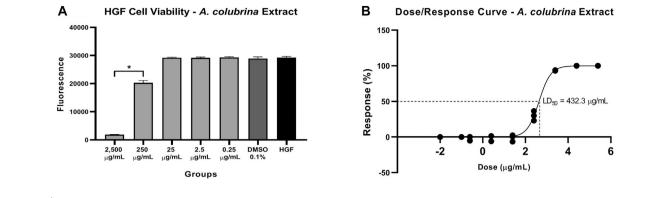


FIGURE 3 | (A) Cytotoxicity effect of *A. colubrina* extract (2,500 μg/ml–0.25 μg/ml) on human gingival fibroblasts after 24 h of treatment, (B) LD₅₀ = 432.3 μg/ml. HGF: only cells; DMSO 0.1%: vehicle control (Values shown with asterisk (*) are statistically significant when compared to the vehicle control (ρ < 0.05).

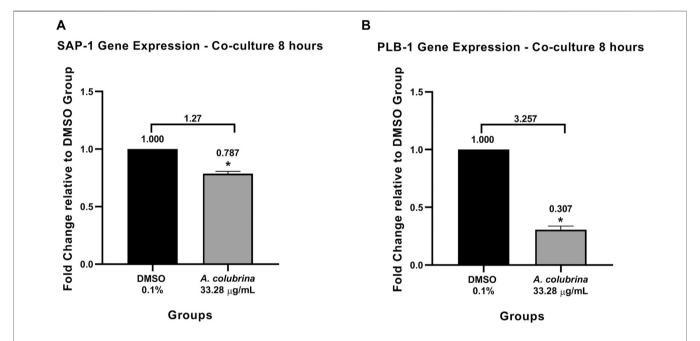


FIGURE 4 | Real-time quantitative information about relative gene expression of (A) SAP-1 and (B) PLB-1 after 8 h of treatment with *A. colubrina* extract treatment (33.28 μg/ml) in human gingival fibroblasts infected by *C. albicans*. DMSO 0.1%: vehicle control. Values shown with asterisk (*) are statistically significant when compared to the vehicle control (ρ < 0.05).

cytokine IL-10, following treatments with *A. colubrina* extract (33.28 µg/ml). The extract has resulted in a significant reduction (p < 0.05) in the expression of IL-6 and IL-8 when compared to the vehicle control group. On the other hand, there was no detection of modulatory effect on the expression of IL-1 β and IL-10 cytokines upon treatment with the extract (**Figure 8**).

DISCUSSION

Recently, the traditional therapeutic use of *A. colubrina* by popular communities in Brazilian culture has encouraged comprehensive studies about its biological properties to be conducted (Damascena et al., 2014; Lima et al., 2014; Barreto et al., 2016; Mota et al., 2017;

Guarneire et al., 2019; Silva et al., 2019; Cardoso-Junior et al., 2020; Maia et al., 2021). In this study, we evaluated the *A. colubrina* extract effects on virulence factor of *C. albicans* and its modulatory effects on host immune response during the fungal infection.

In a previous study, we evaluated the phytochemical composition of the *A. colubrina* extract (Lima et al., 2014), in which was found that the extract presents in its composition a high total polyphenol content (53.18% gallic acid equivalents); tannins (8.77% catechin equivalents) and flavonoids (0.28% quercetin equivalents). This chemical profile seems to support the biological activities evaluated here and discussed ahead, since these classes of compounds are related to a wide range of properties, including antifungal (Ramirez et al., 2013; Kanchanapiboon et al., 2020) and immune response

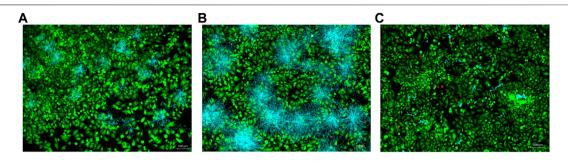


FIGURE 5 | Co-culture fluorescence microscopy after 24 h of treatment with *A. colubrina* extract. (A) *A. colubrina* extract (33.28 μg/ml); (B) Vehicle control (DMSO 0.1%) and (C) Positive control (Fluconazole–10 μg/ml). Scale bar set at 100 μm at 100x magnification power.

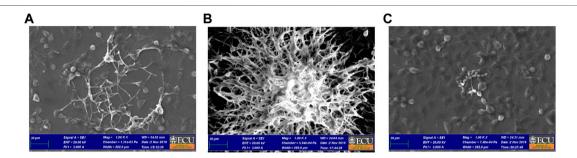


FIGURE 6 | Co-culture SEM after 24 h of treatment with *A. colubrina* extract. (A) *A. colubrina* extract (33.28 μg/ml); (B) Vehicle control (DMSO 0.1%) and (C) positive control (Fluconazole–10 μg/ml). Scale bar set at 30 μm at 1,000x magnification power.

modulatory effects (Fu et al., 2013; Ji et al., 2019; Cardoso Junior et al., 2020).

A. colubrina extract has been reported to present in vitro antifungal properties against Candida spp. and anti-biofilm properties, mainly on C. albicans biofilms (Lima et al., 2014; Silva et al., 2019). The susceptibility assay from our study showed a strong anti-Candida effect (Holetz et al., 2002) of A. colubrina, exerting a fungistatic profile (Siddiqui et al., 2013) over all the strains tested in planktonic form. Candida spp. is not only an important component of oral microbiota, living as a common commensal in immunocompetent individuals (Qin et al., 2016), but also display an important role in shaping the oral microbiome (Xu and Dongari-Bagtzoglou, 2015; Bertolini et al., 2019). Thus, total elimination of yeast from the body is neither desirable nor feasible (Bhattacharya et al., 2020) and its growth inhibition instead its elimination might be positive regarding the infection control, by preventing the rise of pathogenic strains that could lead to more severe infections and antifungal resistance (Ford et al., 2015).

One of the major virulence factors related to *C. albicans* pathogenesis, with significant clinical implications, resides in its ability to form biofilms (Fox et al., 2015; Wall et al., 2019). In oral cavity, hyphae formation and adherence to oral epithelial cells and other abiotic surfaces, such as dentures, leads to the development of this structured community of surface-associated microbial populations embedded in an extracellular matrix (Ghannoum et al., 2015; Hirota et al., 2017). In our study, biofilms treated with *A. colubrina* at 312.4 μ g/ml (20 \times 15.62 μ g/ml) showed

significant decrease in fungal viability in comparison to the vehicle group, by reducing the CFU/mL/g parameter and altering the biofilm composition and structure integrity. For this biofilm assay model, we used *C. albicans* MYA 2876, considering the MFC result of this strain after the treatment with the extract. In addition, higher concentrations of *A. colubrina*, equivalent to $156.2 \,\mu\text{g/ml}$ ($10 \times 15.62 \,\mu\text{g/ml}$) and $312.4 \,\mu\text{g/ml}$ ($20 \times 15.62 \,\mu\text{g/ml}$), were used against *C. albicans* MYA 2876 strain, due to biofilm structured and stable environment, which is tolerant to antifungal agents' diffusion (Tsui et al., 2016).

Once biofilm is established, the expression of C. albicans virulence factors increases (Jabra-Rizk, 2011) also giving rise to the release of extracellular hydrolytic enzymes by the biofilms into the local environment, contributing to candidiasis progression (Vila et al., 2020). Most notable of the secreted enzymes frequently implicated in the pathogenicity of *C*. albicans are Secreted Aspartyl Proteinases (SAPs) and Secreted Phospholipases (PLs), which are involved in host tissue invasion, nutrient acquisition, immune evasion, and organ damage (Jabra-Riks, 2011; Sorgo et al., 2013; Swidergall and Filler, 2017). In order to evaluate the modulating effect of A. colubrina extract over this critical virulence factor, we demonstrated that phospholipase enzyme activities was significant reduced using the extract both at 156.2 μ g/ml (10 × 15.62 μ g/ml) and 312.4 μ g/ ml (20 \times 15.62 $\mu g/ml$) concentrations, while proteinase activity was decreased only by the highest concentration. These results suggest that both antifungal and anti-biofilm activities of A.

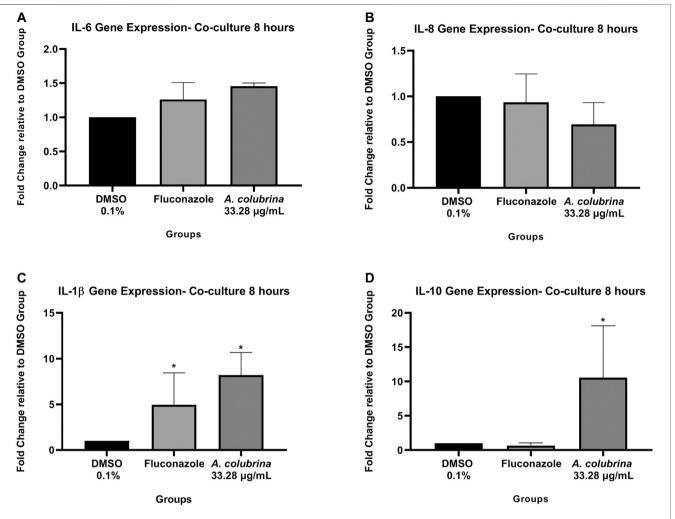


FIGURE 7 | Real-time quantitative information about relative gene expression of (A) IL-6; (B) IL-8; (C) IL-1β; and (D) IL-10 of human gingival fibroblasts after 8 h of infection by *C. albicans* and treatment with *A. colubrina* extract (33.28 µg/ml). DMSO 0.1%: vehicle control; Fluconazole (10 µg/ml): positive control. Values are shown as the fold-change relative to the vehicle control group. Values shown with asterisk (*) are statistically significant when compared to the vehicle control (ρ < 0.05).

colubrina could involve the inhibition of proteolytic enzymes expression as mechanism of action, considering that during *C. albicans* penetration, these enzymes affect epithelial junctions and enable degradation of cell membrane components, facilitating fungal adhesion and biofilm formation to both oral epithelium or abiotic surfaces (Naglik et al., 2011).

To confirm the results obtained over proteolytic enzyme secretion, we assessed gene expression of SAP-1 PLB-1) after treatment with *A. colubrina* at 33.28 μg/ml on co-culture models of immature biofilm of *C. albicans* coexisting with fibroblasts. We demonstrated a significant down-regulation on the gene expression of both enzymes in comparison to the vehicle group. These findings are consistent to the enzymatic secretion results, considering that fungal infections usually present a higher gene expression of SAPs and PLs. Proteinases were shown to induce degradation of a variety of host factors, such as E-cadheryn, present in epithelial cell junction, increasing the hyphae capacity for colonization and penetration into host tissues, and factors involved in the innate and adaptive immune responses, allowing *C*.

albicans to overcome the host immune defenses (Kumar et al., 2017). On the other hand, phospholipases expression displays an active role in epithelial adherence and tissue invasion, since their catalytic action results in disruption of epithelial cell membrane allowing the penetration of yeasts into host cell cytoplasm (Sanitá et al., 2014). Thus, our results suggest that the *A. colubrina* can act by interfering with yeast invasion mechanisms, which could prevent the development of candidiasis.

The cytotoxicity assay was conducted on human gingival fibroblasts (LD $_{50}=432.3\,\mu g/ml$) in order to verify the therapeutic safety level previously, regarding further *in vivo* and human clinical researches. *A. colubrina* extract maintained the cell viability higher than 70% at concentrations up to 250 $\mu g/ml$, representing a relatively low cytotoxic activity. This finding is consistent with results recently reported, which verified the low toxicity of the bark extract of *A. colubrina* on human cells lines, such macrophages (Silva et al., 2019; Cardoso-Junior et al., 2020), keratinocytes and also on tumoral cell strains (Lima et al., 2014). These data corroborate to the results found in this study related to

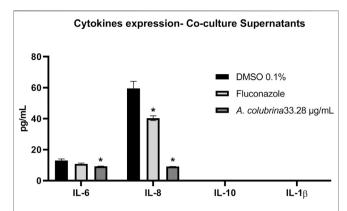


FIGURE 8 | Pro and anti-inflammatory cytokines expression of IL-6, IL-8, IL-10 e IL-1β by human gingival fibroblasts after 8 h of infection with C. albicans and treatment with A. colubrina extract (33.28 μg/ml). HGF: only cells; DMSO 0.1%: vehicle control; Fluconazole (10 μg/ml): positive control. Values shown with asterisk (*) are statistically significant when compared to the vehicle control (p < 0.05).

the low toxic potential effect of this product, shown to be pharmacological safe *in vitro*, by maintaining the cell viability.

Considering the purpose to evaluate the regulating effects of *A. colubrina* extract on *C. albicans*-host interaction, we used a coculture model to provide comprehensions about the complex system of an immature *C. albicans* biofilm coexisting with fibroblast cells incubated with the tested extract. Recent studies had been conducted in order to evaluate *in vitro* the modulatory effects of natural compounds on the interaction between *C. albicans* and the host using a co-culture model (Seleem et al., 2016a; Seleem et al., 2016b; Chen et al., 2018). Moreover, co-cultures have demonstrated to be an effective tool to stimulate physiological conditions and induce interactions between the cells that triggers important host response pathways (Serrano et al., 2017).

Microscope images obtained from the co-culture model were helpful to evaluate qualitatively the distribution of C. albicans and fibroblasts in response to *A. colubrina* and the controls groups. The pattern imaging observed through fluorescence microscopy demonstrated a considerable reduction in C. albicans growth without affecting significantly the fibroblasts viability, showing a strong antifungal effect with minimal toxicity. Similarly, the arrangement observed on co-culture SEM imaging in a higher magnification and topographic view, showed significant alterations of the biofilm structure treated with A. colubrina. When compared to the vehicle group, it is possible to observe structural alterations, such as notable decrease of the density biofilm and de-structuring of the hyphae morphology in the areas where the extract was able to penetrate. In addition, hyphae decreased, indicating a potential reduction of the biofilm virulence, since the formation of hyphae is associated to tissue invasion.

Host immune defense against *C. albicans* infection requires a wide range of complex molecular mechanisms involving the recognition of fungal cell wall components, the activation of host immune cell signaling cascades and the release of cytokines and chemokines (Brown et al., 2012; Pappas et al., 2018). Some reviews were recently published regarding the

interplay between *C. albicans* and host cells and the immune response during *C. albicans* mucosal infection (Höfs et al., 2016; Naglik et al., 2017; Nikou et al., 2019; Swidergall, 2019; Vila et al., 2020), serving as a guidelines to improve our understanding that relies on this complex interaction.

Therefore, to evaluate the modulatory activity of *A. colubrina* on the host pro-inflammatory response during the *Candida* infection, we employed a transcriptomic approach in conjunction with a proteomic profiling, regarding the analysis for the host cells' gene expression and the release of pro-inflammatory and anti-inflammatory cytokines. We choose a panel of inflammatory markers according to the host immune response mechanisms upon *Candida* recognition, considering the activation of transmembrane Toll Like Receptors (TRLs) (Salvatori et al., 2016; Pappas et al., 2018), which triggers signaling pathways and results at the release of pro-inflammatory cytokines, mainly IL-1α, IL1β, IL-6, IL-8, and CCL5 (RANTES) by the host cells (Hebecker et al., 2014; Verma et al., 2017; Verma et al., 2018).

The assessment of gene expression demonstrated that A. colubrina affects the expression of host inflammatory cytokines by down-regulating IL-8 gene expression and up-regulating IL-6, IL-1β, and IL-10 gene expression. However, there was no statistical difference when compared to vehicle control group. On the other hand, the analysis for expression of host pro-inflammatory and anti-inflammatory cytokines was found significant reduction on the secretion of pro-inflammatory cytokines IL-6 and IL-8, suggesting a modulatory role of A. colubrina on the host proinflammatory response, which could help to eradicate the fungal infection. A possible reason for the differences between gene expression and production profile of IL-1β, IL-6 an IL-10 is based on a negative feedback mechanism modulating gene expression. Cytokines gene expression may play an important role in regulating the release of them. However, as indicated by the significant reduction in expression of these molecules, there may be a negative feedback inhibition mechanism involving the transcription and translation processes, which regulates their respective gene expression. However, this hypothesis needs to be confirmed through further molecular studies.

As mentioned before, IL-6 and IL-8 play a crucial role in innate immune response. While IL-8 is a known neutrophil recruiter from the circulating blood to the site of infection (Höffs et al., 2016), IL-6 is related to immune response to microorganisms and its expression is directly influenced by the secretion of other pro-inflammatory cytokines, especially IL-1 (Tanaka et al., 2014). Some reports state that *C. albicans* infection is crucial for the modulation and release of IL-1a, IL-6, and IL-8, promoting a higher production of these cytokines (Feller et al., 2014; Figueira et al., 2020; Mo et al., 2020). In this regard, our findings suggest that A. colubrina might reduce proinflammatory IL-6 and IL-8 cytokines expression during the fungal infection, due its strong antifungal activity, which modulates some putative virulence factors of the C. albicans, such as biofilm formation and proteolytic enzyme secretion, reducing the fungus pathogenicity. In addition, the low cytotoxicity of the extract on the host cells does not induce an inflammatory response.

This is the first study reporting the effects of Anadenanthera colubrina (Vell.) Brenan on Candida albicans-Host interaction. A. colubrina extract demonstrated anti-Candida, antibiofilm and antiproteolytic enzyme activities against C. albicans, with relatively low cytotoxicity to the host cells. Furthermore, presented modulatory effects on the host immune response, as indicated by its regulation of IL-6 and IL-8 pro-inflammatory cytokines secretion. In this regard, A. colubrina could be considered as a potential source for an anti-Candida formulation. Further investigations about the regulation activity of A. colubrina on others C. albicans key virulence factors, including expression of cell surface adhesins, proteolytic degradation of host immune factors and invasion and destruction of host tissue mechanisms, must to be conducted in order to reinforce and establish the extract effects over molecular and signaling pathways in Candida pathogenesis.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation, to any qualified researcher.

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AUTHOR CONTRIBUTION

Conceptualization: RM, EC, CN, and CM. Investigation and Data curation: CM and SP. Formal analysis: RM, EC, CM, and SP. Writing-original draft: CM. Writing-review and editing: CM, SP, CN, EC, and RM.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Dendrobium Officinale Polysaccharide Attenuates Insulin Resistance and Abnormal Lipid Metabolism in Obese Mice

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Qu J, Tan S, Xie X, Wu W, Zhu H, Li H, Liao X, Wang J, Zhou Z-A, Huang S and Lu Q (2021) Dendrobium Officinale Polysaccharide Attenuates Insulin Resistance and Abnormal Lipid Metabolism in Obese Mice. Front. Pharmacol. 12:659626. doi: 10.3389/fphar.2021.659626 **Objectives:** Dendrobium officinale polysaccharide (DOP) is the main active ingredient in a valuable traditional Chinese medicine, which exerts several pharmacological activities including hepatoprotection and hypoglycemic effects. However, the effects of DOP on obesity-associated insulin resistance (IR) and lipid metabolism remain unknown. This study aimed to investigate the role of DOP in IR and abnormal lipid metabolism in obese mice.

Methods: IR models were established using 3T3-L1 adipocytes, C2C12 myocytes, and primary cultured hepatocytes exposed to palmitate acid. After treatment with DOP, insulinstimulated glucose uptake, glucose release, and AKT phosphorylation was detected. Fasting blood glucose, fasting serum insulin, the glucose tolerance test (GTT), and the insulin tolerance test (ITT) were measured to evaluate IR of obese mice. Lipid analysis was conducted to evaluate the effects of DOP on lipid metabolism in obese mice.

Results: In vitro, DOP treatment ameliorated palmitic acid-induced IR in adipocytes, myocytes, and hepatocytes. DOP regulated cellular insulin sensitivity via the peroxisome proliferator-activated receptor-γ (PPAR-γ). Furthermore, administration of DOP significantly reduced the IR and visceral adipose tissue (VAT) inflammation of diet-induced obese (DIO) and the genetically-induced obesity mice (ob/ob) mouse models. In addition, DOP treatment attenuated the high-fat diet (HFD)-induced liver lipid accumulation by reducing liver triglycerides (TG), plasma free fatty acid (FFA), serum cholesterol (TC), and low-density lipoprotein cholesterol (LDL-C) levels, while increasing HDL-C levels.

Conclusion: DOP could improve obesity-associated IR and abnormal lipid metabolism through its activities on PPAR- γ , and may serve as a potential therapeutic agent for obesity-associated insulin resistance and lipid metabolism disorder.

Keywords: abnormal lipid metabolism, Dendrobium officinale polysaccharide, insulin resistance, obesity, peroxisome proliferator-activated receptor- γ

Abbreviations: DIO, Diet-induced obese; DOP, Dendrobium officinale polysaccharide; FFA, Free fatty acid; GTT, Glucose tolerance test; HDL-C, High-density lipoprotein cholesterol; HFD, High-fat diet; HOMA-IR, Homeostasis model assessment of insulin resistance; IR, Insulin resistance; ITT, Insulin tolerance test; LDL-C, Low-density lipoprotein cholesterol; PPAR-γ, Peroxisome proliferator-activated receptor-γ; TC, Serum cholesterol; TG, Triglycerides; VAT, Visceral adipose tissue.

INTRODUCTION

With rapid economic growth, obesity is becoming an increasing health concern worldwide. Understandably, obesity was defined as a disease by the Obesity Society (TOS) in 2008 (Belkina and Denis, 2010; Jastreboff et al., 2019). Obesity is characterized by increased circulating fatty acid levels resulting from excessive lipolysis and absorption of basal adipose tissue, which in turn promote the development of ectopic lipid deposition and insulin resistance (IR) (Crowe et al., 2009). Consistently, studies have shown that obesity is a risk factor for metabolic syndrome, which includes IR and dyslipidemia, impaired fasting blood glucose, and hyperinsulinemia (Laaksonen et al., 2002; Meigs et al., 2006). In addition, obesity increases the risk and mortality of many diseases Council of the Obesity (2008), González-Domínguez et al. (2020), especially type 2 diabetes, cardiovascular disease, hypertension, and dyslipidemia (De Lorenzo et al., 2019).

IR refers to the reduction of insulin sensitivity and response to insulin target organs and tissues (liver, adipose tissue, skeletal muscle) due to varied reasons (Samuel and Shulman, 2012). This leads to a decrease in glucose uptake and utilization. Therefore, the body will compensatively secrete excess insulin to maintain the stability of blood sugar, leading to hyperinsulinemia, which in turn leads to dyslipidemia. Dyslipidemia manifests as increased total cholesterol (TC), triglycerides (TG), and free fatty acids (FFA), normal or slightly increased low-density lipoprotein cholesterol (LDL-C), and decreased high-density lipoprotein cholesterol (HDL-C) (Klop et al., 2013). Moreover, the symptoms of IR are impaired glucose absorption in muscles and increased gluconeogenesis in the liver during fasting and postprandial conditions, leading to hyperglycemia (Moller and Kaufman, 2005). Insulin-sensitive tissues (adipose tissue, heart, and liver) are significantly affected by obesity at biomolecular and functional levels (Barazzoni et al., 2018). Excessive fat accumulation can change the function of adipose organs and leads to obesity-related diseases (Ling and Ronn, 2019). In addition, a close relationship between the mechanisms implicated in lipid metabolic disorders and IR has also been reported (Savage et al., 2007). Further, obesity and IR are closely related to inflammation of metabolic tissues, including the liver, muscle, and adipose tissue (Winer et al., 2016; Wu and Ballantyne, 2017; Ghorpade et al., 2018). Excessive fat accumulation and abnormal lipid metabolism caused by obesity induce the transformation of macrophages from the anti-inflammatory M2 polarized state to the pro-inflammatory M1 polarized state, leading to VAT inflammation, thus promoting the development of obesity-related IR (Xu et al., 2003; Lumeng et al., 2007; Kojta et al., 2020). At the same time, IR further aggravates lipid metabolism disorders, leading to a series of metabolic disorders such as diabetes and cardiovascular diseases. The specific manifestations of visceral adipose tissue (VAT) inflammation are increased levels of proinflammatory cytokines such as tumor necrosis factor (TNF)-a and interleukin (IL)-6 Hotamisligil et al. (1993), Kern et al. (2001), and decreased levels of anti-inflammatory cytokines IL-10 and IL-4 in obesity-related IR patients (Esposito et al., 2003). Therefore, the prevention or treatment of IR and lipid

metabolism disorders may be an effective way to inhibit obesity-related diseases.

Dendrobium officinale Kimura et Migo is a valuable traditional Chinese medicine that has been used to treat diabetes, obesity, rheumatoid arthritis, and many other diseases. It has been reported that Dendrobium officinale Kimura et Migo can inhibit the effects of oxidative stress and pro-inflammatory cytokines (Teixeira da Silva et al., 2015). Oxidative stress and inflammation may also lead to obesity-related IR (Xu et al., 2003; Gortan Cappellari et al., 2016). Dendrobium officinale polysaccharide (DOP) is the main active component of Dendrobium officinale Kimura et Migo, which exerts pharmacological activities including antioxidation, lowering blood lipids and blood sugar levels, and hepatoprotection (Huang et al., 2016). In type 2 diabetic rats, DOP treatment reduced hepatic lipid metabolism disorders and alleviated symptoms of hepatic lipid accumulation (Yang et al., 2020). These studies indicated that DOP is expected to be a novel therapeutic agent for obesity-related diseases including IR and abnormal lipid metabolism. However, to date, there are almost no available mechanistic studies investigating mechanistic studies on the effects of DOP in IR and abnormal lipid metabolism. Meanwhile, the mechanism of DOP in obesity-related IR and abnormal lipid metabolism is still unclear.

The purpose of this study was to explore the effects and mechanisms of action of DOP on obesity-related IR and lipid metabolism disorders. First, at the cellular level, we measured glucose uptake, glucose output, and Akt phosphorylation in insulin-stimulated hepatocytes, muscle cells, and adipocytes, respectively. The results showed that DOP treatment could improve IR-induced obesity. Subsequently, we conducted a mechanism study and found that DOP mainly acted on peroxisome proliferator-activated receptor-γ (PPAR-y)signaling to regulate insulin sensitivity in diet-induced obesity (DIO) mice. We evaluated how DOP could improve IR in DIO mice by assessing fasting blood glucose and fasting serum insulin levels, the glucose tolerance test (GTT), the insulin tolerance test (ITT), and the inflammation related indicators of VAT. Furthermore, lipid analysis showed that DOP attenuated the abnormal lipid metabolism in DIO mice. We also validated the therapeutic effects of DOP in the genetically-induced obesity mice (ob/ob mice) model. Overall, we expect that our study can provide a basis for the clinical application of DOP in obesity-related IR and lipid metabolism disorders.

MATERIALS AND METHODS

Animal Models

To establish a diet-induced obese (DIO) mice model, two-month-old male C57BL6 mice were fed a high-fat diet (HFD, 60% fat, 20% protein, and 20% carbohydrate) for 3 months. Ob/ob mice are a classical experimental model of obesity-induced IR as evidenced by a plethora of studies. Ob/ob mice harbor a recessive mutation in leptin and are characterized by hyperphagia, obesity, hyperinsulinemia, insulin-resistance (IR), and hyperglycemia; thus, they are commonly used as a model for

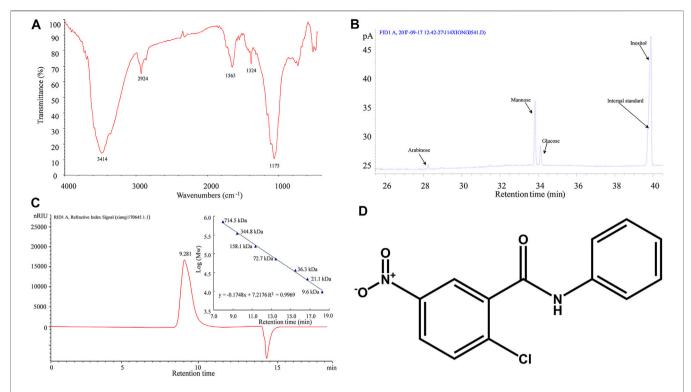


FIGURE 1 | Characterization of DOP (A) The FT-IR spectrogram of DOP (B) GC chromatogram of monosaccharide composition showed that DOP is allocated to O-H stretching vibrations, C-H stretching vibrations and C-C or C-O stretching vibrations, respectively. These is the characteristic absorption profile of polysaccharides. The monosaccharide composition of DOP was mannose, glucose, and arabinose with a molar ratio of 5.55:1:0.12. (C) The average molecular weight of DOP was 393.8 kDa by HPLC profiles of molecular weight measurement. (D)The chemical structure diagram of the PPARy antagonist GW9662.

studies of diabetes and obesity. Ob/ob mice were purchased from Hunan SJA Laboratory Animal Co., Ltd. (license number: SCXK 2019-0004). All animals were housed under 12-h light/dark cycles and were provided unrestricted access to food and water unless otherwise specified.

For in vivo DOP treatment, after 3 months of a HFD, the DIO mice were divided into two groups, the control group and the experimental group, the control group received normal saline (NS) orally, and the experimental group was administrated DOP (150 mg/kg) orally, once daily for 3 months. The DOP involved in this study was prepared by the laboratory of Mathematical Engineering Academy of Chinese Medicine, Guangzhou University of Chinese Medicine (Liang et al., 2018; Liang et al., 2019). The proportion of total polysaccharides in the DOP was 93.80%. Moreover, the FT-IR spectrogram showed that DOP has an intense and broad absorption peak around 3414 cm-1, a weak absorption peak at 2924 cm-1 and 1324 cm-1, and an asymmetrical extension at 1175 cm-1 (Figure 1A). And GC chromatogram of monosaccharide composition showed that DOP had the characteristic absorption profile of polysaccharides. DOP is composed of mannose, glucose, and arabinose with a molar ratio of 5.55:1:0.12 (Figure 1B). Meanwhile, the average molecular weight of DOP determined by HPLC profiles of molecular weight measurement was 393.8 kDa (Figure 1C). The structure composition of DOP showed that its

formulation was identical to the DOP prepared by Hua (Hua et al., 2004).

All protocols pertaining to animal care and experiments were reviewed and approved by the Institutional Animal Care and Use Committee of the Laboratory Animal Research Center at Xiangya Medical School of Central South University, China.

Cell Culture and Treatment

Primary hepatocytes, C2C12 myoblasts, and 3T3-L1 preadipocytes were cultured in a humidified incubator at $37^{\circ}C$ and supplemented with 5% CO2. Standard protocols were utilized to induce differentiation of these cells. To establish IR models, primary hepatocytes, C2C12, myoblasts and 3T3-L1 preadipocytes were treated with 0.5 mmol/L palmitate acid (PA; Sigma) for 24 h. Glucose levels in the medium were measured to determine whether the IR model was successful. For *in vitro* DOP treatment, 200 $\mu g/ml$ DOP was added to the culture medium for 48 h.

Cell Viability

The Cell Counting Kit-8 (CCK-8) was used to assess the viability of 3T3-L1 adipocytes after DOP treatment, as per the manufacturer's protocol. Absorbance was measured at 450 nm *via* a microplate reader (Thermo Electron Corp).

TABLE 1 | Primer sequences used for real-time PCR analysis.

Gene	Forward primer	Reverse primer
Actin (mouse)	GGCTGTATTCCCCTCCATCG	CCAGTTGGTAACAATGCCATGT
PPAR-γ (mouse)	GGAAAGACAACGGACAAATCAC	TACGGATCGAAACTGGCAC
TNFα (mouse)	TATGGCTCAGGGTCCAACTC	CTCCCTTTGCAGAACTCAGG
IL-6	AGTTGCCTTCTTGGGACTGA	CAGAATTGCCATTGCACAAC
IL-10	GCCCTTCCTATGTGTGGTTTG	TTGAGTTTCCGTACTGTTTGAGG
IL-4	CCCCAGCTAGTTGTCATCCTG	CAAGTGATTTTTGTCGCATCCG

Glucose Uptake and Glucose Output Assay

The glucose uptake and glucose output assays were performed as described previously (Su et al., 2019). The medium glucose levels were measured by a Glucose Assay Kit (Abcam, ab65333) according to the manufacturer's instructions.

Western Blot and gRT-PCR Analysis

Western blotting analysis was conducted as previously described (Li et al., 2009). Primary antibodies p-AKT (CST9272s; Dilution 1:1,000) and AKT (CST9272s; Dilution 1:1,000) were purchased from Cell Signaling Technology, and PPAR- γ (ab209350, Dilution 1:1,000) was purchased from Abcam. All primary antibodies were incubated at 4°C overnight, the secondary antibodies were diluted to 1:5,000, and specific proteins were visualized by ECL Plus. For qRT-PCR analysis, the total RNA from cultured cells were isolated by TRIzol (Thermo Fisher Scientific). The list of primers used for real-time PCR analysis are described in **Table 1**.

Blood Glucose, Serum Insulin, Insulin Tolerance Test, Glucose Tolerance Test, and HOMA-IR Index

The measurement of blood glucose levels and serum insulin, and the performance of the ITT and GTT, have been reported previously (Ying et al., 2017; Xiao et al., 2020). The following formula was used to calculate the homeostasis model assessment of IR (HOMA-IR) index: [fasting blood glucose levels (mmol/L)] \times [fasting serum insulin levels (μ U/ml)]/22.5 (Su et al., 2019).

Lipid Analysis

Approximately, 0.1 g liver was homogenized in phosphate-buffered saline (PBS) solution (1:9 ratio). The mixture was centrifuged at 2,500 rpm for 10 min at 4°C after which the supernatant was collected. The cytoplasm of L02 cells was collected with 2% Triton X-100. Hepatic and hepatocellular TG were quantified using chemical reagent kits from Nanjing Jiancheng Bioengineering Institute (Nanjing, China). In addition, serum lipids including TC, TG, LDL-C, and HDL-C levels were determined using kits from Nanjing Jiancheng Bioengineering Institute (Nanjing, China). Plasma-free fatty acid (FFA) levels were measured enzymatically using a kit from WAKO Chemicals. Absorbance values of all samples were measured using a spectrophotometric system.

Hematoxylin and Eosin Staining and Oil Red O Staining

Livers samples (4–5 micron in thickness) were placed in cassettes and submerged in 10% formalin solution overnight. Samples were processed in a dehydrating ethanol gradient, followed by xylene incubation and paraffin embedding. Serial 8-µm sections were used for hematoxylin and eosin (H&E) staining and Oil Red O staining.

Quantification and Statistical Analysis

All data are presented as mean \pm SD. For comparisons between two groups, a two-tailed Student's t-test was used. Comparisons between multiple groups were performed using ANOVA followed by Bonferroni's post-hoc correction. A *p*-value < 0.05 was considered statistically significant.

RESULTS

DOP Ameliorated Cellular Insulin Resistance *In Vitro*

The cytotoxicity of DOP was assessed by the CCK-8 assay, which revealed DOP did not affect cell viability at concentrations of 100, 200, and 400 µg/ml (Figure 2A). To explore whether DOP participated in the regulation of insulin sensitivity, we treated PA-induced adipocytes, myocytes, and hepatocytes with DOP. As expected, DOP treatment significantly promoted the insulinstimulated glucose uptake of 3T3-L1 adipocytes and C2C12 myocytes (Figures 2B,C), while the glucose output of primary cultured hepatocytes decreased (Figure 2D). In addition, the insulin-stimulated AKT phosphorylation of 3T3-L1 adipocytes, C2C12 myocytes, and primary cultured hepatocytes was increased following DOP treatment (Figure 2E). Taken together, these results suggested that DOP ameliorated cellular IR of adipocytes, myocytes, and hepatocytes *in vitro*.

DOP Regulated Cellular Insulin Sensitivity by Activating PPAR-γ

Pharmacological activation of PPAR-γ has emerged as an effective method for treating diabetes. We found that the transcript levels of PPAR-γ mRNA in 3T3-L1 adipocytes, C2C12 myocytes, and primary cultured hepatocytes treated with DOP were elevated (**Figures 3A-C**). Western blotting analysis further confirmed that DOP could promote the protein expression levels of PPAR-γ (**Figure 3D**). These

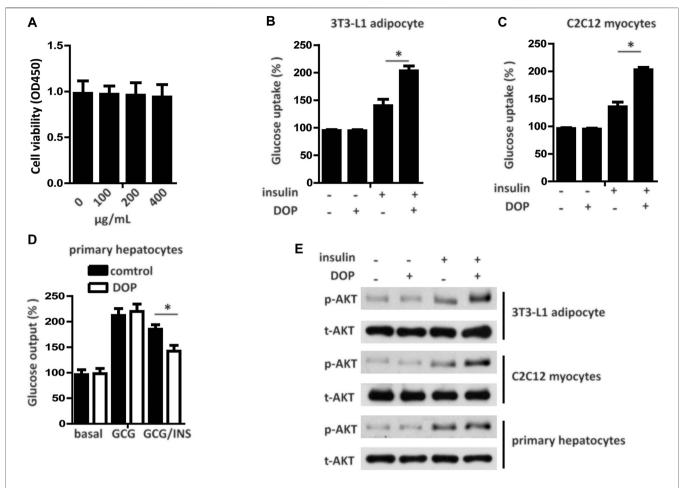


FIGURE 2 | DOP ameliorated cellular insulin resistance in vitro. (A) 3T3-L1 adipocytes were seeded into 96-well plates at a density of 8×103 cells/well and were treated with different concentrations of DOP for 48 h. Cell viability was determined using CCK-8 assay. (B-D) Influence of DOP on glucose uptake of 3T3-L1 adipocytes and C2C12 myocytes as well as glucose output of primary cultured hepatocytes (E) Insulin stimulated AKT phosphorylation in 3T3-L1 adipocytes, C2C12 myocytes, and primary cultured hepatocytes. Data are presented as mean \pm SD. Statistical significance was determined using analysis of variance (ANOVA) for A, and Student's t-test for B, C, and D.* means p < 0.05.

observations suggested that DOP increased the expression of PPAR- γ .

To validate whether DOP regulated cellular insulin sensitivity through the activation of PPAR- γ , we treated PA-induced adipocytes and myocytes with GW9662, a PPAR- γ antagonist. GW9662 is a potent and selective PPAR- γ antagonist with an IC50 of 3.3 nM, showing 10 and 1000-fold selectivity over PPAR α and PPAR- δ , respectively. The chemical structure is shown in **Figure 1D**. The effects of DOP on 3T3-L1 adipocytes and C2C12 myocytes was abrogated by GW9662, which indicated that DOP failed to improve the insulin sensitivity if PPAR- γ was inhibited (**Figures 3E,F**). Taken together, these results indicated that DOP regulated cellular insulin sensitivity by activating PPAR- γ .

Administration of DOP Reduced the Insulin Resistance of Obese Mice

To explore the therapeutic potential of DOP on the IR of obese mice, we treated obese mice with normal saline (NS) or DOP.

Notably, mice treated with DOP had lower fasting blood glucose levels and fasting serum insulin (**Figures 4A,B**). The HOMA-IR index was also lowered in the DOP-treated group (**Figure 4C**). Moreover, DOP could also suppress VAT inflammation. The levels of pro-inflammatory cytokines IL-6 and TNF α were also decreased, while the anti-inflammatory cytokines IL-10 and IL-4 were increased (**Figure 4D**). Furthermore, the results of the GTT and ITT revealed that glucose tolerance and clearance in mice were increased after administration of DOP (**Figures 4E,F**). Together, these findings suggested that administration of DOP reduced IR and adipose tissue inflammation in obese mice.

DOP Impaired Lipid Metabolism Disorder in Obese Mice

To further explore the effect of DOP on lipid metabolism in obese mice, serum, and hepatic lipid levels were assayed. DOP-treated mice exhibited significantly lower TG levels in the liver when compared with untreated mice (**Figure 5A**). In addition, FFA,

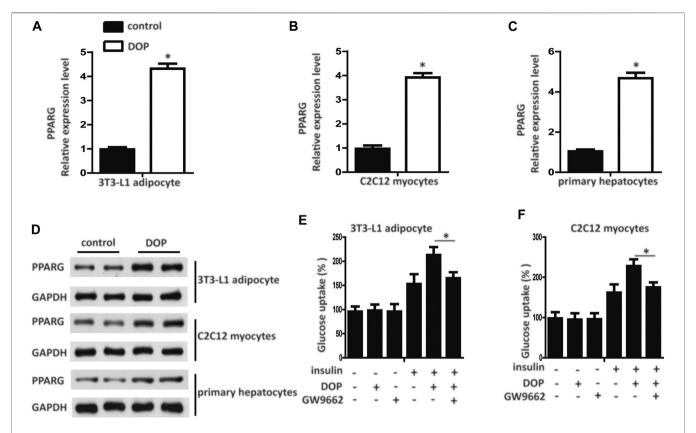


FIGURE 3 DOP regulated cellular insulin sensitivity by activating PPAR- γ (A-C) Expression levels of PPAR- γ in 3T3-L1 adipocytes, C2C12 myocytes, and primary cultured hepatocytes treated with DOP (200 µg/ml, 48 h) (**D**) Western blot analysis of the protein levels of PPAR- γ of 3T3-L1 adipocytes, C2C12 myocytes, and primary cultured hepatocytes treated with DOP. (**E-F**) Effects of GW9662 (10 µM, 24 h) on insulin-stimulated glucose uptake of 3T3-L1 adipocytes and C2C12 myocytes. Data are presented as mean \pm SD. Statistical significance was calculated by two-tailed Student's t-test. * means p < 0.05.

serum TC, TG, and LDL-C levels in DOP-treated mice were also lower than in the control group (**Figures 5B–E**). Importantly, DOP treatment was effective in increasing HDL-C levels (**Figure 5F**). The H&E staining and Oil Red O staining of the liver samples indicated that compared with the control group, the lipid levels and volumes were decreased in DOP treatment group in ob/ob mice (**Figure 5G**). Taken together, these results showed that DOP could ameliorate lipid metabolism disorders in obese mice.

DOP Treatment Alleviated Insulin Resistance in Ob/Ob Mice

To further confirm the therapeutic effect of DOP, ob/ob mice were orally administered DOP as mentioned above. Similar to the observations in obese mice, ob/ob mice treated with DOP also exhibited decreased fasting blood glucose levels, fasting serum insulins, and a lower HOMA-IR index (**Figures 6A–C**). In addition, VAT inflammation was also restrained by DOP treatments exhibited by reduced levels of inflammatory cytokines (IL-6 and TNF α) and elevated expression of anti-inflammatory cytokines (IL-10 and IL-4) (**Figure 6D**). The results from the GTT and ITT indicated that the application of DOP could improve the glucose intolerance of ob/ob mice

(**Figures 6E,F**). Thus, all these results indicated that DOP treatment could alleviate IR and adipose tissue inflammation in ob/ob mice.

DISCUSSION

Obesity is the basis of IR, which is a potential cause of a complex metabolic syndrome, including hypertension, elevated fasting blood glucose, low HDLC, and elevated TG levels (Beale, 2013). Therefore, there is an urgent need to identify potential therapeutic agents and suitable targets to attenuate IR and abnormal lipid metabolism in obese patients. In this study, we confirmed the potential therapeutic target of PPAR- γ in obese mice and the role of DOP in attenuating IR and abnormal lipid metabolism.

IR is defined as the decreased sensitivity to insulin and response of insulin to target organs and tissues (liver, adipose tissue, skeletal muscle) (Samuel and Shulman, 2012). IR can lead to an increase in intracellular glucose concentration and a decrease in glucose uptake. However, for the liver, IR is characterized by an inability to inhibit liver glucose production and glycogen decomposition (Randle et al., 1963; Randle et al., 1964; Randle et al., 1965). AKT protein kinase in adipocytes,

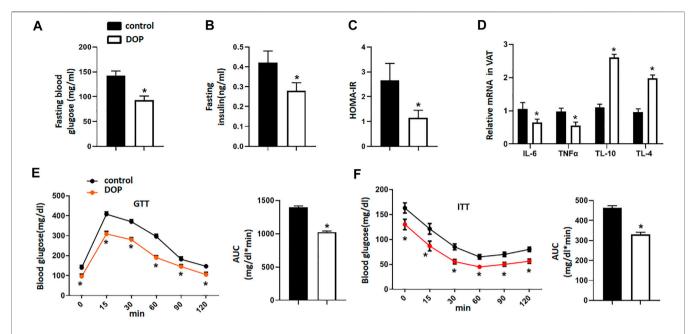


FIGURE 4 Administration of DOP reduced insulin resistance in obese mice **(A–C)** The fasting blood glucose levels, fasting serum insulin, and HOMA-IR index of obese mice administered NS or DOP **(D)** Inflammation-related mRNA levels of VAT in obese mice treated with NS or DOP **(E–F)**. The GTTs and ITTs in obese mice treated with NS or DOP (n = 5 per group). AUC: area under curve. Data are presented as mean n = 5 Statistical significance was calculated using the two-tailed Student's t-test. * means n = 5 means n = 5 co.05.

muscle cells, and liver cells is the key kinase regulating glucose homeostasis (Czech, 2017). Previous studies have found that fatty acid stimulation is an early event of IR (Lee et al., 2014). In this study, we used PA to treat adipocytes, myocytes, and hepatocytes to establish IR models of the three cell types. We then measured glucose uptake or output and insulin-stimulated AKT phosphorylation in these insulin-resistant cells with or without DOP treatment. As expected, DOP treatment significantly promoted the insulin-stimulated glucose uptake of 3T3-L1 adipocytes and C2C12 myocytes, while the glucose output from hepatocytes decreased. Therefore, it is likely that DOP is an agent for potential treatment or prevention of IR.

Multiple mechanisms are involved in the IR of type 2 diabetes. PPAR- γ is a subfamily of nuclear receptors. Activation of PPAR- γ has been reported to improve blood glucose control and systemic insulin sensitivity in patients with type 2 diabetes (Semple et al., 2006). The activation of nuclear receptor PPAR- γ in adipose tissue, liver, and muscle is a determinants of insulin sensitivity (Lu et al., 2011; Germoush et al., 2019). In accordance with previous studies, our results showed that DOP could up-regulate the expression of PPAR- γ in adipocytes, myocytes, and hepatocytes.

IR can lead to hyperinsulinemia and impaired fasting blood glucose (elevated fasting blood glucose). Further, ITT, and GTT are also effective methods to evaluate IR (Guerre-Millo et al., 2001). IR can be diagnosed clinically by a homeostasis model of IR (HOMA-IR) based on fasting blood glucose and fasting serum insulin levels (Yee et al., 2019). To further explore the therapeutic effects of DOP on IR, we conducted *in vivo* experiments using and obese IR mouse model. The results showed that the levels of

fasting blood glucose and fasting serum insulin in the DOPtreated group were significantly lower than those in the control group. Through the ITT and GTT, we found that the blood glucose concentration of mice treated with DOP decreased significantly, which indicated that DOP treatment could significantly increase the glucose tolerance of obese mice and clearance rate of insulin to blood glucose. Furthermore, an increase in obesity-induced lipid storage leads to adipose tissue dysfunction and promotes adipocyte secretion of proinflammatory cytokines, including TNF-α and IL-6. Moreover, due to the transformation of M2 macrophages to M1 in obesity tissues, the expression of anti-inflammatory cytokines IL-10 and IL-4 secreted by M2 macrophages is decreased (Taylor, 2021). Changes in the expression of these markers lead to VAT inflammation, which in turn promotes IR. However, our study showed that DOP treatment can reverse the changes in proinflammatory and anti-inflammatory cytokines caused by obesity. These results once again confirmed the therapeutic effects of DOP on obesity-induced IR.

Typical obesity-induced dyslipidemia includes elevation in TC, TG, and FFA levels; normal or mildly elevated LDL-C; and decreased HDL-C levels (Klop et al., 2013). Multiple studies have shown that these changes in lipid metabolism are closely related to IR (Reaven et al., 1988; Frayn, 1993; Boden et al., 1994; Ormazabal et al., 2018). Therefore, we analyzed the levels of serum and liver lipids in obese mice with or without DOP treatment. The FFA and serum TC, TG, and LDL-C levels were lower and the serum HDL-C levels were higher in DOP-treated mice than control mice. These results were similar to the study by Yang et al. study, whereby DOP treatment reduced the

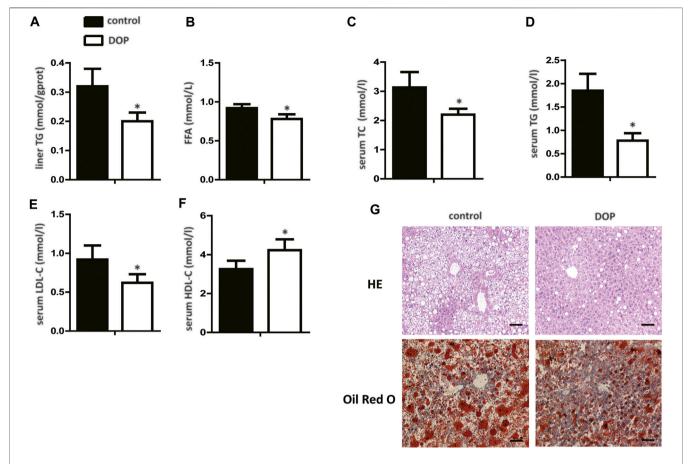


FIGURE 5 | DOP impaired lipid metabolism disorder in obese mice **(A)** TG levels in the liver after treatment with DOP. **(B–F)** The serum levels of TC, TG, LDL-C, and HDL-C after treatment with DOP (n = 5 per group) **(G)** Representative images of H&E staining (G, top) and Oil Red O staining (G, bottom). Scale bars: 300 μ m. Data are presented as mean \pm SD. Statistical significance was calculated using the two-tailed Student's t-test. * means p < 0.05.

metabolic disorder of liver lipids (fatty acids, TG, and glycerolipids) and reduced the symptoms of lipid accumulation in the liver of type 2 diabetic rats (Yang et al., 2020). Thus, we believe that DOP treatment can improve disorders of obesity-induced lipid metabolism.

Interestingly, only a handful of studies have been published in areas related to DOP and obesity to date. The present study investigated whether DOP could improve IR and lipid metabolism disorders in DIO mice. In order to better demonstrate the therapeutic effects of DOP, we used the ob/ob mouse, a genetic model of obesity. Leptin-deficient (ob/ob) mice are an excellent model of obesity and IR Tomita et al. (1992) and are characterized by elevated insulin and glucose levels and by elevated plasma TG and TC, dyslipidemia, and IR (Dubuc, 1976; Fellmann et al., 2013). Concordant with DIO mice, DOP treatment significantly improved glucose tolerance and insulin clearance of blood glucose in ob/ob mice. Remarkably, DOP has also been shown to inhibit VAT inflammation and liver lipid deposition in the ob/ob mouse model of hereditary obesity. Further, this model was used to further confirm the therapeutic effects of DOP on obesity-related IR and lipid metabolism disorders.

There is a limitation to be noted in our study. Hyperinsulinemic-euglycemic clamp studies are the "gold standard" for evaluating IR, but in our study, we did not adopt this method due to the limitations of the experimental conditions. Nonetheless, an important strength of our study is that it is the first to confirm that DOP can reduce IR and improve abnormal lipid metabolism in obese mice.

In conclusion, DOP can improve insulin sensitivity by upregulating the expression of PPAR- γ , thus improving obesity-related IR. In addition, DOP can treat disorders of lipid metabolism in obese mice. To our knowledge, our study is the first to confirm that DOP can reduce IR and improve abnormal lipid metabolism in obese mice, which provides a novel therapeutic option for the treatment of obesity-related IR and lipid metabolism disorders.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/Supplementary Material, further inquiries can be directed to the corresponding authors.

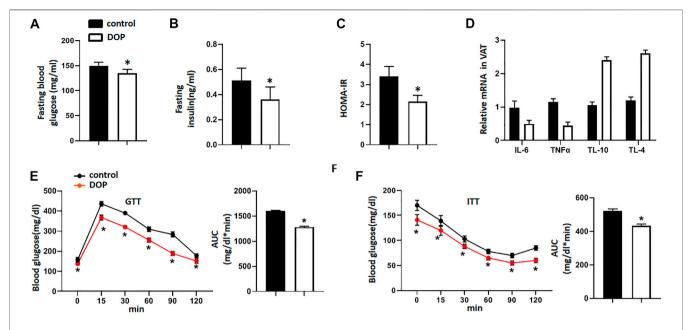


FIGURE 6 DOP treatment alleviated insulin resistance in ob/obmice **(A–C)** The fasting blood glucose levels, fasting serum insulin, and HOMA-IR index of ob/ob mice administered NS or DOP **(D)** Inflammation-related mRNA levels of VAT in ob/ob mice treated with NS or DOP **(E–F)**. The GTTs and ITTs in ob/ob mice treated with NS or DOP (*n* = 5 per group). AUC: area under curve. Data are presented as mean ± SD. Statistical significance was calculated using the two-tailed Student's t-test. * means p < 0.05.

ETHICS STATEMENT

The animal study was reviewed and approved by the Institutional Animal Care and Use Committee of the Laboratory Animal Research Center at Xiangya Medical School of Central South University, China.

AUTHOR CONTRIBUTIONS

Study design: QL, SH; Study conduct: XX, WW, HZ, HL, and JW; Data collection: XX, WW, ZZ, HL, HZ, and JW; Data analysis: QL, XX, XL, and JQ; Data interpretation: QL, XX, XL, and JQ; Drafting manuscript: XX and WW; Revising manuscript content:

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QL, XX, ST; Approval of the final manuscript: QL, XX, WW, HZ, HL, XL, JW, ZZ, and SH are responsible for the integrity of the data analysis, and all authors take responsibility for and attest to the integrity of the data analysis. QL and SH are responsible for sharing the editors' comments with the other authors.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Variable Secondary Metabolite Profiles Across Cultivars of *Curcuma longa* L. and *C. aromatica* Salisb.

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Kulyal P, Acharya S, Ankari AB, Kokkiripati PK, Tetali SD and Raghavendra AS (2021) Variable Secondary Metabolite Profiles Across Cultivars of Curcuma longa L. and C. aromatica Salisb.. Front. Pharmacol. 12:659546. doi: 10.3389/fphar.2021.659546 **Background:** Curcuma spp. (Zingiberaceae) are used as a spice and coloring agent. Their rhizomes and essential oils are known for medicinal properties, besides their use in the flavoring and cosmetic industry. Most of these biological activities were attributed to volatile and nonvolatile secondary metabolites present in the rhizomes of Curcuma spp. The metabolite variations among the species and even cultivars need to be established for optimized use of Curcuma spp.

Objectives: We compared the phytochemical profiles of rhizomes and their essential oils to establish the variability among seven cultivars: five of *Curcuma longa* L. (Alleppey Supreme, Duggirala Red, Prathibha, Salem, Suguna) and two of *C. aromatica* Salisb. (Kasturi Araku, Kasturi Avidi). The GC-MS and LC-MS-based analyses were employed to profile secondary metabolites of these selected cultivars.

Methods: Rhizomes of *Curcuma* spp. were subjected to hydro-distillation to collect essential oil and analyzed by GC-MS. The methanol extracts of fresh rhizomes were subjected to LC-MS analyses. The compounds were identified by using the relevant MS library databases as many compounds as possible.

Results: The essential oil content of the cultivars was in the range of 0.74–1.62%. Several compounds were detected from the essential oils and rhizome extracts by GC-MS and LC-MS, respectively. Of these, 28 compounds (13 from GCMS and 15 from LCMS) were common in all seven cultivars, e.g., α -thujene, and diarylheptanoids like curcumin. Furthermore, a total of 39 new compounds were identified from *C. longa* L. and/or *C. aromatica* Salisb., most of them being cultivar-specific. Of these compounds, 35 were detected by GC-MS analyses of essential oils, 1,2-cyclohexanediol, 1-methyl-4-(1-methylethyl)-, and santolina alcohol, to name a few. The other four compounds were detected by LC-MS of the methanolic extracts of the rhizomes, e.g., kaempferol-3,7-O-dimethyl ether and 5,7,8-trihydroxy-2',5'-dimethoxy-3',4'-methylene dioxyisoflavanone.

 $\textbf{Abbreviations:} \ \text{CU, curcumin; cvs, cultivars; DMC, demethoxy curcumin; BDMC, bisdemethoxy curcumin.}$

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Conclusions: We identified and recorded the variability in the metabolite profiles of essential oils and whole rhizome extracts from the seven cultivars of *Curcuma longa* L. and *C. aromatica* Salisb. As many as 39 new metabolites were detected in these seven Indian cultivars of *Curcuma* spp. Many of these compounds have health benefits.

Keywords: Curcuma longa L., Curcuma aromatica Salisb, essential oil, metabolomics, secondary metabolites, GC-MS, LC-MS

INTRODUCTION

Turmeric (Curcuma longa L.) is a perennial rhizomatous herb that belongs to the family Zingiberaceae (Prasath et al., 2018). It has been used traditionally in India for its medicinal value and as a spice (Srinivasan et al., 2004; Aggarwal et al., 2007; Esatbeyoglu et al., 2012). In Ayurvedic medicine, turmeric is used internally (as a stomachic, tonic, and blood purifier) or externally (prevention and treatment of skin diseases) (Gounder and Lingamallu, 2012). Turmeric was scientifically validated for several pharmacological benefits, including antioxidant, antiinflammatory, and chemoprotective properties (Miquel et al., 2002; Krup et al., 2013; Kanase and Khan, 2018; Umar et al., 2020). The rhizomes of turmeric are enriched with several bioactive metabolites, though the attention was mostly on curcuminoids. Besides curcumin (a curcuminoid), the essential oil of C. longa L. showed antimicrobial activity and ability to suppress aflatoxins production (Ferreira et al., 2013).

Out of 110 species of genus *Curcuma*, only ~20 species were used so far for phytochemical studies (Nahar and Sarker, 2007). *Curcuma longa* L. is popularly known as turmeric, while *C. aromatica* Salisb. and *C. caesia* Roxb. are known as wild turmeric and black turmeric, respectively. *C. longa* L. and a few other species, including *C. aromatica* Salisb., produce curcumin, a yellow colored curcuminoid. So far, at least 235 compounds, primarily phenolics, terpenoids, and alkaloids, were identified from *Curcuma* spp. (Li et al., 2011). About 70 varieties of *C. longa* L. are cultivated in India (Sasikumar, 2005; Parthasarathy and Chempakam, 2008), but very few are chemically profiled.

The essential oil of *Curcuma* spp. is used in traditional medicine for many ailments (Dosoky and Setzer, 2018). The volatile component of *C. longa*'s rhizome is responsible for its aromatic flavor and odor (Gounder and Lingamallu, 2012). Its essential oil is considered safe for human use (Tisserand and Young, 2013). The oils of *C. longa* L. and *C. aromatica* Salisb. have applications in the food and pharmaceutical industries due to their antioxidant, antibacterial, and anti-inflammatory properties (Dosoky and Setzer, 2018). The essential oil also improved the bioavailability of curcumin, thereby its bioactivity (Shishu and Maheshwari, 2010). Preliminarily clinical trials indicated that the essential oil from *C. longa* L. and *C. aromatica* Salisb. was helpful against cancer, asthma, and other ailments (Cheng et al., 1999; Joshi et al., 2003; Li Y. et al., 2009). Thus, there is a need to identify high-yielding cultivars containing curcuminoids and essential oil.

Since the pharmacological properties of *Curcuma* spp. are dependent on their chemical profiles, studies on the chemical constituents of turmeric/wild turmeric and their essential oils gained significance. Thin-layer chromatography (TLC)

is one of the methods employed to quantify curcumin (Setyaningsih et al., 2016) and other curcuminoids (Phattanawasin et al., 2009) in *Curcuma longa* L. A few different techniques used were HPTLC (Pathania et al., 2006; Paramasivam et al., 2009), nuclear magnetic resonance (NMR) spectroscopy (Li W. et al., 2009), and the HPLC method (Kulyal et al., 2016).

Our present study on metabolite profiles would pave the way for metabolomics by providing the identity of several metabolites. Metabolomics is a practical approach for the comprehensive profiling and comparison of metabolites in plant systems (De Vos et al., 2007). It is crucial for quality evaluation and scientific validation of medicinal plants and their products (Mukherjee et al., 2016). Mainly information on secondary metabolites of medicinal plants/spices is of great importance in health, food, and nutrition sectors, due to the antioxidant nature, color, or flavor of these secondary compounds (Beekwilder et al., 2005; Dixon et al., 2006; Hall, 2006). The quality of turmeric and other spices depends on factors, such as cultivation, collection, storage, milling, and processing, apart from genetics and adulteration issues. Therefore, metabolomics provides a practical approach for quality control (Mukherjee et al., 2016; Tetali et al., 2021).

Over the past decade, several methods suitable for large-scale analysis of metabolites in plant extracts were developed (Dixon et al., 2006; Hall, 2006). However, to date, no single analytical method can successfully detect the entire metabolome of higher plants, especially of medicinal and aromatic plants, as they are highly rich in chemically diverse metabolites (Tetali et al., 2021). The GC-MS and LC-MS techniques mutually complement each other in unraveling secondary metabolomes comprising a wide range of volatile and nonvolatile compounds. These compounds belonged to terpenes, phenolic acids, phenylpropanoids, saponins, alkaloids, polyamines, and their derivatives (Huhman and Sumner, 2002; Moco et al., 2006).

Essential oils from different *Curcuma* species, including *C. longa* L. and *C. aromatica* Salisb, were studied for their chemical constituents (Choudhury et al., 1996; Angel et al., 2014; Nampoothiri et al., 2015; Dosoky and Setzer, 2018) to establish their variability. Variation in the volatile compositions of *Curcuma* spp. such as *C. longa* L. and *C. zedoaria*, was done using GC-MS (Dosoky et al., 2019). A combination of GC-MS and LC-MS techniques was used for metabolite analysis of *C. domestica* L. (*C. longa* L.) (Herebian et al., 2009). In the present study, the volatile (essential oil) and nonvolatile (total extract) components of the fresh rhizome of the seven cultivars of *Curcuma* spp. were analyzed by the GC-MS and LC-MS techniques. The present study is the first report revealing such detailed

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TABLE 1 | Essential oil content and total number of compounds detected by GC-MS in the rhizomes of Curcuma species.

SI. No.	Cultivar (species)	Essential oil (%)	Identified (Reported in	Unidentified		
			Curcuma spp. or another plant species)	Unknown	Not reported from any plant species	
1	Alleppey Supreme	1.42	31	58	111	
	(C. longa L.)					
2	Duggirala Red	0.74	36	56	108	
	(C. longa L.)					
3	Prathibha	1.20	44	60	96	
	(C. longa L.)					
4	Salem	1.00	30	39	131	
	(C. longa L.)					
5	Suguna	0.80	35	51	114	
	(C. longa L.)					
6	Kasturi Araku	0.78	29	64	107	
	(C. aromatica Salisb.)					
7	Kasturi Avidi	1.62	31	60	109	
	(C. aromatica Salisb.)					

metabolite profiles of the selected cultivars to the best of our knowledge. These cultivars, except Alleppey Supreme, are typically cultivated in Telangana and Andhra Pradesh, and these states are among the largest producers of turmeric in India (Parthasarathy and Chempakam, 2008).

Most of the studies worldwide on *Curcuma* spp., for their curative properties, were with *C. longa* L., followed by *C. aromatica* Salisb, *C. aeruginosa* Roxb. (Simoh and Zainal, 2015), and *C. kwangsiensis* S. K. Lee & C. F. Liang (Zeng et al., 2009). Several cultivars exist within these species, which vary in their chemical profiles. The present article is the first attempt to characterize both volatile (essential oil) and nonvolatile (crude extract) components of fresh rhizomes of seven cultivars of *Curcuma* spp. by the GC-MS and LC-MS techniques. Our results using GC-MS and LC-MS analyses revealed high variability in their metabolite profiles of seven cultivars of genus *Curcuma*. We emphasize that such an approach could be exploited to distinguish cultivars for a specific application based on their metabolite profile.

MATERIALS AND METHODS

Materials and Reagents

LC-MS grade methanol, water, and acetonitrile were purchased from Fisher Scientific (Pittsburgh, PA, United States). Ammonium formate, formic acid, 4-fluoro-4'-hydroxy benzophenone (97%), and *n*-hexane were from Sigma-Aldrich, India. Anhydrous sodium sulfate (99.99%) was from Merck Millipore, India.

Fresh rhizomes of four cultivars of *Curcuma longa* L. (Duggirala Red, Prathibha, Salem, and Suguna) and two cultivars of *C. aromatica* Salisb. (Kasturi Araku and Kasturi Avidi) were collected from Turmeric Research Station, Kammarpally, Telangana State, India. Alleppey Supreme cultivar of *C. longa* L. was from the Indian Institute of Spices Research, Marikunnu (IISR) Kozhikode, Kerala, India. The mature rhizome samples were collected during the postharvest

season of turmeric (May-Jun) in 2011 and 2012 and cryopreserved at -80°C until extraction and analysis.

Isolation of Essential Oil by Hydrodistillation for GC-MS Analysis

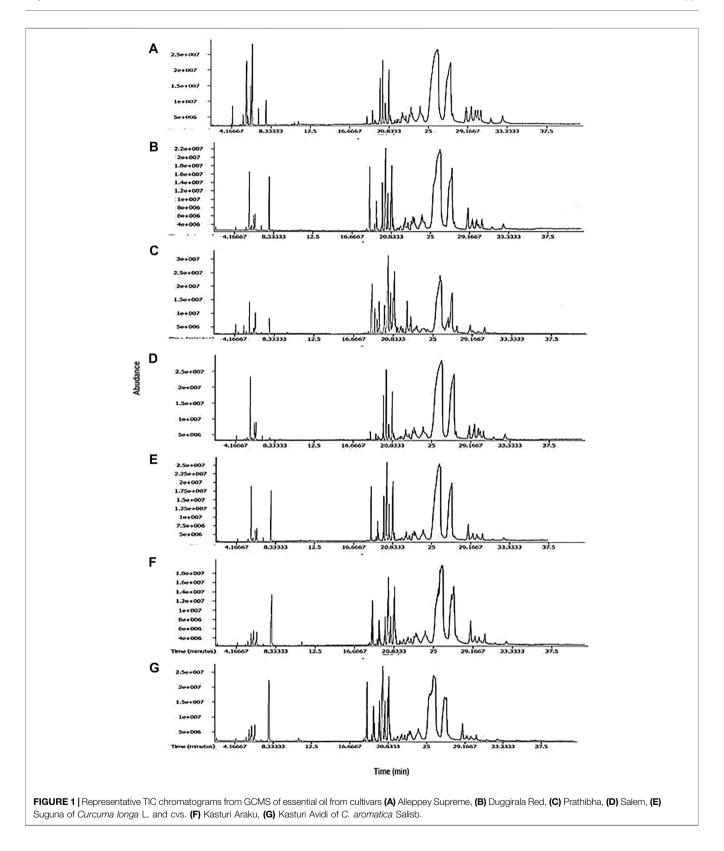
50 g each of fresh turmeric rhizome of five cultivars of C. longa L. cvs. Alleppey Supreme, Duggirala Red, Prathibha, Salem, Suguna, and two cultivars of C. aromatica Salisb. cvs. Kasturi Araku and Kasturi Avidi were taken out from a -80° C freezer, made into pieces, and ground in a pestle with a mortar to a fine powder under liquid nitrogen. The powder was subjected to hydrodistillation in a Clevenger-type apparatus for 7 h. The essential oil obtained after distillation was dried over anhydrous sodium sulfate and kept at -80° C until GC-MS analysis.

GC-MS Running Conditions and Metabolite Identification

The chemical composition of the Curcuma spp. essential oil was analyzed by the GC-MS technique using Agilent 7890 A gas chromatograph coupled with a Leco Pegasus HT TOF mass spectrometer equipped with a 29.8 m \times 320 μ m HP-5MS 5% phenyl methyl siloxane capillary column with 0.25 µm film thickness. The oven temperature was programmed at 65°C for 2 min and then increased from 65 to 90°C at 5°C/min (held for 3 min). Then the temperature was increased from 90 to 103°C (held for 3 min) and from 103 to 150°C (held for 15 min) at 20°C/ min and 8°C/min, respectively. The temperature was raised finally from 150 to 280°C at 20°C/min. The injector, interphase, and ion source were maintained at 250°C, 280°C, and 250°C, respectively. The detector voltage was 1500 V. A solvent delay of 2 min was selected. One microliter (diluted with *n*-hexane; 1:10) of essential oil sample was injected into the GC-MS system using split mode (50: 1). Helium was used as a carrier gas at a flow rate of 1 ml/min. GC-MS data were measured at 70 eV; mass scan 40-1000 amu.

The compounds were identified by comparing their mass spectra with the data available in the literature, National

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Institute of Standards Technology NIST, and Leco-Fiehn Rtx5 libraries. The compounds originated from the GC-MS data file were identified by matching most resembling spectra with the

NIST library. Each search produced a hit list of compounds according to match factor or similarity with the library spectra. All the compounds showing similarity more than 70% with the

TABLE 2 | Cultivar-specific compounds identified, in one of the seven cultivars of *Curcuma longa* L. or *C. aromatica* Salisb. by GC-MS in the essential oil from rhizomes. The structures of the compounds (serial numbers from 1 to 23) are given in Figure 2 (panel numbers: 1–23), and this is the first report of these compounds from the genus *Curcuma* L. These compounds, however, were reported from genus other than *Curcuma* L. The compounds from serial numbers 24 to 41 are already reported in *Curcuma* species. Structures for few compounds (serial numbers 24–30) are given in Figure 3 (panel numbers: 1–7). Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

SI. No.	Compound name	Cultivar	RT (Min)	Area/ abundance	Formula	Mass	Mass fragmentations	Class of compound	Reported from plant species	References
1	1,2-Cyclohexanediol, 1-methyl-4-(1-methylethyl)-	AS	6.38	958955880	C ₁₀ H ₂₀ O ₂	172.146	43, 71, 111 154	Monoterpenoid	Citrus medica L. Leaf and peel essential oil	Bhuiyan et al. (2009)
2	Trans, trans-Octa-2,4-dienyl acetate	AS	8.22	84981	C ₁₀ H ₁₆ O ₂	168.115	43, 77,79	Dienyl acetate	Kaempferia galanga L. Dried rhizomes	Othman et al. (2006)
3	Phenol, 2-methoxy-3-(2-propenyl)-	AS	17.05	200016	$C_{10}H_{12}O_2$	164.083	77,131 164	Phenolic monoterpenoid	Dalberga stevensonii Standl. Wood extracts	Jiang et al. (2018)
4	3-Isopropyl-4-methyl-1-pentyn-3-ol	DR	13.59	805101	C ₉ H ₁₆ O	140.120	43,97 107	Alcohol constituent	Anethum sowa Roxb. ex, Fleming Leaf and stem essential oil	Saleh-e-in et al. (2010)
5	5,9-Tetradecadiyne	DR	19.45	11283632	C ₁₄ H ₂₂	190.172	41,105, 147	Unsaturated hydrocarbon	Ferula vesceritensis Coss. & Durieu ex Trab. Leaves	Zellagui et al. (2012)
6	Naphthalene, 5-butyl-1,2,3,4-tetrahydro-	DR	20.62	1290163	C ₁₄ H ₂₀	188.156	91,145 188	Tetralin Type	Meconopsis punicea Maxim. and M. delavayi (Franch.) Franch. Ex Prain, essential oil	Yuan et al. (2003)
7	Santolina alcohol	DR	23.63	547909	C ₁₀ H ₁₈ O	154.135	59,81 121	Tertiary alcohol	Achillea filipendulina Lam., aerial part	Sharopov and Setzer (2010)
8	2-Pentanone, 4-mercapto-4-methyl-	PR	5.32	1330293	C ₆ H ₁₂ OS	132.060	43,55 132	Ketone	Camellia sinensis (L.) Kuntze	Kumazawa et al. (2005)
9	8-Methylene-3-oxatricyclo[5.2.0.0(2,4)] nonane-	PR	11.72	25554	C ₉ H ₁₂ O	136.08	40,79, 92	Hydrocarbon	Schisandra chinensis (Turcz.) Baill., essential oil dried fruit	Wang et al. (2005)
10	7-Tetracyclo[6.2.1.0(3.8)0(3.9)] undecanol, 4,4,11,11 tetramethyl-	PR	19.16	21297856	C ₁₅ H ₂₄ O	220.182	77,119 159	Sesquiterpene alcohol	Cyperus articulatus L., essential oil roots/rhizome	Metuge et al. (2014)
11	Bicyclo(2.2.1)hept-2-ene, 2,3-dimethyl-	PR	19.41	23461594	C_9H_{14}	122.109	79,94 122	Cyclic hydrocarbon	Abies alba Mill leaf and twig	Yang et al. (2009)
12	1H-3a,7-methanoazulene, 2,3,4,7,8,8a-hexahydro-3,6,8,8-tetramethyl-, [3R-(3à,3aá,7á,8aà)]-	PR	19.69	1483176	C ₁₅ H ₂₄	204.187	93,119 161	Sesquiterpene	Lindera aggregata (Sims) Kosterm., essential oil	Hong (2011)
13	Cholesta-8,24-dien-3-ol, 4-methyl-, (3á,4à)-	PR	21.56	84686714	C ₂₈ H ₄₆ O	398.354	69,105 119	Triterpenoid	Parkia speciosa Hassk. seed	Salman et al. (2006)
14	4-Ethylphenethylamine	PR	25.88	507899185	$C_{10}H_{15}N$	149.120	63,120	Amine	Psidium guajava L. stem bark essential oil	Fasola et al. (2011)
15	Cyclohexanol, 2-methyl-5-(1-methylethenyl)-	PR	26.57	3965291	C ₁₀ H ₁₇ O	154.135	67,107 136	Monoterpenoid	Mentha spicata L. aerial parts	Mohammed et al. (2017)
16	Cyclohexane, 1,2-dimethyl-3,5-bis(1-methylethenyl)-	PR	26.59	26170712	C ₁₄ H ₂₄	192.187	107,149	Monoterpenoid	Rhanterium adpressum Coss. & Durieu Aerial parts	Kala et al. (2009)
17	5,8,11,14-Eicosatetraenoic acid, phenylmethyl ester, (all-Z)-	SA	5.39	15244294	C ₂₇ H ₃₈ O ₂	394.287	67,91 205	Mster	Petiveria alliacea L., whole plant	Sathiyabalan et al. (2014)
18	11-Dodecen-2-one	SA	36.83	511982	C1 ₂ H ₂₂ O	182.167	43,124 182	Ketone	Ficus hispida L. f Fresh male and female receptive figs, leaves	Song et al. (2001)
19 20	E-11-Tetradecenoic acid 2-Nonen-4-yn-1-ol, (Z)-	SA SU	37.15 10.68	335669 287984	C ₁₄ H ₂₆ O ₂ C ₉ H ₁₄ O	226.193 154.135	41,55,69 41,67	Fatty acid Alcohol	Coriandrum sativum L., leaf oil Alpinia speciosa (J.C. Wendl.) K. Schum	Bhuiyan et al. (2009) Ho (2010)
									(Con	tinued on following page)

TABLE 2 (*Continued*) Cultivar-specific compounds identified, in one of the seven cultivars of *Curcuma longa* L. or *C. aromatica* Salisb. by GC-MS in the essential oil from rhizomes. The structures of the compounds (serial numbers from 1 to 23) are given in Figure 2 (panel numbers: 1–23), and this is the first report of these compounds from the genus *Curcuma* L. These compounds, however, were reported from genus other than *Curcuma* L. The compounds from serial numbers 24 to 41 are already reported in *Curcuma* species. Structures for few compounds (serial numbers 24–30) are given in Figure 3 (panel numbers: 1–7). Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

SI. No.	Compound name	Cultivar	RT (Min)	Area/ abundance	Formula	Mass	Mass fragmentations	Class of compound	Reported from plant species	References
							95, 138		Seeds and leaves	
21	3-Cyclohexen-1-one, 3,5,5-trimethyl-	SU	21.81	10709364	C ₉ H ₁₄ O	138.104	96, 138	Cyclohexenone	Crocus sativus L. Dried saffron	D'Auria et al. (2006)
22	6,10-Dodecadien-1-yn-3-ol, 3,7,11-trimethyl-	SU	23.27	18320904	C ₁₅ H ₂₄ O	220.182	41,67, 95, 138	Sesquiterpenoid	Hiptage benghalensis (L.) Kurz, leaves	Venkataramani and Chinnagounder (2012)
23	3-Octen-5-yne, 2,7-dimethyl-, (Z)-	KAv	7.91	132889991	C ₁₀ H ₁₆	136.125	93, 121, 136	Monoterpene	Litsea glutinosa (Lour.) C.B. Rob Fruit oil	Chowdhury et al. (2008b)
24	Aromadendrene	PR	21.68	32839807	C ₁₅ H ₂₄	204.187	41,67,161	Hydrocarbon	Curcuma purpurascens Blume, rhizome, essential oil	Hong et al. (2014)
25	Isoborneol	PR	10.16	931077	C ₁₀ H ₁₈ O	154.135	41,67,95	Monoterpenoid	Curcuma aromatica Salisb, rhizome Essential oil	Sasikumar (2005)
26	β-Elemene	PR	17.87	8265459	C ₁₅ H ₂₄	204.187	41,67193	Sesquiterpene	Curcuma longa L., rhizome Essential oil	Ma and Gang (2006)
27	α-Santalene	PR	19.15	167463111	C ₁₅ H ₂₄	204.187	41,94, 122	Sesquiterpene	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
28	2-Tridecanone	PR	36.82	145399		198.198	43,57	Ketone	Curcuma albiflora Thwaites, rhizome Essential oil	Herath et al. (2017)
29	Nonanoic acid	SU	37.82	1054190	C ₉ H ₁₈ O2	158.1307	41,60,129	Fatty acid	Curcuma longa L., rhizome Essential oil	Nieman et al. (2012)
30	Eucalyptol	KAr	6.34	73923505	C ₁₀ H ₁₈ O	154.135	51,71, 139	Monoterpene	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
31	Carvacrol	AS	15.46	800060	C ₁₀ H ₁₄ O	150.104	91, 135	Monoterpene	Curcuma longa L., rhizome, essential oil	Awasthi and Dixit (2009)
32	endo-Borneol	PR	25.95	762477	C ₁₀ H ₁₈ O	154.135	95, 140	Monoterpene	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
33	1,3,5-Cycloheptatriene, 3,7,7-trimethyl-	KAv	22.26	44959671	C ₁₀ H ₁₄	134.109.120	41,91,119	Cyclic hydrocarbon	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
34	p-Cymen-8-ol	KAr	11.08	28783214	C ₁₀ H ₁₄ O	150.104	51,91, 135	Monoterpenoid	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
35	Camphor	PR	9.68	7985363	C ₁₀ H ₁₆ O	152.120	41,95,152	Terpenoid ketone	Curcuma longa L., rhizome Essential oil	Leela et al. (2002)
36	α-Bisabolol	PR	22.60	26108003	C ₁₅ H ₂₆ O	222.198	41,69, 119	Sesquiterpenoid	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
37	α -Elemenone	PR	22.99	5795701	C ₁₅ H ₂₂ O	218.167	67,119, 216	Sesquiterpene	Curcuma longa L., rhizome Essential oil	Singh et al. (2010)
38	Caryophyllene oxide	PR	21.85	84236617	C ₁₅ H ₂₄ O	220.182	21,96,138	Sesquiterpenoid oxide	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
39	Citral	KAr	10.81	4942325	C ₁₀ H ₁₆ O	152.120	69,119	Monoterpene	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
40	Neoisolongifolene, 8,9-dehydro-	KAr	20.92	956644398	C ₁₅ H ₂₄	204.187	44,131, 187	Bicyclic hydrocarbon	Curcuma longa L., rhizome Essential oil	Chowdhury et al. (2008a)
41	Sabinene hydrate	KAv	19.81	30005835	C ₁₀ H ₁₈ O	154.135	79,93,121	Monoterpene	Zingiber Officinale Roscoe, rhizome essential oil	(2000a) Koo and Gang (2012)

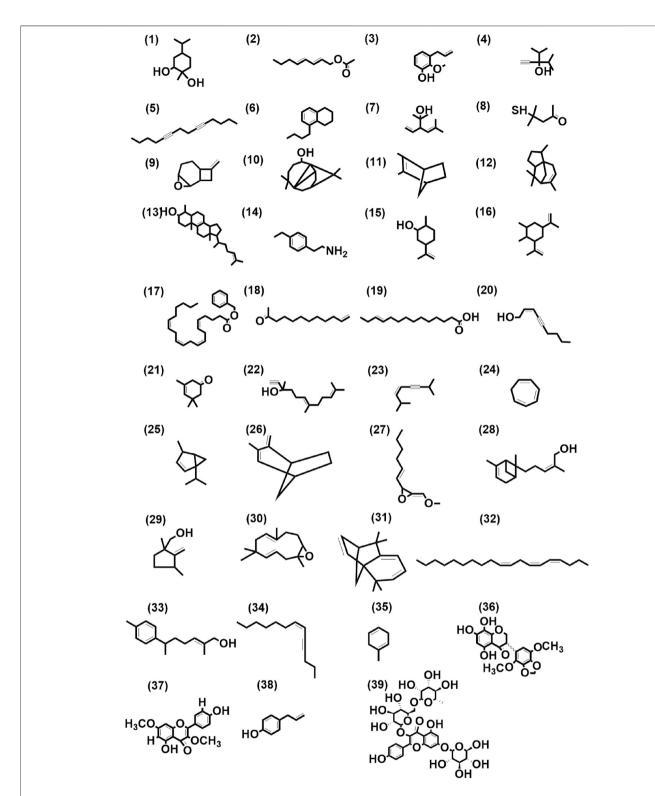


FIGURE 2 | Structures of first-time reported (total 39) from the genus Curcuma, identified from cultivars of Curcuma longa L. and C. aromatica Salisb. detected in essential oil (panel numbers 1–23 and 24–35 corresponding to serial numbers 1–23 and 1–12 of Tables 2, 3 respectively) and rhizome extracts (panel numbers 36 and 37–39 corresponding to serial numbers 1 and 1–3 of Tables 6, 7 respectively) by GC-MS and LC-MS, respectively. Details of all these compounds are given in Supplementary Tables S3, S4. (1) 1,2-Cyclohexanediol, 1-methyl-4-(1-methylethyl)-, (2) trans, trans-octa-2,4-dienyl acetate, (3) phenol, 2-methoxy-3-(2-propenyl)-, (4) 3-isopropyl-4-methyl-1-pentyn-3-ol, (5) 5,9-tetradecadiyne, (6) naphthalene, 5-butyl-1,2,3,4-tetrahydro-, (7) santolina alcohol, (8) 2-pentanone, 4-mercapto-4-methyl-, (9) 8-methylene-3-oxatricyclo[5.2.0.0(2,4)]nonane, (10) 7-tetracyclo[6.2.1.0(3.8)0(3.9)]undecanol, 4,4,11,11 tetramethyl-, (11) bicyclo(2.2.1)hept-(Continued)

FIGURE 2 | 2-ene, 2,3-dimethyl-, (12) 1H-3a,7-methanoazulene, 2,3,4,7,8,8a-hexahydro-3,6,8,8-tetramethyl-, [3R-(3à,3aá,7á,8aà)]-, (13) cholesta-8,24-dien-3-ol, 4-methyl-, (3á,4à)-, (14) 4-ethylphenethylamine, (15) cyclohexanol, 2-methyl-5-(1-methylethenyl)-, (16) cyclohexane, 1,2-dimethyl-3,5-bis(1-methylethenyl)-, (17) 5,8,11,14-eicosatetraenoic acid, phenylmethyl ester, (all-Z)-, (18) 11-dodecen-2-one, (19) E-11-tetradecenoic acid, (20) 2-nonen-4-yn-1-ol, (Z)-, (21) 3-cyclohexen-1-one, 3,5,5-trimethyl-, (22) 6,10-dodecadien-1-yn-3-ol, 3,7,11-trimethyl-, (23) 3-octen-5-yne, 2,7-dimethyl-, (Z)-, (24) 1,3,5-cycloheptatriene, (25) bicyclo(3.1.0)hexane, 4-methyl-1-(1-methylethyl)-, didehydro deriv., (26) bicyclo(3.2.1)oct-2-ene, 3-methyl-4-methylene-, (27) oxirane, 2-(hexyn-1-yl)-3-methoxymethylene-, (28) bergamotol, Z-α-trans-, (29) (1,3-dimethyl-2-methylene-cyclopentyl)-methanol, (30) 12-oxabicyclo(9.1.0)dodeca-3,7-diene, 1,5,5,8-tetramethyl-, [1R-(1R*,3E,7E,11R*)]-, (31) isolongifolene, 4,5,9,10-dehydro-, (32) Z,Z,Z-4,6,9-nonadecatriene, (33) 6-(p-tolyl)-2-methyl-2-heptenol, (34) 6-tridecen-4-yne, (Z)-, (35) 1,4-cyclohexadiene, 1-methyl-, (36) kaempferol-3,7-O-dimethyl ether, (37) 5,7,8-trihydroxy-2',5'-dimethoxy-3',4'-methylene dioxyisoflavanone, (38) chavicol, (39) kaempferol-3-O-rutinoside-7-O-glucoside.

NIST library were selected by the software (Software: Version 4.22 optimized for Pegasus®). Software searches (identifies) compound from their mass spectra and includes MS interpretation programs for analyzing mass spectra based on chemical structure, molecular formula, isotopic pattern, etc. The similarity of 70% or above between the m/z values of the compound detected in the respective cultivar and the MS-libraries' mass fragmentation pattern was considered as identification. Furthermore, mass spectra of all compounds were also matched with ranges available as per their CAS number. Compounds for which the CAS number was not generated, the PubChem CID was used. Compounds below the similarity level of 70% were not considered and grouped as unknown. The data obtained with the samples collected in 2012 are presented in this article.

Preparation of Rhizome Extracts for LC-MS Analysis

Samples for LC-MS analysis were prepared by grinding the fresh rhizome to a fine powder in a mortar and pestle under liquid nitrogen. 1 g of the rhizome powder was suspended in 2 ml of MeOH (LC-MS grade). The samples were sonicated for 30 min and centrifuged for 25 min at 1500 rpm, and the supernatants were separated by filtering through a 0.45- μ m Nylon filter disk. These extracts were freshly prepared for the analysis. A 200 μ l aliquot of the extract was diluted quantitatively with internal standard (IS) 200 μ l 4-fluoro-4'-hydroxy benzophenone solution. It was prepared freshly for each analysis by dissolving in methanol for a final concentration of 0.58 mg/ml. The samples were subjected to LC-MS analysis for the complete metabolite profile. The data obtained with the samples collected in 2012 were presented in this article.

LC-MS/MS Conditions and Metabolite Identification

LC-MS analyses of the crude extract of fresh rhizome of *Curcuma* spp. were performed according to Jiang et al. (2006) using Agilent 6520 Accurate Q-TOF (Agilent Santa Clara, CA), and the column used was Zorbax Eclipse XDB-C 18, 4.6×50 mm, $1.8\,\mu$; Mobile phase: A) buffer (5 mM ammonium formate, 0.1% formic acid, in deionized and distilled H₂O) and B) acetonitrile; gradient (in buffer A): 0–2 min, 5% B; 2–57 min, 5–100% B; 57–60 min, 100% B; 60–65 min, 100–5% B; flow rate: 0.25 ml/min; temperature, 40°C; injection volume 5 μ l. For the MS detection, Agilent MSD-Trap-SL

was equipped with electrospray ionization (ESI) interface as the ion source. The acquisition parameters for the negative mode were: drying N_2 temperature, 350° C, 8 l/min; nebulizer pressure 40 psi; HV capillary 4000 V; skimmer 65.0 V; mass range measured: 110-1700 m/z; Spray voltage: 4 kV; scan rate 1.4. We analyzed the results in both the positive and the negative ion mode acquired by Agilent TOF/Q-TOF mass spectrometry and full MS scan, in the form of total ion current (TIC) chromatogram, and the metabolites were identified based on their MS/MS spectra and fragmentation rules reported previously (Jiang et al., 2006).

RESULTS

Essential Oil Content

The oil was obtained by hydro-distillation, in a Clevenger-type apparatus, of the fresh rhizomes of five cultivars (Alleppey Supreme, Duggirala Red, Prathibha, Salem, and Suguna) of *Curcuma longa* L. and two cultivars (Kasturi Araku and Kasturi Avidi) of *C. aromatica* Salisb. The yield of essential oil from the seven cultivars was in the range of 0.74–1.62% on a fresh weight basis, with the highest yield of 1.62% in cv. Kasturi Avidi (*C. aromatica* Salisb.) followed by cv. Alleppey Supreme (*C. longa* L.) with an amount of 1.42% and the lowest yield of 0.74% in cv. Duggirala Red (*C. longa* L.). The essential oil yields from the other five rhizomes were in between these values (**Table 1**). The oil yields of *C. longa* L. varieties were higher than those of *C. aromatica* Salisb.

GC-MS Analysis of Essential Oil

Essential oils of seven cultivars of *Curcuma* spp. were subjected to GC-MS analysis, and the results from one of such studies for each cultivar are presented in this article. The representative TIC chromatograms of these cultivars are shown in **Figure 1**. Several compounds were detected in each cultivar's essential oil (**Table 1**). Only a few of the identified compounds were confirmed based on their match with the compound profiles found in the NIST databases and Leco-Fiehn Rtx5 library. Up to 44 compounds were identified from the five cvs. of *C. longa* L. and 31 compounds from two cvs. of *C. aromatica* Salisb. (**Table 1**). Altogether 80 compounds were grouped into three categories: cultivar-specific (41), present in more than one cultivar (26), and common in all seven cultivars (13).

These 41 cultivar-specific compounds were detected in the essential oil of one of the cultivars of *C. longa* L. or *C. aromatica* Salisb. (**Table 2**). The essential oil of *C. longa* L. cv. Prathibha had the highest number of cultivar-specific compounds, whereas *C.*

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TABLE 3 Compounds detected in more than one cultivar of *C. longa* L. and *C. aromatica* Salisb. identified by GCMS in the essential oil from rhizomes. The structures of the compounds from serial numbers 1–12 are given in **Figure 2** (panel numbers: 24–35), and the compounds with Sl.No. 13–18 are shown in **Figure 3**, with corresponding panel numbers: 8–13 respectively. Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

SI No.	Compound name	Cultivar	RT (Min)	Area/ abundance	Formula	Mass	Mass fragment ions	Class of compound	Reported from plant species	References
1	1,3,5-Cycloheptatriene	AS, PR, SA, SU, KAr, KAv	2.16	6243556	C ₇ H ₈	92.0626	65,91	Closed ring organic compound	Ceropegia woodii Schltr	Meng et al. (2010)
2	Bicyclo(3.1.0)hexane, 4-methyl-1-(1-methylethyl)-, didehydro deriv	DR, PR, SA, SU	5.70	89775296	C ₁₀ H ₁₆	136.1252	41, 77, 93	Monoterpene	Zingiber Officinale Roscoe	Tang et al. (2012)
3	Bicyclo(3.2.1)oct-2-ene, 3-methyl-4-methylene-	DR, SU, KAv	9.35	559996	C ₁₀ H ₁₆	134.1096	91, 105, 134	Monoterpene	Seseli daucifolium C.B. Clarke	Mohiuddin et al. (2012)
4	Oxirane, 2-(hexyn-1-yl)-3- methoxymethylene-	DR, KAr, KAv	9.75	71555	C ₁₀ H ₁₄ O ₂	166.0994	79, 110	Cyclic ether and epoxide	Hyptis spicigera Lam	Ladan et al. (2011)
5	Bergamotol, Z-α-trans-	AS, SA	20.90	39326774	C ₁₅ H ₂₄ O	220.182	91, 93,119,187	Sesquiterpene alcohol	Pogostemon deccanensis (Panigrahi) Press	Kumar et al. (2019)
6	(1,3-Dimethyl-2-methylene-cyclopentyl)- methanol	AS, DR, SA, SU, KAv	21.05	25037989	C ₉ H ₁₆ O	140.1201	67, 77, 94, 109	alcohol H	Elsholtzia argyi H. Lév	Peng and Yang (2005)
7	12-Oxabicyclo[9.1.0]dodeca-3,7-diene, 1,5,5,8-tetramethyl-, [1R- (1R*,3E,7E,11R*)]-	DR, KAr	21.67	21304483	C ₁₅ H ₂₄ O	220.1827	67, 96, 109, 138	Epoxide	Eugenia Caryophyllus (Spreng.) Bullock & S.G. Harrison	Mani and Boominathan (2011)
8	Isolongifolene, 4,5,9,10-dehydro-	AS, DR, SA, SU, KAr	22.10	350003	C ₁₅ H ₂₀	200.1565	77, 91, 143, 157, 185	Polycyclic hydrocarbon	Cymbopogon citratus (DC.) Stapf	Tajidin (2012)
9	Z,Z,Z-4,6,9-Nonadecatriene	DR, KAv	22.33	169215573	C ₃₄ H ₁₉	262.2661	79, 93	Hydrocarbon	Papaver somniferum L.	Kumaravel et al. (2019)
10	6-(p-Tolyl)-2-methyl-2-heptenol	AS, SU, KAv	22.98	60406564	C ₁₅ H ₂₂ O	218.167	91, 119, 202	Aromatic alcohol	Zingiber officinale Roscoe	Choudhari and Kareppa (2013)
11	6-Tridecen-4-yne, (Z)-	DR, PR, SU	23.14	153999724	C ₁₃ H ₂₂	178.1722	43, 79, 94	Hydrocarbon	Ambrosia trifida L.	Wang et al. (2005)
12	1,4-Cyclohexadiene, 1-methyl-	KAr, KAv	23.15	156905042	C ₇ H ₁₀	94.0783	55, 79,94	Aromatic alcohol	Capsicum annuum L.	Eggink et al. (2012)
13	Camphene	AS, DR, PR, SU	4.56	930505	C ₁₀ H ₁₆	136.125	93, 121	Monoterpene	Curcuma longa L.	Chowdhury et al. (2008a)
14	α-Phellandrene	AS, DR, SA, SU, KAr	5.72	2645357306	C ₁₀ H ₁₆	136.125	77, 93	Monoterpene	Curcuma longa L.	Chowdhury et al. (2008a)
15	Limonene	AS, SU, KAr, KAv	6.27	202198637	C ₁₀ H ₁₆	136.125	68, 93	Monoterpene	Curcuma longa L.	Singh et al. (2010)
16	α-Terpineol	AS, PR, SA, SU, KAr, KAv	11.25	35019844	C ₁₀ H ₁₈ O	154.135	59 93, 121	Monoterpenoid	Curcuma longa L.	Gopalan et al. (2000)
17	β-Sesquiphellandren	DR, SA, SU, KAv	20.83	962609070	C ₁₅ H ₂₄	204.187	68, 79	Sesquiterpene	Curcuma longa L.	Chowdhury et al. (2008a)
18	Nerolidol	DR, PR, SA, SU, KAv	21.79	15626126	C ₁₅ H ₂₆ O	222.198	69, 93	Sesquiterpinol	Curcuma longa L.	Awasthi and Dixit (2009)
19	Bicyclo(4.1.0)hept-2-ene, 3,7,7-trimethyl-	DR, KAv	5.63	227551	C ₁₀ H ₁₆	136.125	93, 121	Monoterpene	Curcuma longa L.	Chowdhury et al. (2008a)
20	α -Terpinene	AS, DR, SA, KAr, KAv	6.00	28366949	C ₁₀ H ₁₆	136.125	93, 121, 136	Monoterpene	Curcuma longa L.	Chowdhury et al. (2008a)
21	cis-Ocimene	DR, PR, SA, SU, KAr, KAV	6.74	466438	C ₁₀ H ₁₆	136.125	41, 93	Monoterpene	Curcuma longa L.	Usman et al. (2009)
22	γ -Terpinene	AS, DR, PR, SA, SU, KAr	7.01	26650014	C ₁₀ H ₁₆	136.125	93, 119,136	Monoterpene	Curcuma longa L.	Curcuma longa L. Usman et al. (2009)
23	Linalool	AS, DR, PR, SU	8.15	500594	C ₁₀ H ₁₈ O	154.135	71, 93, 121	Alcohol	Curcuma longa L.	Curcuma longa L. Leela et al. (2002)
		111,00							(Continu	ued on following page)

Metabolomics of Curcuma spp.

TABLE 3 (*Continued*) Compounds detected in more than one cultivar of *C. longa* L. and *C. aromatica* Salisb. identified by GCMS in the essential oil from rhizomes. The structures of the compounds from serial numbers 1–12 are given in Figure 2 (panel numbers: 24–35), and the compounds with Sl.No. 13–18 are shown in Figure 3, with corresponding panel numbers: 8–13 respectively. Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

SI No.	Compound name	Cultivar	RT (Min)	Area/ abundance	Formula	Mass	Mass fragment ions	Class of compound	Reported from plant species	References
24	Terpinene-4-ol	AS, DR, PR, SA, SU	10.83	2557284	C ₁₀ H ₁₈ O	154.135	73, 94, 154	Monoterpene	Curcuma longa L.	Curcuma longa L. Singh et al. (2010)
25	cis-α-Bisabolene	PR, KAr	20.40	11244271	C ₁₅ H ₂₄	204.187	67, 93, 161, 204	Sesquiterpene	Curcuma longa L.	Curcuma longa L. Chowdhury et al. (2008a)
26	Ar-Tumerone	DR, SA, KAv	25.87	328137262	C ₁₅ H ₂₀ O	216.151	83, 119, 173, 216	Sesquiterpene	Curcuma longa L.	Curcuma longa L. Chowdhury et al. (2008a)

TABLE 4 | Compounds common in the seven cultivars of *Curcuma* spp detected by GC-MS in essential oil obtained from rhizomes. The structures of the two compounds with serial numbers 10 and 13 are given in **Figure 3** (panel numbers: 14–15 respectively).

SI No.	Compound name	RT (Min)	Area/abundance	Formula	Mass	Mass fragment ions	Class of compound	Reported from plant species	References
1	α-Thujene	4.13	9407392	C ₁₀ H ₁₆	136.125	93, 136	Monoterpenoid	Curcuma longa L.	Raina et al. (2005)
2	1s-α-Pinene	4.27	122103688	C ₁₀ H ₁₆	136.125	39, 41, 93	Monoterpenoid	Curcuma longa L.	Singh et al. (2002)
3	Sabinene	5.05	3901899	C ₁₀ H ₁₆	136.125	93, 136	Monoterpenoid	Curcuma longa L., leaves	Behura et al. (2002)
4	β or m-Cymene	6.20	338719033	C ₁₀ H ₁₄	134.109	65, 91, 119	Aromatic hydrocarbon	Curcuma longa L.	Singh et al. (2002)
5	Terpinolene	7.82	225186296	C ₁₀ H ₁₆	136.125	93, 121	Monoterpenoid	Curcuma longa L.	Leela et al. (2002)
6	trans-α-Bergamotene	18.86	2365810	$C_{15}H_{24}$	204.187	69, 93, 119, 161	Sesquiterpene	Curcuma longa L.	Raina et al. (2005)
7	α-Caryophyllene	19.23	6097261	$C_{15}H_{24}$	204.187	93, 121	Sesquiterpene	Curcuma longa L., leaves	Behura et al. (2002)
8	trans-β-Farnesene	19.37	211225438	$C_{15}H_{24}$	204.187	69, 93, 133	Sesquiterpene	Curcuma longa L.	Singh et al. (2002)
9	Ar-Curcumene	19.88	482956678	$C_{15}H_{22}$	202.172	132, 202	Sesquiterpene	Curcuma longa L.	Singh et al. (2002)
10	α-Zingiberene	20.25	1117738917	$C_{15}H_{24}$	204.187	69, 93, 119, 204	Sesquiterpene	Curcuma longa L.	Chowdhury et al. (2008a
11	Tumerone	22.16	67277186	$C_{15}H_{22}O$	218.167	83, 157	Sesquiterpene	Curcuma longa L.	Singh et al., 2002)
12	Curlone	27.34	439832546	C ₁₅ H ₂₂ O	218.167	83, 120, 218	Sesquiterpene	Curcuma longa L.	Leela et al. (2002)
13	2-Heptadecanone	39.17	152911	C ₁₇ H ₃₄ O	254.261	43, 55, 71, 125	Ketone	Curcuma angustifolia Roxb	Srivastava et al. (2006)

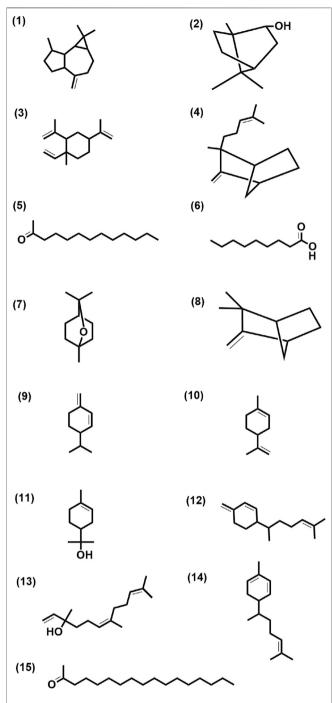


FIGURE 3 | Structure of few selected cultivar-specific (panel numbers 1–7 corresponding to serial numbers 24–30 of **Table 2**); detected in more than one cultivar (panel numbers 8–13 corresponding to serial numbers 13–18 of **Table 3**) and common (panel numbers 14–15 corresponding to serial numbers 10 and 13 of **Table 4**) compounds already reported from the genus *Curcuma* in essential oils isolated from rhizomes by GCMS analysis of seven cultivars of *Curcuma* L.: five of *Curcuma longa* L. (cvs. Alleppey Supreme, Duggirala Red, Prathibha, Salem, and Suguna) and two of *C. aromatica* Salisb. (cvs. Kasturi Araku and Kasturi Avidi). (1) Aromadendrene, (2) isoborneol, (3) β-elemene, (4) α-santalene, (5) 2-tridecanone, (6) nonanoic acid, (7) eucalyptol, (8) camphene, (9) α-phellandrene, (10) limonene, (11) α-terpineol, (12) β-sesquiphellandren, (13) nerolidol, (14) α-zingiberene, (15) 2-heptadecanone.

FIGURE 4 | Structure of few selected cultivar-specific (panels 3, 5-11 corresponding to serial numbers 2, 3-9 of Table 6); detected in more than one cultivar (panels 1-2, 4, 12 corresponding to serial numbers 4-5, 6, 7 of Table 7) and common (panels 13, 14-15, 16, and 17 corresponding to serial numbers 10, 5-6, 15, and 1, respectively, of Table 8) compounds already reported from genus Curcuma in methanolic extract from rhizomes by LCMS analysis of seven cultivars of Curcuma spp.: five of Curcuma longa L. (cvs. Alleppey Supreme, Duggirala Red, Prathibha, Salem, and Suguna) and two of C. aromatica Salisb. (cvs. Kasturi Araku and Kasturi Avidi). (1) Kaempferol-3-rhamnoside, (2) 3-acetyl coumarin, (3) luteolin-7-O-glucoside, (4) turmeronol, (5) 1,7-bis(4-hydroxy-3,5-dimethoxyphenyl)-1,6-heptadiene-3,5-dione, (6) 1,7-bis(3,4-dimethoxyphenyl)-1,6-heptadiene-3,5-dione, (7) (6S)-2-methyl-6-[(1R,5S)-(4-methene-5-hydroxyl-2-cyclohexen)-2-hepten-4one, (8) 1,7-bis(4-hydroxyphenyl)-3,5-heptanediol, (9) 1,7-bis(3,5-diethyl-4hydroxyphenyl)-1,6-heptadiene-3,5-dione, (10) 1-(4-hydroxy-3methoxyphenyl)-5-(4-hydroxyphenyl)-1,4-pentadiene-3-one, (11) (-)-(12E,2S,3S,4R, 5R,6R, 9S,11S, 15R)-3,15-dibenzoyloxy-5,6-epoxylathyr-12-en-14-one, (12) 7-(3,4-dihydroxyphenyl)-5-hydroxy-1-phenyl-(1E)-1heptene, (13) 1-(3,4-dihydroxyphenyl)-7-(4-hydroxy-3-methoxyphenyl)hepta-1,6-diene-3,5-dione, (14) 1-(4-hydroxyphenyl)-7-(4-hydroxy-3methoxyphenyl)-1,4,6-heptatrien-3-one, (15) 1,7-bis(4-hydroxy-3methoxyphenyl)-1,4,6-heptatrien-3-one, (16) 1-heptene-3,5-dione, 1,7-bis-(4-hydroxy-3-methoxyphenyl)-, (17) 1,5-bis(4-hydroxy-3-methoxyphenyl)-1,4-pentadien-3-one.

TABLE 5 | Total number of compounds detected by LC-MS from the rhizome extract of C. longa L. and C. aromatica Salisb.

SI. No.	Cultivar (Species)	Total number of Metabolites detected	Metabolites identified	Unknown Metabolites
1	Alleppey Supreme	86	43	43
	(C. longa L.)			
2	Duggirala Red	107	23	84
	(C. longa L.)			
3	Prathibha	60	28	32
	(C. longa L.)			
4	Salem	91	28	63
	(C. longa L.)			
5	Suguna	96	30	66
	(C. longa L.)			
6	Kasturi Avidi	90	30	60
	(C. aromatica Salisb.)			
7	Kasturi Araku	92	29	63
	(C. aromatica Salisb.)			

aromatica Salisb., cv. Kasturi Araku had the least (Table 2). Of these, 23 cultivar-specific compounds were reported for the first time from the genus Curcuma. The chemical structures of these 23 compounds (Table 2, Sl. Nos. 1-23) are presented in Figure 2 (panels 1-23). In addition to 41 cultivar-specific compounds, 26 compounds were present in more than one cultivar (Table 3). Among these, 12 were detected first time in the genus Curcuma (Table 3, Sl. Nos. 1 to 12; Figure 2, panels: 24-35). The remaining 14 were already known in C. longa L. A total of 13 compounds were common in all seven cultivars of C. longa L. and C. aromatica Salisb. (Table 4) and the representative structures of two of these compounds are given in Figure 3 (panel numbers 14-15, corresponding to serial numbers 10 and 13 respectively of Table 4). Most of these compounds belong to mono, di, and sesquiterpene. A summary of all 80 compounds identified by GC-MS in the essential oils of the seven cultivars is presented in Supplementary Table S1.

LC-MS Analysis of Methanol Extracts

Methanolic extracts of rhizomes from the seven cultivars of *Curcuma* spp. were subjected to LC-MS analysis. The results from one of such analyses for each cultivar are presented in this article. The use of "positive" and "negative" modes of LC-MS was quite helpful. TIC chromatograms of all seven cultivars of *Curcuma longa* L. and *C. aromatica* Salisb. were shown in **Supplementary Figure S1A** for negative mode and **Supplementary Figure S1B** for positive mode.

A typical LC-MS analysis of methanolic extracts from rhizomes of *C. longa* L. cv. Alleppey Supreme revealed the presence of up to 86 compounds. Out of these, 43 were identified, and the remaining 43 compounds remained unknown. The (-) ESI-LC-MS detected 30 known compounds, and the (+) ESI-LC-MS detected 23 known compounds with an overlap of 10 compounds, detected by both negative and positive ion modes. A similar assessment of data was done with all seven cultivars of *Curcuma* spp. (**Table 5**). Altogether 62 compounds were identified, as presented in **Supplementary Table S2**. These compounds were grouped into three categories: cultivar-specific,

detected in more than one cultivar, and common. There were 23 cultivar-specific compounds present in any one cultivar of C. longa L. or C. aromatica Salisb. (Table 6). 24 compounds were present in more than one cultivar of C. longa L. and/or C. aromatica Salisb. (Table 7). The remaining 15 were common in all seven cultivars (Table 8). Of these 15 common compounds found in the LC-MS/MS chromatograms, only one was a "Bisabolane" sesquiterpene (Parthasarathy et al., 2009) and all other 14 were diarylheptanoids. These were identified based on the MS/MS spectra reported by Jiang et al. (2006), including curcumin (CU), demethoxycurcumin (DMC), and bisdemethoxycurcumin (BDMC). Among the other diarylheptanoids, 1-(4-hydroxyphenyl)-7-(4-hydroxy-3-methoxyphenyl)-1,4,6-heptatrien-3-one; 1,5-bis(4-hydroxy-3-methoxyphenyl)-1,4-pentadien-3-one, etc., were common in all the cultivars of C. longa L. and C. aromatica Salisb. (Table 8). The structure of the five common compounds was given in Figure 4 (panels 13, 14-15, 16, and 17 corresponding to serial numbers 10, 5-6, 15, and 1, respectively, of Table 8). In addition to diarylheptanoids, several other classes (phenolic acids, flavonoids, ketonic sesquiterpenes, and fatty acid derivatives) were also detected in the turmeric rhizomes.

Compounds Reported First Time From the Genus Curcuma Using GC-MS and LC-MS Analysis

A total of 39 compounds were detected (**Figure 2**) for the first time from the genus *Curcuma*. Out of these, 35 and 4 compounds were identified respectively in the essential oils and whole rhizome extracts of *C. longa* L. and *C. aromatica* Salisb. by the GC-MS and LC-MS techniques. Details of the compounds, including the class of compound, molecular weight, are given in **Tables 2**, **3**, **5**, and **6**; structures of all these compounds are shown in **Figure 2** (panels: 1–39). The MS and MS/MS spectra of these compounds are presented in **Supplementary Figure S2** (panels: 1–39). These compounds were reported earlier from plants belonging to any genus other than *Curcuma*, and this is the first report from genus

TABLE 6 Cultivar-specific compounds identified by LC-MS in the rhizome extracts from one of the seven cultivars of *Curcuma longa* L. and *C. aromatica* Salisb. The structure of the compound with the serial number "1" is given in **Figure 2** (panel number: 36) and compounds with Sl. Nos. 2, 3–9 are given in **Figure 4** with the corresponding panel nos. 3, 5–11, respectively. Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

SI. No.	Compound name	Cultivar	RT (Min)	Area/ abundance	Formula	Mass (m/z)	Mass fragment ions	Class of compound	Reported from plant species	References
1	Kaempferol-3,7-O-dimethyl ether	AS	12.77	25537	C ₁₇ H ₁₄ O ₆	313.0721 M- H ⁻	108; 123; 152; 153 167	Flavonoid	Lumnitzera racemosa Willd and Artemisia vulgaris L.	Nikolova (2006); DeSouza et al. (2010)
2	Luteolin-7-O-glucoside	AS	42.2	5324	C ₂₁ H ₂₀ O ₁₁	447.2733 M-H	110; 185; 279; 280	Flavonoid	Curcuma Zedoaria (Christm.) Roscoe	Mass bank ACCESSION: TY00-0145; Rahmatullah et al. (2012)
3	1,7-Bis(4-hydroxy-3,5-dimethoxyphenyl)-1,6-heptadiene-3,5-dione	PR	32.9	186331	C ₂₃ H ₂₄ O ₈	428.2 M-H	109; 123; 137; 159; 191; 209	Diarylheptanoid	Curcuma longa L.	Nurfina et al. (1997)
4	1,7-Bis(3,4-dimethoxy phenyl)-1,6- heptadiene-3,5-dione	PR	38.3	335360	C ₂₃ H ₂₄ O ₆	396.2 M-H	105; 107; 119; 129; 137; 145; 155; 195	Diarylheptanoid	Curcuma longa L.	Chen et al. (2006)
5	(6S)-2-Methyl-6-[(1R,5S)-(4-methene-5-hydroxyl-2-cyclohexen)-2-hepten-4-one	PR	40.2	229164	C ₁₅ H ₂₄ O ₂	236.1 M-H	105; 106; 107; 108; 109; 119; 120; 121; 133; 135	Bisabolane	Curcuma longa L.	Li et al. (2011)
6	1,7-Bis(4-hydroxyphenyl)-3,5-heptanediol	KAr	22.8	8120	C ₁₉ H ₂₄ O ₄	316.1 M-H	105; 106; 107; 119; 121; 147; 148	Diarylheptanoid	Curcuma longa L.	Ma and Gang (2006)
7	1,7-Bis(3,5-diethyl-4-hydroxyphenyl)-1,6- heptadiene-3,5-dione	KAr	60.6	129145	C ₂₇ H ₃₂ O ₄	420.3 M-H	106; 107; 119; 120; 121; 122; 123; 144; 145; 146; 147; 171; 172; 175; 187; 197; 201; 209; 211; 213; 223; 237; 239; 321; 323	Aromatic	Curcuma longa L.	Li et al. (2011)
8	1-(4-Hydroxy-3-methoxyphenyl)-5-(4- hydroxyphenyl)-1,4-pentadiene-3-one	KAv	28.8	8009	C ₁₈ H ₁₆ O ₄	296.1 M-H	105; 109; 117; 119; 133; 145; 159; 161; 171; 173; 181; 185; 1207; 209; 223; 233; 239; 251; 279	Diarylheptanoid	Curcuma longa L.	Park and Kim (2002)
9	(-)-(12E,2S,3S,4R, 5R,6R, 9S,11S, 15R)- 3,15-Dibenzoyloxy-5,6-epoxylathyr-12-en- 14-one	KAv	39.8	5683	C ₃₄ H ₃₈ O ₆	542.2 M-H	119; 145; 183; 211; 212; 237	Diterpenoid	Euphorbia micractina Boiss	Tian et al. (2011)
10	5'-methoxycurcumin	PR	35.56	388655	C ₂₂ H ₂₂ O ₇	398.1 M-H	117; 119; 129; 137; 145; 149; 161; 175; 207	Diarylheptanoid	Curcuma longa L.	Ravindran (2000)
11	Methyl-7-methoxycoumarin,4-	SU	34.4	67927	C ₁₁ H ₁₀ O ₃	190.1953	115; 116; 117; 119; 120	Coumarin	none	NIST CAS register No. 2555–28–4 Mass Bank ACCESSION: PR100013
12	Hydroferulic acid	KAr	16.8	13992	C ₁₀ H ₁₂ O ₆	195.10 M-H	109; 121; 122	Phenolic acid	Curcuma longa L.	Ma and Gang (2006)
13	1,2,3,4-Tetraphenylbutane-2,3-diol	KAr	11.1	3926	C ₂₈ H ₂₆ O ₂	394.1 M-H	112; 129; 133; 180; 207; 243; 247; 263; 339	Aliphatic diol	none	Pubchem Compound ID: 344369
14	4-Hepten-3-one, 5-hydroxy-1,7-bis(4-hydroxyphenyl)-	PR	25.2	1418	C ₁₉ H ₂₀ O ₄	312.1 M-H	118; 119; 120; 146; 161	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
15	5,7-Dihydroxy-2-(4-hydroxyphenyl)- chroman-4-one	PR	26.8	12833	C ₁₅ H ₁₂ O ₅	272.0 M-H	107; 119; 120	Phenolic acids	none	Chromadex
16	Tetradecanoic acid/myristic acid	AS	29.47	2381	C ₁₄ H ₂₈ O ₂	228.0 M-H	128; 130; 143; 155; 158; 182; 183; 184; 210	Fatty acid	none	NIST CAS 544-63-8
17	1-(4-Hydroxy-3-methoxyphenyl)-7-(4- hydroxy-3,5-dimethoxypheny)-4,6- heptadiene-3-one	PR	32.0	194388	C ₂₂ H ₂₄ O ₆	384.1 M-H and M + H	150; 151; 158; 165	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
18	Tumerone	AS	35.3	6120	C ₁₅ H ₂₂ O	218.0 M-H		Bisabolane sesquiterpene	Curcuma longa L.	He (2000)
								d sulpania	(Co	ontinued on following page)

ABLE 6 (Continued) Cultivar-specific compounds identified by LC-MS in the rhizome extracts from one of the seven cultivars of Curcuma longa L. and C. aromatica Salisb. The structure of the compound with the serial number "1" is given in Figure 2 (panel number: 36) and compounds with SI. Nos. 2, 3-9 are given in Figure 4 with the corresponding panel nos. 3, 5-11, respectively. Abbreviations used: AS, Alleppey Supreme; DR Duggirala Red;

į ė	Compound name	Cultivar	Min)	Area/ abundance	Formula	Mass (m/z)	Mass fragment ions	Class of compound	Reported from plant species	References
							101; 103; 117; 129; 130; 131; 132; 133; 134; 145; 157; 146; 157; 158; 173; 201			
19	4-Methylene-5-hydroxybisabola-2,10-diene- 9-one	H.	44.6	321246	C ₁₅ H ₂₂ O ₂	234.1 M + H	105; 107; 115; 117; 119; 121; 122; 129; 135	Sesquiterpene	Curcuma heyneana Valeton & Zijp	Sirat and Meng (2009)
20	1,7-Bis(3,4-dimethoxyphenyl)-4,4-dimethyl-1,6-heptadiene-3,5-dione	H.	54.4	9854	C ₂₅ H ₂₈ O ₆	447.2 M-H	286; 298; 316; 317	Diarylheptanoid	Curcuma longa L.	Liang et al. (2009)
21	25-Benzylpentacyclo-(22.3.1.0.)-octacosa- 1(27),3 (8),4,6,10(15),11,13,17(22), 18,20, 24(28), 25-dodecaen	AS	54.96	42646	C ₃₅ H ₃₀	450.2 M + H	105; 107; 119; 121; 122	Cyclic diarylheptanoid	Myrica rubra (Lour.) Siebold & Zucc	Ishida et al. (2002)
22	Palmitic acid	SA	59.5	16809	C ₁₆ H ₃₂ O ₂	256.2 M-H	120; 166	Fatty acid	Curcuma kwangsiensis S.K. Lee & C.F. Liang	Jiang et al. (1989)
23	Stearic acid	SA	63.8	76620	C ₁₈ H ₃₆ O ₂	284.1 M-H	197; 199; 200	Fatty acid	Curcuma longa L.	Ma and Gang (2006)

Curcuma. Out of the total of 62 compounds detected by LC-MS analyses of rhizome extracts, four compounds were reported for the first time from the Curcuma genus. One was cultivar-specific (**Table 6**; Sl. Nos. 1; **Figure 2**, panels: 36), and three were present in more than one cultivar (**Table 7**; Sl. Nos. 1–3). The structures of these first-time reported compounds are given in **Figure 2** (panels: 37–39), and their corresponding mass fragmentation spectra are shown in **Supplementary Figure S2** (panels: 36–39).

A comprehensive table each for GCMS (**Supplementary Table S3**) and LCMS (**Supplementary Table S4**) shows the details of compound identification methods used in the present study for the first-time reported compounds from genus *Curcuma* and the previous literature. A list of 80 (GC-MS) and 62 (LC-MS) compounds can be seen in **Supplementary Tables S5, S6** respectively.

DISCUSSION

In one of our previous studies, we reported that the HPLC method could be a valuable tool to differentiate the cultivars of *Curcuma* spp. based on their curcuminoids content ratios (Kulyal et al., 2016). Curcuminoids play a significant role in food, cosmetics, and medicinal compounds. But there are several other secondary metabolites such as terpenoids (e.g., mono-, sesqui-, di-, tri-, so on), alkenes, aromatic compounds, flavonoids, coumarins, etc. that are responsible for various biological activities. All these secondary metabolites are present in either the volatile essential oil or the nonvolatile fraction of the *Curcuma* spp. Employing untargeted metabolomics would be the ideal way to identify as many metabolites as possible. Therefore, in the present study, we analyzed these secondary compounds using GC-MS and LC-MS/MS.

Versatility of GC-MS and LC-MS Techniques to Identify a Large Number of Metabolites

GC-MS analysis is an appropriate technique for analyzing volatile compounds, whereas LC-MS is for detecting polar compounds, and thus, these two techniques are mutually complementary to each other. In the present study, several of the volatile compounds present in the cultivars of C. longa L. and C. aromatica Salisb. belonging to mono- and sesquiterpenoids were detected by GC-MS (Tables 2-4). On the other hand, LC-MS analysis detected phenolic (Tables 6-8) compounds, including several diarylheptanoids in the methanolic extracts of both C. longa L. and C. aromatica Salisb. (Figure 4). Electrospray ionization (ESI), coupled with LC/MS/MS, turned out to be a powerful tool in metabolite profiling and metabolomics research. Studies on chemical derivatization and quantification of several metabolites in turmeric powders and fresh rhizome extracts by LC-MS or LC-MS/MS were made. But the rapid screening within the cultivars of C. longa L. of fresh turmeric rhizome has not yet been reported. To the best of our knowledge, we were able to record the presence of several metabolites, which were not reported so far in the C. longa L. and C. aromatica Salisb. (Tables 2, 3, 6, 7, and Figure 2), using the available literature search, Metlin library, mass bank, and NIST library.

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TABLE 7 Compounds identified by LC-MS in rhizome extracts of more than one cultivar of *Curcuma longa* L. and *C. aromatica* Salisb. The compounds from serial numbers 1–3 are reported first time from the genus *Curcuma*, the structures of these compounds along with few others are given in **Figure 2** (panels: 37–39; panels 1–2, 4, 12 corresponding to serial numbers 4–5, 6, 7). Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

SI. No.	Compound name	Cultivar	RT (Min)	Area/ abundance	Formula	Mass (m/z)	Mass fragment ions	Class of compound	Reported from plant species	References
1	5,7,8-Trihydroxy-2',5'-dimethoxy-3',4'-methylene dioxyisoflavanone	AS, DR, KAv	2.2	51978	C ₁₈ H ₁₈ O ₉	377.1059 M-H ⁻	101; 102; 113; 119; 161; 163; 228; 336	Flavonoid	Terminalia ivorensis A. Chev	Ogundare and Olajuyigbe (2012)
2	Chavicol	AS, SU	38.83	55821	C ₉ H ₂₀ O	135.0794 M + H ⁺	102; 115 116	Terpenoid	Piper betle L.	NIST CAS No: 501–92–8 Nagori et al. (2011)
3	Kaempferol-3-O-rutinoside-7-O-glucoside	PR, SA	33.2	3752	C ₃₃ H ₄₀ O ₂₀	755.2655 M- H ⁻	135; 161; 175; 176; 191; 439; 579; 755; 756	Flavonoid	Lycopersicon esculentum Mill	Le Gall et al. (2003)
4	Kaempferol-3-rhamnoside	AS, DR	10.76	5367	C ₂₁ H ₂₀ O ₁₀	431.9911 M-H	125; 142; 146; 150 176; 184 190; 293; 304; 308 311; 316; 343; 345	Flavonoid	Curcuma Xanthorrhiza Roxb	Ruslay et al. (2007)
5	3-Acetyl coumarin	AS, PR, SA, SU, KAV	34.65	289624	C ₁₁ H ₈ O ₃	188.0534	115; 116; 117; 118 141; 143	Coumarin	None	Pub Chem ID 24852845 NIST 3949-36-8
6	Turmeronol	AS, DR, SU	25.36	87260	C ₁₅ H ₂₀ O ₂	232.1436	103; 104; 105 107; 115; 117; 118 119; 120; 121; 128 129; 131; 141; 142; 143	Bisabolane sesquiterpene	Curcuma longa L.	Ma and Gang (2006)
7	7-(3,4-Dihydroxyphenyl)-5-hydroxy-1- phenyl-(1E)-1-heptene	AS, KAv	35.99	16570	C ₁₉ H ₂₂ O ₃	298.1 M-H	119; 183; 184	Diarylheptanoid	Curcuma xanthorrhiza Roxb	Suksamrarn et al. (1994)
8	1,7-Diphenyl-1,6-heptadiene-3,5-dione	AS, SA	2.49	9697	C ₁₉ H ₁₆ O ₂	276.0	115	Diarylheptanoid	Synthesized the compound	Sundaryono et al. (2003)
9	1-Hepten-3-one, 5-hydroxy-1,7-bis(3,4-dihydroxyphenyl)-	PR, SA, SU, KAr, KAv	21.2	1660	C ₁₉ H ₂₀ O ₆	344.1	107; 121; 134; 135; 136; 159; 161; 162; 177; 178	Diarylheptanoid	Alnus japonica (Thunb.) Steud	Sati et al. (2011)
10	4-(p-Hydroxyphenyl)-3-buten-2-one	AS, DR, SA, KAv	22.16	18641	$C_{10}H_{10}O_2$	162.0	117; 118	Flavonoid	None	NIST CAS 3160-35-8
11	5-Hydroxy-7-(4-hydroxyphenyl)-1- phenyl-(1E)-1-heptene	AS, DR, PR, SA, KAr, KAv	23.11	6169	C ₂₀ H ₂₄ O ₄	328.1	107; 119; 133; 134; 135; 136; 159; 161; 162; 177; 178	Diarylheptanoid	Curcuma xanthorrhiza Roxb	Suksamrarn et al. (1994)
12	1-(4-Hydroxy-3-methoxyphenyl)-7-(4- hydroxy-3,5-dimethoxypheny)-4,6- heptadiene-3-one	AS, DR, SA, KAr, KAv	25.8	6408	C ₂₂ H ₂₄ O ₆	384.1	133; 134; 147; 148; 150; 151; 158; 165; 175; 176; 186; 187; 188; 189; 203; 204; 232	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
13	1,5-Bis(3,4-methylenedioxyphenyl)-1,4- pentadien-3-one	SU, KAv	26.0	9161	C ₁₉ H ₁₄ O ₅	322.0	115; 119; 121; 133; 143; 235; 237; 247; 263; 275	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
14	1-Hydroxy-1-(3,4-dihydroxyphenyl)-7- (4-hydroxy-3-methoxyphenyl)-6- hepten-3,5-dione	AS, KAv	26.7	45589	C ₂₀ H ₂₀ O ₇	372.1	103; 117; 131; 137; 143; 145; 149; 163; 177	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
15	1,7-Bis(4-hydroxyphenyl)-1-heptene- 3,5-dione	AS, DR, PR, SA, SU, KAv	27.4	8495	C ₁₉ H ₁₈ O ₄	310.1	117; 118; 119; 145; 146; 161; 175; 176	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
16	1,7-Bis(4-hydroxyphenyl)-1,4,6- heptatrien-3-one	AS, DR, PR, SA, SU, KAv	30.0	7240	C ₁₉ H ₁₆ O ₃	292.1	115; 117; 119; 120; 143; 145	Diarylheptanoid	Curcuma longa L.	Li et al. (2011)
17	7-(4-Hydroxy-3-methoxyphenyl)-1-(4- hydroxy phenyl)-4,6-heptadien-3-one	AS, KAv	31.8	138675	C ₂₀ H ₂₀ O ₄	324.1	107; 117; 119; 120; 122; 123; 131; 135; 137; 145; 146; 147; 148; 163; 195; 223	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
									(Continued	d on following page)

TABLE 7 (Continued) Compounds identified by LC-MS in thizome extracts of more than one cultivar of Curcuma longa L. and C. aromatica Salisb. The compounds from serial numbers 1-3 are reported first time from the genus Curcuma, the structures of these compounds along with few others are given in Figure 2 (panels: 37–39; panels 1–2, 4, 12 corresponding to serial numbers 4–5, 6, 7). Abbreviations used: AS, Alleppey Salem: 표 Supreme; DR, Duggirala Red;

is S	Compound	Cultivar	(Min)	Area/ abundance	Formula	Mass (m/z)	Mass fragment ions	Class of compound	Reported from plant species	References
18	Coumaran	AS, DR, SA, SU	34.36	6563	C ₈ H ₈ O	120.0	116; 117; 118; 119	Coumarin	None	Chromadex
19	5,7-Dihydroxy-4-methylcoumarin	AS, SA, SU, KAv	34.57	92188	C ₁₀ H ₈ O ₄	192.17	113; 115; 116; 117; 118; 141	Coumarin	None	PubChem CID 5354284
20	1,7-Bis(3,4,5-trimethoxyphenyl)-1,6- heptadiene-3,5-dione	PR, SU, KAr, KAv	35.82	4972	C ₂₅ H ₂₈ O ₈	456.3	280; 281; 298; 299	Diarylheptanoid	Synthesised the compound	Hahm et al. (2002)
21	Ourlone	AS, DR, PR, SU, KAr, KAv	46.50	19540	C ₁₅ H ₂₂ O	218.0	101; 103; 117; 129; 130; 131; 132; 133; 134; 145; 157; 146; 157; 158; 173	Bisabolane sesquiterpene	Curcuma longa L.	He (2000)
22	Hydrocinnamic acid	SU, KAr	35.1	3812	C ₉ H ₁₀ O ₂	150.0	103; 105; 133	Phenolic acid	Curcuma longa L.	Ma and Gang (2006)
23	Ourcumenol	AS, SU, KAr, KAv	36.67	34556	C ₁₅ H ₂₂ O ₂	234.1	105; 107; 109; 117; 123; 125; 133; 137	Sesquiterpene	Curcuma heyneana Valeton & Zijp	Sirat and Meng (2009)
24	Oleic acid	SA, KAr	60.2	15974	C ₁₈ H ₃₄ O ₂	282.1	168; 257	Fatty acid	Curcuma longa L.	Ma and Gang (2006)

Cultivar Variability Based on Secondary Metabolites

Based on the presence or absence of metabolites identified by GC-MS and LC-MS analyses, there was a need to authenticate cultivar variability. Thus, the metabolite library can be constructed based on the cultivar-specific and compounds found in more than one cultivar. There are very few reports on cultivar-specific secondary metabolite variation. Out of a total of 142 compounds identified by both GC-MS and LC-MS, only 28 compounds (13 from GCMS and 15 from LCMS) were common (Tables 4, 8) present in all the cultivars of C. longa L. and C. aromatica Salisb. Ten of 13 common compounds (GCMS) were reported earlier from C. longa L. rhizome. Two compounds, namely sabinene and α-caryophyllene, were reported from the leaves of C. longa L. The remaining one compound, i.e., 2-heptadecanone, was detected for the first time from these two Curcuma species. This compound was earlier reported in the essential oil of Curcuma angustifolia Roxb. rhizome (Srivastava et al., 2006).

As per our analyses, 64 compounds (Tables 2, 6) out of 142 compounds were cultivar-specific. Of these 64 compounds, 41 were identified in essential oils by GC-MS (e.g., carvacrol, endo-borneol) and 23 (e.g., tumerone, methyl-7-methoxycoumarin,4-) in fresh rhizome extracts (LC-MS) of any one of the cultivars of C. longa L. or C. aromatica Salisb. In addition, 50 compounds (Tables 3, 7) were identified to be present in some of the cultivars, present in more than one cultivar but not common to all the cultivars of C. longa L. and C. aromatica Salisb. Out of these 50 compounds, 26 were identified in essential oils through GC-MS. For example, 1,3,5-cycloheptatriene was detected in all six cultivars except cv. Duggirala Red, whereas 12-oxabicyclo(9.1.0)dodeca-3,7-diene, 1,5,5,8-tetramethyl-, [1R-(1R*,3E,7E,11R*)]-, was detected only in cvs. Duggirala Red and Kasturi Araku. The rest 24 compounds were detected in rhizome extracts by LC-MS (e.g., chavicol detected in cvs. Alleppey Supreme and Suguna). The present extensive analyses of both essential oils and whole rhizome secondary metabolome of seven cultivars of C. longa L. and C. aromatica Salisb. established cultivar variability. Variability of the compounds within or/and in between the cultivars of C. longa L. and C. aromatica Salisb. will give a better understanding of their selection. The current study will help select cultivars for use in pharmacology or the food industry.

Discovery of First-Time Reported Metabolites in *C. longa* L. and *C. aromatica* Salisb.

In the present study, as many as 142 compounds were identified in the essential oils and rhizome extracts of *C. longa* L. and *C. aromatica* Salisb. Out of these, 39 compounds were identified for the first time in the genus *Curcuma*. However, these compounds were found in other plant genera. The structures of these compounds are shown in **Figure 2**, and corresponding details, including the class of compound, molecular weight, are given in **Tables 2**, 3, 6, and 7. As an example, cv. Alleppey Supreme of *C. longa* L. showed three cultivar-specific compounds. Among these, 1,2-cyclohexanediol, 1-methyl-4-(1-methylethyl)- (oxygenated

TABLE 8 Compounds commonly detected by LC-MS analysis of rhizomes extract of all seven cultivars of *Curcuma* spp.: five of *Curcuma longa* L. (cvs. Alleppey Supreme, Duggirala Red, Prathibha, Salem, and Suguna) and two of *C. aromatica* Salisb. (cvs. Kasturi Araku, Kasturi Avidi). The structures for the compounds in the serial numbers 10, 5, 6, 15, and 1 are given in **Figure 4** (panels 13, 14, 15, 16, and 17 respectively).

SI. No.	Compound name	RT (Min)	Area/ abundance	Formula	Mass (m/z)	Mass fragment ions	Class of compound	Reported from plant species	References
1	1,5-Bis(4-hydroxy-3-methoxyphenyl)- 1,4-pentadien-3-one	23.5	3535	C ₁₉ H ₁₈ O ₅	325.1247	117; 118; 119; 120 135; 143; 145; 146 159; 161; 187	Diarylheptanoid	Curcuma longa L.	Li et al. (2011)
2	Ar-Turmerone	24.7	23545	C ₁₅ H ₂₀ O	216.1	103; 104; 105; 106; 107; 108; 115; 116; 117; 118; 119; 120	Bisabolane sesquiterpene	Curcuma longa L.	Parthasarathy and Chempakam (2008)
3	Tetrahydroxybisdemethoxycurcumin	25.4	4773	C ₁₉ H ₂₀ O ₄	311.1446	117; 118; 119; 120 146; 161	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
4	Tetrahydrodemethoxycurcumin	25.9	7734	C ₂₀ H ₂₂ O ₅	341.1272	101; 113; 119	Diarylheptanoid	Piper nigrum L.	Ravindran (2000)
5	1-(4-Hydroxyphenyl)-7-(4-hydroxy-3-methoxyphenyl)-1,4,6-heptatrien-3-one	26.1	76458	C ₂₀ H ₁₈ O ₄	321.0938	115; 117; 119; 121 132; 133; 134; 143 145; 174; 235; 237 247; 263'264; 274 275	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
6	1,7-Bis(4-hydroxy-3-methoxyphenyl)- 1,4,6-heptatrien-3-one	26.3	64172	$C_{21}H_{20}O_5$	351.1123	108; 115; 119; 136 143; 148; 164; 195 207; 223; 224; 235 245; 251; 261; 262 263; 279; 291; 307	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
7	Tetrahydroxycurcumin	26.5	81260	C ₂₀ H ₂₀ O ₇	371.1686	133; 134; 135; 148 149; 175; 176; 177	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
8	1-(4-Hydroxy-3-methoxyphenyl)-7-(4-hydroxy-3,5-dimethoxyphenyl)-1,4,6-heptatrien-3-one	26.84	58571	C ₂₂ H ₂₂ O ₆	382.1	149; 159; 173; 197; 209; 211; 221; 233; 237; 239; 249; 261; 267; 277; 289; 293; 295; 305: 309	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
9	1,6-Heptadiene-3,5-dione, 1-(3,4-dihydroxyphenyl)-7-(4-hydroxy phenyl)-	31.6	5753	C ₁₉ H ₁₆ O ₅	324.1	134; 135; 136; 143	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
10	1-(3.4-Dihydroxyphenyl)-7-(4-hydroxy- 3-methoxyphenyl)-hepta-1,6-diene-3,5- dione	32.3	16375	C ₂₀ H ₁₈ O ₆	353.1212	134; 135; 136; 150	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
11	Bisdemthoxycurcumin	34.5	1675644	C ₁₉ H ₁₆ O ₄	307.1132	117; 119; 120; 143 145	Diarylheptanoid	Curcuma Ionga L.	Jiang et al. (2006)
12	Demethoxycurcumin	35.4	1302410	C ₂₀ H ₁₈ O ₅	337.1251	117; 119; 120; 132 134; 143; 145; 158 160; 175; 201	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
13	Dihydrocurcumin	35.8	5151	C ₂₁ H ₂₂ O ₆	369.1533	132; 134; 135; 149	Diarylheptanoid	Curcuma longa L. (Continued	Jiang et al. (2006) on following page

TABLE 8 (*Continued*) Compounds commonly detected by LC-MS analysis of rhizomes extract of all seven cultivars of *Curcuma* spp.: five of *Curcuma longa* L. (cvs. Alleppey Supreme, Duggirala Red, Prathibha, Salem, and Suguna) and two of *C. aromatica* Salisb. (cvs. Kasturi Araku, Kasturi Avidi). The structures for the compounds in the serial numbers 10, 5, 6, 15, and 1 are given in Figure 4 (panels 13, 14, 15, 16, and 17 respectively).

SI. No.	Compound name	RT (Min)	Area/ abundance	Formula	Mass (m/z)	Mass fragment ions	Class of compound	Reported from plant species	References
14	Curcumin	36.2	1503497	C ₂₁ H ₂₀ O ₆	367.1374	158; 160; 175 132; 133; 134; 135 149; 158; 160; 161 175	Diarylheptanoid	Curcuma longa L.	Jiang et al. (2006)
15	1-Heptene-3,5-dione, 1,7-bis-(4-hydroxy-3-methoxyphenyl)-	43.2	5078	C ₂₀ H ₂₀ O ₅	339.1473	117; 119; 120; 134 158	Diarylheptanoid	Curcuma Ionga L.	Jiang et al. (2006)

alcoholic monoterpenoid) was earlier reported from leaf and peel essential oil of *Citrus medica* L. (Rutaceae). This compound is used as a flavoring agent (Bhuiyan et al., 2009); trans, trans-octa-2,4-dienyl acetate, present in common Malaysian *Kaempferia galanga* L. (Zingiberaceae), was used for its food-flavoring property (Othman et al., 2006). Phenol, 2-methoxy-3-(2-propenyl)-, an allyl chain-substituted guaiacol was reported from rosewood extracts (Jiang et al., 2018).

The following four compounds were identified from cv. Duggirala Red (C. longa L.): 3-isopropyl-4-methyl-1-pentyn-3-ol (alcohol constituent) containing leaf and stem of Anethum sowa Roxb. ex, Fleming, used for flavoring of food, beverages and also for many medical preparations (Saleh-e-in et al., 2010); 5,9-tetradecadiyne (unsaturated hydrocarbon) was found to be a major component of Ferula vesceritensis Coss. & Durieu ex Trab. leaf essential oil (Zellagui et al., 2012); naphthalene, 5-butyl-1,2,3,4-tetrahydro- (tetralin type of compounds) found in the essential oil of Meconopsis punicea Maxim. and M.delavayi (Franch.) Franch. Ex Prain (Slavík and Slavíková; Yuan et al., 2003); and santolina alcohol was reported from plant Achillea filipendulina Lam. (Sharopov and Setzer, 2010). A total of nine cultivar-specific compounds were detected in cv. Prathibha (C. longa L.) and the examples of these compounds and their source plants, respectively, are 7-tetracyclo[6.2.1.0(3.8)0(3.9)]undecanol, 4,4,11,11 tetramethyl- in Cyperus articulatus L. (Metuge et al., 2014); bicyclo(2.2.1)hept-2-ene, 2,3-dimethyl- in Abies alba Mill. (Yang et al., 2009). Cultivar-specific compounds of three each were detected in cvs. Salem (C. longa L.) and Suguna (C. longa L.) (Table 2). In C. aromatica Salisb., only one cultivar-specific compound was detected in cv. Kasturi Avidi, i.e., 3-octen-5-yne, 2,7-dimethyl-, (Z)-, and this compound was earlier reported from the medicinally important Litsea glutinosa (Lour.) C.B. Rob. fruit essential oil (Chowdhury et al., 2008a).

Some of the compounds identified in our study were present in more than one cultivar. For example, 6-(p-tolyl)-2-methyl-2-heptenol (**Table 3**) was detected in three cvs.: Alleppey supreme, Suguna of *C. longa* L., and Kasturi Avidi of *C. aromatica* Salisb. This compound was earlier reported from *Zingiber officinale* Roscoe (Zingiberaceae), used as a spice, food products, and beverages (Choudhari and Kareppa, 2013).

Limitations and Strengths of the Present Study

There is significant variability within and between the cultivars of C. longa L. and C. aromatica Salisb, which can be exploited to differentiate the cultivars of Curcuma spp. The feasibility of studies without using any standard compounds was pointed out by Núñez et al. (2020). Similarly, reference compounds were not used in our study to derive arithmetic indices under the experimental conditions. Despite the dilution made in the essential oil sample before injecting into the GC-MS system, the sample was still too concentrated. The high concentration of oil might have restricted the resolution due to overloading the detector. This could be the reason that we could not identify several compounds. We would ensure the further dilution of the oil sample in our future studies. However, the technology employed, GC-TOFMS and LC-QTOFMS, and MS-spectral database/literature search enabled us to establish the cultivar variability of Curcuma spp. The detailed information on the metabolite variability within or/and between the cultivars of C. longa L. and C. aromatica Salisb. may assist us in selecting the cultivars for a specific purpose, like culinary use, coloring, or pharmacological purpose. The studies such as the present one can help to select cultivars, particularly for use in pharmacology or the food industry. Metabolite variability poses a challenge in the use of turmeric in therapy. The practitioners need to be quite careful and use the identified cultivar and avoid mix-up. The caution applies to commercial/industrial use. Once standardized, the protocol should ensure the use of a specific cultivar. Our GC-MS and LC-MS-based metabolite identification is distinct from chemophenetic studies but is a complementary approach to characterize the Curcuma metabolome.

Importance of *Curcuma* spp. Metabolites for Human Health

Curcuminoids (CU, DMC, and BDMC) were identified as the main bioactive compounds of genus *Curcuma* and proved to have a broad spectrum of biological activities based on pharmacological studies. However, rhizomes and their essential oils of *Curcuma* spp. contained several other

TABLE 9 | Pharmacological activity of metabolites identified, other than major curcuminoids (curcumin, demethoxycurcumin, and bisdemethoxy curcumin), in *C. longa* L. and *C. aromatica* Salisb.

SI.	Compound name	Source plant	Tested Compound/	Pharmacological activity/health	References
No.			essential oil/extract	benefit of the compound or compound containing plant product	(Activity assay or compound detection)
1	Carvacrol	Curcuma longa L.	Compound	Antibacterial	Suntres et al. (2015)
2	p-Cymene	Curcuma longa L.	Compound	Antioxidant	(De Oliveira et al. (2015)
				Anti-inflammatory, anticancer, and antimicrobial effects	Marchese et al. (2017)
3	Eucalyptol	Curcuma longa L.	Compound	Antitumor anti-inflammatory relevance to Alzheimer's disease	Murata et al. (2013); Islam et al. (2014)
4 5	α -Pinene α -Terpineol	Curcuma longa L. Curcuma longa L.	Compound Compound	Anti-inflammatory and chondroprotective Anti-inflammatory	Rufino et al. (2014) De Oliveira et al.
6	Terpinolene	Curcuma longa L.	Compound	Anticancer	(2012) Okumura et al. (2012)
7	2-Heptadecanone	Curcuma angustifolia Roxb	Dried rhizome essential oil	As a coolant, demulscent	Srivastava et al. (2006)
8	Santolina alcohol	Achillea filipendulina Lam	Aerial part essential oil	Traditional herbal medicine	Sharopov and Setzer (2010)
9	Cyclohexanol, 2-methyl-5-(1-methylethenyl)-	Mentha spicata L.	Aerial parts essential oil	Antifungal	Mohammed et al. (2017)
10	Cyclohexane, 1,2-dimethyl-3,5-bis(1-	Rhanterium adpressum	Aerial parts	Antifungal	(2017) Kala et al. (2009)
11	methylethenyl)- 4-Ethylphenethylamine	Coss. & Durieu Psidium guajava L.	essential oil Stem bark essential oil	Antioxidant	Fasola et al., 2011)
12	5,9-Tetradecadiyne	Ferula vesceritensis Coss. & Durieu ex Trab	Leaves essential oil	Antibacterial	Zellagui et al. (2012)
13	E-11-Tetradecenoic acid	Coriandrum sativum L.	Leaf essential oil	Spice, flavoring agent, antimicrobial	Bhuiyan et al. (2009)
14	6,10-Dodecadien-1-yn-3-ol, 3,7,11-trimethyl-	<i>Hiptage benghalensis</i> (L.) Kurz	Leaves essential oil	Treatment of skin diseases, cough, asthma, leprosy	Venkataramani and Chinnagounder (2012)
15	Chavicol	Piper betle L.	Leaf oil	Antifungal, antiseptic, and anthelmintic	Nagori et al. (2011)
16	1,2-Cyclohexanediol, 1-methyl-4-(1-methylethyl)-	Citrus medica L.	Leaf and peel essential oil	Antibiotic	Bhuiyan et al. (2009)
17	3-Isopropyl-4-methyl-1-pentyn-3-ol	Anethum sowa Roxb. ex, Fleming	Leaf and stem essential oil	Flavoring of food and beverages, antimicrobial, antioxidant	Saleh-e-in et al. (2010)
18	Bicyclo(2.2.1)hept-2-ene, 2,3-dimethyl-	Abies alba Mill	Leaf and twig essential oil	Radical scavenging activity	Yang et al. (2009)
19	2-Nonen-4-yn-1-ol, (Z)-	Alpinia speciosa (J.C. Wendl.) K. Schum	Seeds and leaves essential oil	As a food and herbal medicine, mosquito larvicidal activity	Ho (2010)
20	8-Methylene-3-oxatricyclo [5.2.0.0(2,4)]nonane	Schisandra chinensis (Turcz.) Baill	Dried fruit essential oil	Antioxidant	Wang et al. (2005)
21	3-Cyclohexen-1-one, 3,5,5-trimethyl-	Crocus sativus L.	Dried saffron oil	Antitumor	(D'Auria et al. (200
22	Ar-Tumerone α-Turmerone	Curcuma longa L.	Rhizome essential oil	Antioxidant	Singh et al. (2010)
	β-Turmerone α-Santalene Ar-Curcumene				
23	7-Tetracyclo[6.2.1.0(3.8)0(3.9)] undecanol, 4,4,11,11 tetramethyl-	Cyperus articulatus L.	Roots/rhizome essential oil	Anti-onchocera activity	Metuge et al. (2014)
24	Cholesta-8,24-dien-3-ol, 4-methyl-, (3á,4à)-	Parkia speciosa Hassk.	Seed essential oil	High nutritional and medicinal value	Salman et al. (2006)
25	3-Octen-5-yne, 2,7-dimethyl-, (Z)-	Litsea glutinosa (Lour.) C.B. Rob	Fruit essential oil	Antirheumatic	Chowdhury et al. (2008b)
26	5,8,11,14-Eicosatetraenoic acid, phenylmethyl ester, (all-Z)-	Petiveria alliacea L.	Whole plant essential oil	Used as folk medicine to enhance memory and in treatment of common cold, flu, other viral, or bacterial infections	Sathiyabalan et al. (2014)
27	Naphthalene, 5-butyl-1,2,3,4-tetrahydro-	Meconopsis punicea Maxim. and M. delavayi (Franch.) Franch. Ex Prain	Whole plant essential oil	As a traditional medicinal plant for anti- inflammatory and analgesic activity	Yuan et al. (2003)
28	1H-3a,7-methanoazulene, 2,3,4,7,8,8a-hexahydro-3,6,8,8- tetramethyl-, [3R-(3à,3aá,7á,8aà)]-	Lindera aggregata (Sims) Kosterm	Root/tubers essential oil	Treatment of decubitus ulcer	Hong (2011)
29	trans, trans-Octa-2,4-dienyl acetate	Kaempferia galanga L.	Dried rhizomes	Spice, food-flavoring agent (Continued (Othman et al. (2006) on following page)

TABLE 9 (Continued) Pharmacological activity of metabolites identified, other than major curcuminoids (curcumin, demethoxycurcumin, and bisdemethoxy curcumin), in C. longa L. and C. aromatica Salisb.

SI.	Compound name	Source plant	Tested Compound/	Pharmacological activity/health	References
No.			essential oil/extract	benefit of the compound or compound containing plant product	(Activity assay or compound detection)
				Vasorelaxant	
30	11-Dodecen-2-one	Ficus hispida L. f	Fresh male and female receptive figs	Hepatoprotective, anti-inflammatory, antipyretic	Song et al. (2001)
31	Kaempferol-3,7-O-dimethyl ether	Lumnitzera racemosa Willd and Artemisia vulgaris L.	Fresh twig methanolic extract; leaf methanolic extract	Antibacterial	Nikolova (2006); DeSouza et al. (2010)
32	5,7,8-Trihydroxy-2',5'-dimethoxy-3',4'-methylene dioxyisoflavanone	Terminalia ivorensis A. Chev	Fresh sawdust methanolic extract	Antifungal	Ogundare and Olajuyigbe (2012)
33	Kaempferol-3-O-rutinoside-7-O-glucoside	Lycopersicon esculentum Mill	Methanolic extract of fruit	Antioxidant	Le Gall et al. (2002)
34	Phenol, 2-methoxy-3-(2- propenyl)-	Dalberga stevensonii Standl	Wood extracts	Used as raw material for medical industries	Jiang et al. (2018)
35	2-Pentanone, 4-mercapto-4-methyl-	Camellia sinensis (L.) Kuntze	Tea leaves	Antioxidant	Kumazawa et al. (2005)

bioactive (volatile and nonvolatile) compounds. A summary of the pharmacological studies with the metabolites detected in the present study is given in Table 9. Some of the studies demonstrated therapeutic activity with the isolated metabolites, e.g., carvacrol (Suntres et al., 2015), p-cymene (De Oliveira et al., 2015), which are commonly found in essential oils of Curcuma spp. A few other reports correlated anti-inflammatory and antioxidant properties of C. longa L. essential oil with its chemical components ar-tumerone, α-santalene (Singh et al., 2010) (Table 9). Several compounds detected in the present study in the essential oil or rhizome extracts of C. longa L. or C. aromatica Salisb. were also found in the essential oil of other medicinal plants, traditionally used for their health benefits. The examples of such compounds are 5,9-tetradecadiyne, a cultivarspecific compound of Duggirala Red (C. longa L.), earlier reported in Ferula vesceritensis Coss. & Durieu ex Trab. leaf essential oil, exhibiting antibacterial activity; 3-octen-5-yne, 2,7-dimethyl-, (Z)-, a hydrocarbon monoterpene, identified from cv. Kasturi Avidi (C. aromatica Salisb.) was earlier reported from fruit essential oil of the medicinally important plant, Litsea glutinosa (Lour.) C.B. Rob. (Chowdhury et al., 2008a). We suggest that the medicinal use of the genus Curcuma can be not only species but also cultivar-specific.

CONCLUDING REMARKS

Essential oils from spices and aromatic plants are enriched with bioactive metabolites, easily isolated and used, unlike the difficulties encountered with synthetic chemical products. The low mammalian toxicity and biodegradable nature of the natural secondary products provide an attractive option to develop them also for crop protection. Metabolomics is a practical and dynamic approach to make a comprehensive

study. Both GC-MS and LC-MS techniques should be used to characterize the metabolite profiles of as many cultivars as possible for building a reference library. Preparative LC can be helpful to collect individual metabolite fractions and establish their identity. Several metabolites detected in 7 selected cultivars of *Curcuma* spp. by GC-MS and LC-MS analyses are reported first time in *Curcuma* spp. We suggest that the seven Indian cultivars of *Curcuma* spp. employed in our study can be used as sources of such compounds. High-throughput analysis of cultivar-specific and first-time detected compounds in the present study may lead to new drug candidates. The metabolites validated for their medicinal or other users can be quantified using simple techniques such as HPLC or TLC to ensure their presence in the herbal preparations.

DATA AVAILABILITY STATEMENT

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found below: https://www.ebi.ac.uk/metabolights/MTBLS2790.

AUTHOR CONTRIBUTIONS

ST and AR planned and designed all the experiments. PK and PKK did the experiments and preliminary data interpretation related to GC-MS and LC-MS/MS, respectively. PK, ST, and AR re-analyzed the data and wrote the draft of the manuscript. SA prepared tables and reference search. AA drew the figures and helped in editing the manuscript. All the authors read and approved the final version of the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.659546/full#supplementary-material

Supplementary Figure 1 | (A) Representative TIC chromatograms from negative ion (-) ESI-HPLC from cultivars (A) Alleppey Supreme, (B) Duggirala Red, (C) Prathibha, (D) Salem, (E) Suguna of Curcuma longa L. and cvs. (F) Kasturi Araku, (G) Kasturi Avidi of C. aromatica Salisb. Peak labelled IS represents internal standard. (B) Representative TIC chromatograms from positive ion (+) ESI-HPLC from cultivars (A) Alleppey Supreme, (B) Duggirala Red, (C) Prathibha, (D) Salem, (E) Suguna of Curcuma longa L. and cvs. (F) Kasturi Araku, (G) Kasturi Avidi of C. aromatica Salisb. Peak labelled IS represents internal standard.

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Supplementary Figure 2 | MS and MS/MS spectra of cultivar-specific compounds first time reported from genus Curcuma, identified from cultivars of Curcuma longa L. and C. aromatica Salisb. detected in essential oil (1-35) and rhizome extracts (36-39) by GC-MS (MS spectra) and LC-MS (MS/MS spectra) respectively. (Spectra 1-23 corresponds to panel numbers: 1-23 of Figure 2 and serial numbers: 1-23 of Table 2. Spectra 24-35 corresponds to panel numbers: 24-35 of Figure 2 and serial numbers: 1-12 of Table 3. Spectra 36 correspond to panel numbers 36 of Figure 2 and serial number 1 of Table 6. Spectra 37–39 correspond to panel number 37-39 of Figure 2 and serial number 1-3 of Table 7). (1) 1,2-Cyclohexanediol, 1-methyl-4-(1-methylethyl)-, (2) trans, trans-Octa-2,4dienyl acetate, (3) Phenol, 2-methoxy-3-(2- propenyl)-, (4) 3-Isopropyl-4methyl-1-pentyn-3-ol (5) 5,9-Tetradecadiyne, (6) Naphthalene, 5-butyl-1,2,3,4-tetrahydro-, (7) Santolina alcohol, (8) 2-Pentanone, 4-mercapto-4-methyl-, (9) 8-Methylene-3-oxatricyclo[5.2.0.0(2,4)]nonane, (10) 7-Tetracyclo[6.2.1.0(3.8)0(3.9)]undecanol, 4,4,11,11 tetramethyl-, (11) Bicyclo[2.2.1]hept-2-ene, 2,3-dimethyl-, (12) 1H-3a,7-Methanoazulene, 2,3,4,7,8,8a-hexahydro-3,6,8,8-tetramethyl-, [3R-(3à,3aá, 7á, 8aà)]-, (13) Cholesta-8,24-dien-3-ol, 4-methyl-, (3á,4à)-, (14) 4-Ethylphenethylamine, (15) Cyclohexanol, 2-methyl-5-(1-methylethenyl)-, (16) Cyclohexane, 1,2-dimethyl-3,5-bis(1methylethenyl)-, (17) 5,8,11,14-Eicosatetraenoic acid, phenylmethyl ester, (all-Z)-, (18) 11-Dodecen-2-one, (19) E-11-Tetradecenoic acid, (20) 2-Nonen-4-yn-1-ol, (Z)-, (21) 3-Cyclohexen-1-one, 3,5,5-trimethyl-, (22) 6,10-Dodecadien-1-yn-3-ol, 3,7,11-trimethyl-, (23) 3-Octen-5-yne, 2,7-dimethyl-, (Z)-, (24) 1,3,5-Cycloheptatriene, (25) Bicyclo[3.1.0] hexane, 4-methyl-1-(1-methylethyl)-, didehydro deriv., (26) Bicyclo[3.2.1]oct-2-ene, 3methyl-4-methylene-, (27) Oxirane, 2-(hexyn-1-yl)-3-methoxymethylene-, (28) Bergamotol, $Z-\alpha$ -trans-, (29) (1,3-Dimethyl-2-methylene-cyclopentyl)-methanol, (30) 12-Oxabicyclo[9.1.0]dodeca-3,7-diene, 1,5,5,8-tetramethyl-, [1R-(1R*,3E,7E,11R*)]-, (31) Isolongifolene, 4,5,9,10-dehydro-, (32) Z,Z,Z-4,6,9-Nonadecatriene, (33) 6-(p-Tolyl)-2-methyl-2-heptenol, (34) 6-Tridecen-4-yne, (Z)-, (35) 1,4-Cyclohexadiene, 1methyl-, (36) Kaempferol-3,7-O-dimethyl ether, (37) 5,7,8-Trihydroxy-2',5'-dimethoxy-3',4'-methylene dioxyisoflavanone, (38) Chavicol, (39) Kaempferol-3-O-rutinoside-7-Oalucoside.

Supplementary Table 1 | A list of secondary metabolites identified by GC-MS in the essential oil from the rhizomes of five cvs. of *C. longa* L. and two cvs. of *C. aromatica* Salisb. Abbreviations: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

Supplementary Table 2 | A list of secondary metabolites identified by LC-MS in the rhizomes extract of five cvs. of *C. longa* L. and two cvs. of *C. aromatica* Salisb. Abbreviations used: AS, Alleppey Supreme; DR, Duggirala Red; PR, Prathibha; SA, Salem; SU, Suguna; KAr, Kasturi Araku; KAv, Kasturi Avidi.

Supplementary Table 3 | Identification parameters of first-time reported compounds by GC-MS in the essential oil from the seven cultivars of *Curcuma* spp. along with the methods used in previous literature.

Supplementary Table 4 | Identification parameters of first-time reported compounds by LC-MS in the rhizome extracts of genus *Curcuma* along with the methods used in related previous literature.

Supplementary Table 5 | The list of 80 compounds identified by GCMS analysis.

Supplementary Table 6 | The list of 62 compounds identified by LCMS analysis.

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Multielemental Analysis and *In Vitro*Evaluation of Free Radical Scavenging Activity of Natural Phytopigments by ICP-OES and HPTLC

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The phytopigments derived from ethnomedicinal plants employed as traditional medicines appear to be the simplest alternative for artificial radical colorants. This can be because of persistent use of synthetic dyes and their harmful impacts linked to human lives as well as to the ecosystem. The literature evidences clearly reveal the complications from growing demands of radical colorants from artificial origin. The planned analysis work hence focuses on screening of the fundamental composition of phytopigments, obtained from plant sources by subtle technique of ICP-OES, with axial plasma combined with nebulizer motor-assisted gas flow approach, utilizing microwave digester for complete digestion of phytopigments, thereby establishing the pigments being safe for consumption. Additionally, the observations from free radical scavenging activity using DPPH by HPTLC concluded that the natural pigments obtained from plant sources are rich in flavonoids with potent antioxidant property. Thus, an effort has been made through the developed ICP-OES methodology, to beat the distinct imprecise practice of food labeling, once natural pigments are utilized in a variety of additives, as food colorants with amounts of components detected as arsenic, lead, and metal, within specified limits of FSSAI, demonstrate and establish safety of natural foodstuff agents, as compared over hazardous synthetic azo dyes.

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INTRODUCTION

Colors form an integral component of food and related consumer goods because of their intrinsic indispensable fundamental property of imparting unique characteristic hues to the product to which they are added. These food colors not only define nature of food but also are linked to human desires for types of food consumed; for example, yellow to light green for raw fruits with citrus flavor (acidic), whereas red and pink for ripe condition with sweet taste. Routine food colors are classified into tetrapyrroles, tetraterpenoids, flavonoids, *etc.* Some class of pigments were also further categorized into anthocyanins (from blue berries), betalains (from beetroot), and annatto (from bixin seeds).

On the basis of their source of origin, colors may be classified as follows:

- 1. Natural: bixin, anthocyanins, betanins, chlorophylls, curcumin, lycopene, etc.
- 2. Nature identical: orange, watermelon, etc.

- 3. Artificial colors: blue-1, blue-2, tartrazine, erythrosine, citrus red-2, indigo carmine, Ponceau 4R, *etc*.
- 4. Inorganic: TiO₂ (from metals) (Mortensen, 2006).

The recent advancements in technology for extraction and assessment of biological activities like antiaging phenomena as well as therapeutic efficacy like treating blood disorders, anemia, beneficial effect on lungs, free radical scavenging activity, and the newer phytopigments like anthocyanins, betanins, curcumins, indigotin, and isatin are the preferred choice of coloring agents in foods by public considering focal point of their safety as well as for manufacturers in regards to expanding their extensive business (Graham et al., 1990; Micozzi et al., 1990; Zhang et al., 1991; Sies et al., 1992; Van Poppel, 1993). In terms of food frauds, the establishment of accurate and rapid instrumental techniques for natural colorings is required, especially for the phytopigments like anthocyanins and betalains; oleo-resins like paprika and turmeric; carotenoids; and quinoids, that are off late frequently utilized in different foods and related consumer matrices (Fujii et al., 2001). Frugal, fast, and concurrent analytical techniques need to be established. Elemental estimation is another parameter of great significance for determining beneficial and toxic effects of plant pigments, like anthocyanin, betanin, paprika oleoresin, annatto, and turmeric oleoresin, that contain adequate basic components additionally for human well-being (Kohen and Nyska, 2002). Most recent innovations in Foodomics as well as farsighted toxicological studies have been applied for screening potential hazardous synthetic contaminants such as heavy metals and aflatoxins in early medication improvement/new drug lead molecule discoveries. Hence, such novel innovations would surely be utilized to add to the scientific evidence to plant pigments in regards to its safety (Jordan et al., 2010). The overall expanding enthusiasm for natural cycles just as the synthetic structure of plants for dietary, restorative, and ecological issues has led to advanced metal-related studies (Adriano, 2001). Recent dossiers and newer regulations regarding stringent food norms and laws prompt more noteworthy entry of toxic metals into the climate. with the indication that a critical aspect of the populace is currently routinely exposed to these toxic metals (Goyer, 1997). Plants are probable sources for micro- and macroessential nutrients, since there are different take-up courses for fundamental components such as uptake of minerals, salts, and metals from soil (Barthwal et al., 2008). These components are utilized, for instance, keeping up osmotic balance, as basic parts in sugars and proteins, as segments of natural atoms associated with typical digestion (e.g., magnesium (Mg) in chlorophyll, phosphorous (P) in ATP, iron (Fe) in photosynthesis, copper (Cu) in root digestion, and zinc (Zn) for development), and as chemical activators (e.g., potassium (K) in tissue cells and layers, calcium (Ca) for stress reaction, (K) as development controller, and nickel (Ni); Hepler, 2005; Tanhan et al., 2007; Soetan et al., 2010; Wang et al., 2013). Adjacent to the fundamental components, a few metals, for example, arsenic (As), cadmium (Cd), and lead (Pb), are toxic to the creature even in exceptionally low levels, while other do not show any positive or negative impact. It is vital, particularly for spices, that they contain adequate fundamental components (micro-macro nutrients)

additionally for human well-being. Besides, micro-components in plants are associated with the arrangement cycles of dynamic synthetic elements, which permit their utilization for treating various disorders, for example, iron (Fe) supplement for blood-related disorders. The detrimental impact results from the reality that heavy metals migrate from soils, harvests, or plants, entering the food chain (Antonijević et al., 2012), or by therapeutic applications from medicaments (Cheng, 1955; Garcia et al., 2000; Başgel and Erdemoğlu, 2006; Adeyolanu et al., 2016). Considering the aforementioned points, the World Health Organization (WHO) has specified the permissible levels in crude plant material for the presence of heavy metals, thereby maintaining a stringent watch of negative effects on human wellbeing by plant utilization or its clinical use (WHO, 1991; Zeiner et al., 2015).

Antioxidant assays might depend on the probable type of anticancer agents (lipophilic or hydrophilic, and enzymatic or nonenzymatic) (Huang et al., 2005). The DPPH test by HPTLC is one of the reliable mainstreams and frequently preferred technique among diagnostic tools for identifying the presence of radical scavenging/antioxidant activity. The technique is basic, productive, moderately reasonable, and fast. The shading change occurs from purple color of the reagent to lemon yellow color components possessing free radical scavenging property, permitting the spectrophotometric assurance of the agent possessing possible free radical scavenging (antioxidant) activity (Molyneux, 2004; Kedare and Singh, 2011).

In the proposed research, an effort has been made to feature the biotherapeutic potential of phytopigments utilized in foods and related food merchandises, by chromatographic fingerprints *via* free radical activity, along with multielemental assessment using inductive coupled plasma-optical emission spectroscopy (ICP-OES), with a viewpoint to screen heavy metals such as lead, arsenic, and cadmium, in addition to micro- and macro-minerals like Mg, Fe, and Zn. Therefore, the novel strategy developed above would surely be employed in routine quality control for monitoring food.

EXPERIMENTAL

Reagents

Natural pigments like anthocyanins, betanins, curcumin oleoresin, paprika oleoresin, and annatto were procured from Neelikon Food Dyes Pvt. Ltd., Mumbai. 98% nitric acid-reagent grade (Fisher Scientific, Fair Lawn, NJ, United States). Hydrogen peroxide (H₂O₂)-30% reagent grade (J.T. Baker, Phillipsburg, NJ, United States). Micro laboratory cleaner (International Products Corporation, Trenton, NJ, United States. Distilled, deionized water, 18 M Ω (Continental Water Systems, San Antonio, TX, United States). For HPTLC analysis, n-butanol, glacial acetic acid, water, and DPPH (1,1-diphenyl-2-picrylhydrazyl) were of analytical grade and purchased from Merck and Sigma Chemical, Germany.

Apparatus

ICP AVIO 200 inductively coupled plasma optical emission spectrometer was purchased from Perkin-Elmer, Ahmedabad, Gujarat. Titan MPS microwave digestor. Teflon® PFA microwave

TABLE 1 | Plasma specification and optimum conditions for ICP-OES.

Optimum conditions	Parameters
Plasma power	1,350–1,500 w
Gas flow	0.2 (nebulizer)/0.8 auxiliary (liters/minutes)
Coolant	15°C (55°F)
Nebulizer type	Cross flow
Nebulizer flow rate	0.2-0.8 (liters/minutes)
Pump speed	6.2 RPM
Stabilization time	60 s
No. of probes for each measuring	3
Plasma observation	Axial (low concentration), radial (high concentration)

vessels rated to 120 psi (CEM, Matthews, NC, United States). Lined digestion vessels rated to 200 psi (CEM, Matthews, NC, United States). Food processor was designed for home use. High-density polyethylene bottles, Nalgene®, or equivalent were purchased from Nalge Company, Rochester, NY, United States. The HPTLC system purchased from Camag was used for TLC analysis, and data interpretation was performed using digitally optimized vision CATS Software. Camag derivatizer was employed for derivatization to demonstrate free radical antioxidant activity using DPPH.

Instrumentation

A Titan MPS microwave digestor 950 W power with temperature and pressure monitoring and control was utilized to digest all the samples. The microwave was aligned after the U.S. Environmental Protection Agency (EPA) calibration procedure that involves heating a known volume of water at specific powers (Hepler, 2005). Individual experience directs that the sample weights should be kept at or below the prescribed weights to minimize the potential for overpressuring and venting during the microwave digestion process. Samples containing high levels of sugars are apt to react more quickly and to generate more pressure. If these products are substituted for the materials analyzed in this work, using smaller sample sizes and lower powers are strongly recommended to prevent overpressuring.

The ICP-OES analysis was performed on the Perkin-Elmer ICP AVIO 200 inductively coupled plasma-optical emission spectrometer equipped with an axial standard torch using crossflow nebulizer. Autosampler featuring a quartz sample probe to minimize sample cross contamination was used. The working specifications of ICP-OES Avio 200 and optimal conditions of plasma are given in Table 1. ICP AVIO 200 was used because of its extremely sensitive precision to detect metals at trace levels. Also, due to the simultaneous measurement, no reduction in sample throughput was observed from making measurements at multiple wavelengths of an element. Therefore, multiple emission lines were measured simultaneously for each element to verify analytical results. The analysis of different types of the samples of phytopigments was performed on different days and because each sample was in a different acid matrix, optimum background correction points (BGC) and peak windows were determined as a function of sample before the analysis was performed. The standard concentrations were matched to the anticipated levels in the diluted

samples (Fikarová, 2020). The Camag HPTLC system was employed for chromatographic analysis.

Sample Pretreatment for Inductive Coupled Plasma-Optical Emission Spectroscopy Analysis Using Avio 200 Perkin Elmer System

The phytopigments obtained from Neelikon Pvt Ltd. were pretreated using digestion mixture of concentrated nitric acid (HNO₃) and sulfuric acid (H₂SO₄), utilizing the Perkin Elmer Titan MPS microwave digestor (Liu et al., 2020).

Digestion Procedure for Inductive Coupled Plasma-Optical Emission Spectroscopy Analysis

- Step 1: 10 gm of each selected phytopigments were accurately weighed into the Teflon PFA digestion vessels.
- Step 2: Concentrated, ultrapure HNO₃ and 2 mL concentrated, ultrapure H₂SO₄ were added to the sample.
- Step 3: Cap the vessel in the capping station.
- Step 4: Phytopigment powders were digested as per Table 2.
- Step 5: Cool for approximately five minutes and vent vessels.
- Step 6: Repeat Step 4 for juices containing pulp.
- Step 7: Cool for five minutes, vent, and open the vessels using the capping station.
- Step 8: Add 3 mL 30% H₂O₂ to the samples.
- Step 9: After effervescence subsides, transfer the samples into clean, acid-washed volumetric flasks, and dilute to 100 mL with double distilled water.
- Step 10: Transfer the samples to clean HDPE bottles.

Standard Preparation for HPTLC Analysis

Standard solutions of selected phytopigments (anthocyanins, betanins, turmeric oleoresin, paprika oleoresin, and annatto) were of 100 ppm using methanol.

Sample Preparation for HPTLC Analysis

Marketed food samples such as locally available jams, squashes, ice cream flavors, and chili powders, containing anthocyanins, betanins, paprika oleoresin, and annatto, were accurately weighed as per requirement (100 ppm) and mixed with a mixture of methanol and water (8:2 v/v). For turmeric samples, locally available turmeric powder was obtained from the market, and 10 ppm solution was prepared and further subjected to spectroscopic and chromatographic analyses by ICP-OES and HPTLC techniques.

Optimized Conditions for HPTLC

Chromatography was performed on 20 \times 10 cm aluminum-coated silica gel 60 F_{254} HPTLC plates (C.A.S. No. 105642, Merck, Darmstadt, Germany). Sample application was done using Camag Linomat V with 100 μL (Hamilton syringe, United States). Development was done using a solvent system of n-butanol: glacial acetic acid: water (4:4:1 v/v/v) up to 70 mm in twin-trough chamber with saturation of 10 min with 5 min

TABLE 2 | Microwave digestion parameters for phytopigment analysis.

Parameter	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5
Power (%)	10	45	45	45	45
Power (watts)	51	366	366	366	366
Pressure (PSI)	20	40	80	120	160
Run time (min)	2	10	10	10	20
Time at parameter (min)	2	5	5	5	10
Temperature at parameter (oC)	0	75	85	100	120
Fan speed (% of maximum)	100	100	100	100	100

TABLE 3 | Quantification of heavy metals observed in selected phytopigments with prescribed limits.

SI. no Name of the color		Heavy metals				
		Arsenic (mg/kg) ≤ 1	Lead (mg/kg) ≤ 1	Cadmium (mg/kg) ≤ 1	Mercury (mg/kg) ≤ 2	
1	Anthocyanins	0.11	0.103	0.043	<0.1	
2	Paprika	0.014	0.120	0.042	0.013	
3	Betanin	0.022	0.167	0.045	0.014	
4	Turmeric	_	0.061	0.049	_	
5	Annatto	-	2.864	0.033	_	

TABLE 4 | ICP-OES results for selected phytopigments with reference values in mg/mL.

Phytopigment	Annatto	Anthocyanin	Betanins	Paprika	Turmeric
Minerals in highest quantity with observed amounts	Iron (Fe) 6.345 ± 0.40 mg/ L, calcium (Ca) 4.868, and magnesium (Mg) 2.478	Iron (Fe) 20.58 ± 0.40 mg/L	Magnesium (Mg) 17.85 \pm 0.4 mg/L with iron (Fe) 5.097 \pm 0.40 mg/L and calcium (Ca) 5.368 \pm 0.7 mg/L	Calcium (Ca) 5.958 ± 0.7 mg/L, iron (Fe) 0.278, and magnesium (Mg) 0.064 mg/L	Magnesium (Mg) 19.40 \pm 0.40 mg/L and iron (Fe) 4.942 \pm 0.40 mg/L mg/L

plate equilibrium. Spectrodensitometric scanning was performed post-derivatization using the DPPH reagent at 540 nm.

1,1-Diphenyl-2-picrylhydrazyl Radical Scavenging

After development, the plates were dried for 10 min using a Camag plate heater III. Derivatization was done using 0.5 mM arrangement of 1,1-diphenyl-2-picrylhydrazyl (DPPH) as the reagent in ethanol for 5 s (Anuyahong et al., 2020). HPTLC plates were dried at room temperature (23°C) for 90 s and then warmed for 30 s at 60°C in a dark room. Densitometric scanning was performed at 540 nm using a Camag TLC scanner four under programming control of vision CATS, v 2.5 Muttenz, Switzerland. Zones were recognized promptly as lemon yellow regions against light violet/purple zones (bands). Estimations were done in duplicate. Ascorbic acid was utilized as a positive control.

RESULTS AND DISCUSSION

For heavy metal analysis of phytopigments, nine references of heavy metal standards, Ba, Cd, Cr, Co, Cu, Pb, Ni, As, and Se, were calibrated for analysis of anthocyanins, betanins, and paprika oleoresin, from which toxic heavy metals, when subjected to ICP-OES analysis, particularly, Pb, As, and Cd,

were found to be well below the specified limits of the U.S. FDA and FSSAI regulations. The concentrations of As, Cd, Pb, and Hg were under the detection limit in each sample, which means that the investigated phytopigment samples of interest were free of toxic metals (Table 3). On a beneficial note, the nutritive profile of frequently used phytopigments was determined. Several studies have shown that the peel of beetroot was characterized by the largest betalain content (Kujala et al., 2002; Shing and Hathan, 2014; Slatnar et al., 2015; Sawicki et al., 2016). In this study, test sample of blue berry squashes and jams demonstrated anthocyanins with the highest content of iron (20.52 mg/L), and beetroot juices demonstrated betanins with the highest quantity of magnesium (17.85 mg/L), along with considerable amounts of iron (5.097 mg/L) and calcium (5.368 mg/L). Locally marketed turmeric samples reported turmeric oleoresins with the highest concentration of magnesium (19.40 mg/L) followed by the iron content of 4.942 mg/L, whereas chili powders demonstrated paprika oleoresin, reporting the calcium content of 5.958 mg/ L. Element composition with respect to macro- and microelemental concentrations of different phytopigment parts is shown in Tables 4, 5. The results in the proposed study indicate that multielemental estimation of natural pigments was successfully performed by the ICP-OES technique, proving it to be a preferred and precise tool in routine quality control of food and related merchandized goods, ensuring and assuring

TABLE 5 | Elemental analysis of phytopigment analysis with respective wavelengths and observed experimental values by ICP-OES AVIO 200 with reference values in mg/mL.

Element	Wavelength	Experimental	Label	
Ca	396.845	51.3 ± 0.7	<115	
Cu	224.702	0.137 ± 0.03		
Fe	238.200	0.59 ± 0.40	<2.1	
K	766.515	0.681 ± 7.3		
Mg	279.553	42.70 ± 0.4		
Na	589.589	24.79 ± 0.02	57.5	
Р	177.436	139.51 ± 1.3		
Zn	206.198	0.79 ± 0.2		

safety profile of food additives and contaminants in the form of heavy metals, if any.

The utilization of HPTLC and a sophisticated scanner with a photodiode detector makes possible utilization of selected phytopigments on TLC plates without prior preparation steps (Pozharitskaya et al., 2007a; Pozharitskaya et al., 2007b). In a similar fashion, chromatographic separation, in situ radical scavenging activity examination of selected phytopigments was done by online HPTLC-DAD and HPTLC-DPPH techniques simultaneously. In this study, a simple and rapid HPTLC densitometric method for the analysis of selected phytopigments was developed. Different trial compositions of the solvent systems were put to task in order to obtain highresolution and reproducible peaks. From preliminary experiments, the best results were obtained using the mobile phase of n-butanol: glacial acetic acid: water (4:4:1, v/v/v). Selected phytopigment samples were applied directly onto the plates without any prechromatographic separations. The DPPH reagent has a unique absorption maximum in the range of 510 and 520 nm, which is diminished in the

presence of a compound capable of reducing it to its hydrazine form. The kinetic behavior of antioxidants is a significant factor in the assessment of antiradical activity. A reaction time of 30 s at 50°C was seen as the optimum antioxidant-DPPH response period. After chromatographic separation, *in situ* DPPH radical scavenging properties of phytopigments were controlled by an online HPTLC-DPPH technique. This is viewed as in **Figure 1**, by derivatized image of silica plates with DPPH radicals reducing light violet/purple bands to lemon yellow bands. These zones demonstrated antioxidant activity. The intensity of the lemon yellow color depended upon the amount and nature of radical scavenging activity in the sample.

DISCUSSION

The phytopigments were subjected to elemental estimation by the ICP-OES (AVIO-200 model) technique in accordance with pharmacopeial dossiers USP 231 and USP 233. The elemental characterization of selected natural pigments utilizing the Perkin Elmer TITAN MPS digestor equipped with nebulizer and dual axial plasma assisted fast elemental analysis. The developed protocol was validated by performing calibration using heavy metal reference standards of mercury (Hg), lead (Pb), cadmium (Cd), arsenic (As), selenium (Se), chromium (Cr), copper (Cu), cobalt (Co), and antimony (Sb). The ICP-OES method designed for elemental analysis gave accurate and precise nutritional profile for selected phytopigments in regards to inherent micro-macro essential elements like iron (Fe), calcium (Ca), zinc (Zn), and phosphorus (P). The ICP-OES outcome determined that heavy metals like arsenic (As), cadmium (Cd), lead (Pb), and mercury (Hg) were reported ≤1 ppm as specified within herbal

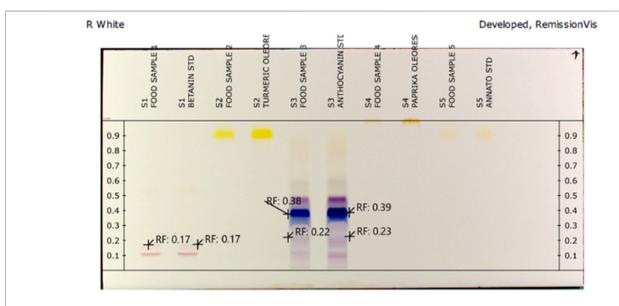


FIGURE 1 | HPTLC fingerprint of selected phytopigments exhibiting antioxidant property post-derivatization by the DPPH reagent.

the selected phytopigments labeling pharmacopeia, nonhazardous and safe for human consumption. The selected phytopigments reported essential minerals as follows: anthocyanins pigment reported the highest iron (Fe) content of 20.52 mg/L, and betanin pigment reported the highest magnesium (Mg) content of 17.85 mg/L, along with considerable amounts of iron (Fe) and calcium (Ca), of 5.097 mg/L and 5.368 mg/L, respectively; paprika oleoresin pigment reported only calcium (Ca) content of 5.958 mg/L. USP compliant DPPH assisted HPTLC protocol, developed for selected phytopigments, indicated that lemon yellow bands of phytopigments possess radical scavenging property with inherent chemical structure proving them to be antioxidant agents, suggesting them as future "Nutraceuticals."

CONCLUSION

The microwave-assisted digestion using the Perkin Elmer Titan MPS digestor gave a contamination-free sampling with minimal overall analysis time, providing faster, simpler, effective, and accurate estimation of elements. Toxic heavy metals, when subjected to the ICP-OES analysis, were within the specified limits of U.S. FDA and FSSAI regulations. On a beneficial note, the essential nutritive profile of frequently used phytopigments was determined. Annatto from butter had highest amounts of iron (Fe: 6.345 mg/L), calcium (Ca: 5.368 mg/L), and magnesium content (2.478 mg/L). Anthocyanins had the highest content of iron (Fe: 20.52 mg/L). Betanins had the highest quantity of magnesium (Mg: 17.85 mg/L) along with considerable amounts of iron (Fe: 5.097 mg/L) and calcium (Ca: 5.368 mg/L), with paprika oleoresin reporting calcium (Ca) content of 5.958 mg/L, whereas turmeric oleoresin from locally purchased turmeric powder demonstrated the highest content of magnesium (Mg: 19.40 mg/L), followed by the iron (Fe) content of 4.942 mg/L. The lemon yellow florescent bands indicated the presence of antioxidant property of the pigment.

The results in the proposed study indicate that multielemental estimation of phytopigments was successfully performed by the ICP-OES technique, proving it to be a preferred and precise tool as a routine quality control method ensuring and assuring safety profile of food additives and contaminants in the form of heavy metals, if any. The effect directed, antioxidant activity of the

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phytopigments was proven by 2,2-diphenyl-1-picrylhydrazyl (DPPH) test, using the CAMAG HPTLC system, where DPPH was used as a derivatizing reagent.

This work portrays the screening and identification of essential nutrients like iron, calcium, and magnesium as well as heavy metals in accordance with guidelines of FSSAI for foods (food industries) may be performed simultaneously utilizing the ICP-OES technique. The radical analysis carried out by the HPTLC-DPPH assay demonstrated possible inherent antioxidant properties of selected phytopigments.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**; further inquiries can be directed to the corresponding author.

AUTHOR CONTRIBUTIONS

NSM: conceptualization, methodology, original draft preparation, software analysis and interpretation, supervision, investigation, and final draft check. 2. HP: editing and final draft check. 3. BCM: original draft preparation, visualization, image graphics reviewing, data curation, supervision, investigation, and final draft check. 4. GM: data curation, language corrections, and final draft check.

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SUPPLEMENTARY MATERIAL

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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The Effects of Erchen Decoction on Gut Microbiota and Lipid Metabolism Disorders in Zucker Diabetic Fatty Rats

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Obesity is a chronic metabolic disease caused by genetic and environmental factors that has become a serious global health problem. There is evidence that gut microbiota is closely related to the occurrence and development of obesity. Erchen Decoction (ECD), a traditional Chinese medicine, has been widely used for clinical treatment and basic research of obesity and related metabolic diseases in recent years. It can significantly improve insulin resistance (IR) and lipid metabolism disorders. However, there is no microbiological study on its metabolic regulation. In this study, we investigated the effects of ECD on obesity, especially lipid metabolism and the composition and function of gut microbiota in Zucker diabetic fatty (ZDF) rats, and explored the correlation between the biomarkers of gut microbiota and metabolite and host phenotype. The results showed that ECD could reduce body weight, improve IR and lipid metabolism, and reduce the concentration of free fatty acids (FFA) released from white adipose tissue (WAT) due to excessive lipolysis by interfering with the insulin receptor substrate 1 (IRS1)/protein kinase B (AKT)/protein kinase A (PKA)/hormone-sensitive triglyceride lipase (HSL) signaling pathway in ZDF rats. Additionally, ECD gradually adjusted the overall structure of changed gut microbiota, reversed the relative abundance of six genera, and changed the function of gut microbiota by reducing the content of propionic acid, a metabolite of gut microbiota, in ZDF rats. A potentially close relationship between biomarkers, especially Prevotella, Blautia, and Holdemania, propionic acid and host phenotypes were demonstrated through correlation analysis. The results suggested that the beneficial effects of ECD on obesity, especially lipid metabolism disorders, are related to the regulation of gut microbiota in ZDF rats. This provides a basis for further research on the mechanism and clinical application of ECD to improve obesity via gut microbiota.

Keywords: obesity, Erchen decoction, lipid metabolism disorders, insulin resistance, gut microbiota, short-chain fatty

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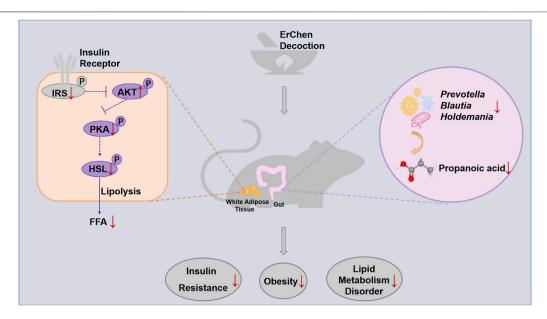
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INTRODUCTION

With the improvement of living standards and changes in lifestyles, the number of obese people is increasing sharply. The latest data has showed that, there were more than 1.9 billion adults worldwide who were overweight (about 39% of the total), and 650 million who were obese (about 13% of the total). 38 million children under the age of five were overweight or obese¹. Obesity is

¹World Health Organization. (2020). Obesity and overweight. https://www.who.int/news-room/fact-sheets/detail/obesity-and-overweight. [Accessed December 20, 2020].



GRAPHICAL ABSTRACT | Erchen Decoction could inhibit excessive lipolysis and improve lipid metabolism disorders by regulating the IRS1/AKT/PKA/HSL signaling pathway in white adipose tissue of ZDF rats. The delay in developing obesity was related to changes in gut microbiota composition and function in ZDF rats.

an important risk factor for many metabolic diseases (Saltiel and Olefsky, 2017), cardiovascular diseases (Luo et al., 2018), and even certain types of cancers (Majchrzak et al., 2019). At present, obesity, especially primary obesity, is considered to be a common disease. How to effectively prevent obesity and reduce the occurrence and development of related diseases has become a major research focus.

Adipose tissue is a main depot for storing and releasing energy and plays a key role in energy homeostasis, especially lipid metabolism balance. Dysfunction and metabolic disorder in adipose tissue is a characteristic pathological change in obesity and an important cause of local inflammation and systemic insulin resistance (IR) (Caprio et al., 2017). Insulin signaling is of crucial importance for maintaining adipose tissue function (Czech, 2017), whether from circulation or central insulin signaling (Scherer et al., 2011). Adipose tissue IR, especially an impaired insulin-signaling pathway, affects the key enzymes of lipolysis (Frühbeck et al., 2014), which leads to enhanced lipolysis as an important manifestation of metabolic disorders in adipose tissue.

Erchen Decoction (ECD), a traditional Chinese medicine formula, was first recorded in the Taiping Huimin Formula Bureau in the Song Dynasty, and is mainly used to treat phlegm dampness syndrome due to spleen dysfunction and dampness accumulation. Modern studies have found that ECD has beneficial weight loss, anti-inflammatory, and anti-oxidation effects, and significantly improves decreased insulin sensitivity (Zhang et al., 2017) and glucose and lipid metabolism disorders, especially lipid metabolism in metabolic diseases (Gao et al., 2015; Ding et al., 2018; Zhang et al., 2020b; Lee et al., 2020). In recent years, growing evidence has linked changes in gut microbiota with insulin sensitivity (Pedersen et al., 2016) and lipid metabolism (Kindt et al., 2018), and is now a target for obesity treatment

(Maruvada et al., 2017). The potential therapeutic mechanism of Chinese herbal medicines to ameliorate related metabolic diseases by improving the gut microbiota is also gradually being discovered (Gong et al., 2020). Previous studies have reported that the metabolism improvement of main traditional Chinese medicines (such as Wolfiporia extensa (Peck) Ginns (syn. Poria cocos (Schwein.) F.A.Wolf) and Zingiber Officinale Roscoe (Wang et al., 2020)) and their extracts (such as Citrus reticulata Blanco extract (Zhang et al., 2020c)) and active ingredients (such as glycyrrhiza polysaccharide (Zhang et al., 2018)) in ECD was closely related to the modulation of gut microbiota. A series of studies have been conducted on the effects by which ECD improves obesity. However, the role of ECD as a compound recipe in gut microbiota and whether the effect of ECD on improving IR or lipid metabolism disorders is related to changes in intestinal microbiota are still unclear.

The aim of this study was to observe whether ECD intervention could induce changes in IR and lipid metabolism disorders, delay the development of obesity, and affect the composition and function of gut microbiota in Zucker diabetic fatty (ZDF) rats, a spontaneous obesity model. More importantly, our goal was to determine the underlying correlation between the biological effects of ECD and the changes of gut microbiota and to provide a theoretical basis by which ECD improves obesity and related metabolic diseases via a gut microbiological mechanism.

MATERIALS AND METHODS

Preparation of ECD

ECD is composed of six components, as shown in **Table 1**. All herbs were purchased from Sanyue Chinese Traditional Medicine

TABLE 1 | The components of ECD.

Herbal name	Botanical Latin name	Place of origin	Part used	Amount used
Ban-Xia	Pinellia ternata (Thunb.) Makino	Jiangsu	dried tuber	15 g
Chen-Pi	Citrus × aurantium L.	Zhejiang	dried mature pericarp	15 g
Fu-Ling	Wolfiporia extensa (Peck) Ginns (syn. Poria cocos (Schwein.) F.A.Wolf)		dried sclerotia	9 g
Gan-Cao	Glycyrrhiza uralensis Fisch. ex DC.	Gansu	dried root and rhizome	4.5 g
Sheng-Jiang	Zingiber Officinale Roscoe	Jiangsu	fresh rhizome	7 pieces
Wu-Mei	Prunus mume (Siebold) Siebold and Zucc.	Fujian	dry near-mature fruit	1 piece

Co., Ltd. (Nantong, China) and prepared according to the Chinese Pharmacopeia method (Chinese Pharmacopoeia Commission, 2015). The medicines were soaked in eight weight/volume (1:8, w/v) distilled water for 2 h. After boiling on high heat, they were simmered at low heat for 30 min. They were extracted twice, and the filtrate combined and concentrated until the final crude drug concentration was 0.23 g/ml for low dose, 0.46 g/ml for medium dose, and 0.92 g/ml for high dose. The medium dose is clinically effective dose of ECD. The samples were stored in a refrigerator at 4°C.

Chemical Composition of ECD Samples

High performance liquid chromatography (HPLC) was performed on a Waters 2,695 system (Waters Corporation, Milford, MA, United States), consisting of a binary solvent delivery manager, an auto-sampler, and a PDA detector. Chromatographic separations were performed on an Alltima C18 column (250 \times 4.6 mm, 5 μ m). Flow rate and column temperature were set at 1 ml min⁻¹ and 30°C, respectively. A mobile phase system consisting of 0.1% formic acid in H₂O (A)acetonitrile (B) was applied with the following gradient program: 0-5 min, 95% A; 5-15 min, 95-75% A; 15-24 min, 75% A; 24-29 min, 75-65% A; 29-34 min, 65% A; 34-39 min, 65-55% A; 39–44 min, 55–50% A; 44–50 min, 50% A; 50–55 min, 50–30% A; 55-60 min, 30% A; 60-70 min, 30-10% A; 70-75 min, 10% A; 75-80 min, 10-0% A; 80-83 min, 0% A; 83-86 min, 0-95% A; 86–90 min, 95% A. The injection volume was 10 μL. Ultraperformance liquid chromatography-electrospray ionization-quadrupole-time of flight-mass spectrometry (UHPLC-ESI-Q-TOF-MS) was also performed on ECD samples. Details of the detection method are described in the supplementary materials.

Animal Model

We used 32 ZDF rats (Fa/Fa) with body weights of 130 \pm 10 g, and six Zucker lean (ZL) rats (Fa/+) with body weights of 102 \pm 12 g. All rats were 5 weeks old, male, with animal quality certificate No. SCXK (Beijing) 2016–0,006 provided by Vital River Laboratories (Beijing, China). They were raised in the specific pathogen-free animal experiment center at Nanjing University of Chinese medicine (Nanjing, China) at a temperature of 24 \pm 2°C, humidity of 65 \pm 5%, light/dark cycle of 12 h/12 h, and were provided food and water *ad libitum*. All animal experiments were approved by the Animal Ethics Committee of Nanjing University of Chinese Medicine (approval No. 201909A017). All studies were conducted in

accordance with the recommendations of Guide for the Care and Use of Laboratory Animals.

Experimental Design

After adaptive feeding, rats were randomly divided into five groups: control group (L, n = 6), model group (Z, n = 8), ECD low-dose group (EC-L, n = 8), medium-dose group (EC-M, n = 8), and high-dose group (EC-H, n = 8). Group L was fed with a normal diet (MD17121, Mediscience, China), and the others were given formula feed (Purina#5008, Lab diet, United States). Dietary composition is shown in **Supplementary Table 1**. From 5 to 9 weeks old, ECD treatment groups (EC-L, EC-M, and EC-H groups) were orally administered the low (2.28 g/kg), medium (4.57 g/kg), or high (9.14 g/kg) doses of ECD, and the L and Z groups were given high-pressure-sterilized water instead of ECD once a day with a volume of 1 ml/100 g. These dosages were calculated from the equivalent conversion of the body surface area between animals and humans.

Fresh fecal samples were collected into sterile tubes, avoiding contact with skin or urine of rats, at the end of adaptive feeding (5-week-old rats) and before the end of the experiment (9-week-old rats), then stored at -80° C before processing for 16S rRNA gene sequencing. The body weights, abdominal circumferences, and food intakes of rats in all five groups were measured weekly. At the age of 9 weeks, an insulin tolerance test (ITT) was performed by intraperitoneal injection of insulin (5 U/kg) after fasting for 6 h, and the area under the curve (AUC) was calculated.

After the experiment, the rats were fasted for 12 h and then anesthetized with isoflurane. Blood was taken from the abdominal aorta. The supernatant was collected after centrifugation at 4°C and 180 g for 10 min, and the levels of total cholesterol (TC), high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), and triglycerides (TG) also with alanine aminotransferase (ALT), aspartate aminotransferase (AST), blood urea nitrogen (BUN) and creatinine (Cr) were measured by an automatic biochemical analyzer (Chemray 240, Rayto, China). Fasting serum insulin levels were determined by enzyme-linked immunosorbent assay (10-1,250-01, Mercodia, Sweden), and the Homeostasis Model Assessment-Insulin Resistance (HOMA-IR) index was calculated as follows: HOMA-IR = fasting plasma glucose (mmol/L) × fasting serum insulin (mIU/L)/22.5 (Matthews et al., 1985). The remaining samples were used for determination of fasting serum free fatty acids (FFA). The weights of perirenal WAT and epididymal WAT were measured, and the fat body ratio was calculated as follows: Fat body ratio = (perirenal or epididymal)

WAT weight (mg)/body weight (g) \times 100%; Total fat body ratio = (perirenal + epididymal) WAT weight (mg)/body weight (g) \times 100%. The epididymal WAT from the same part of each rat was collected for hematoxylin-eosin (HE) staining and western blotting. Cecal contents (fresh feces in the cecum) were collected for targeted metabolomics analysis. EC-M group was used as the representative of EC groups for subsequent HE staining, western blotting, FFA determination, gut microbiota sequencing, and short-chain fatty acids (SCFAs) content detection. Except the paraformaldehyde fixed WAT was stored at 4°C, all samples were stored at -80°C.

HE Staining

To detect the difference of cell morphology in WAT, the three most representative rats in groups L, Z, and EC were respectively selected and their WAT were dehydrated and embedded, and then prepared into 5- μ M paraffin sections (RM2245, Leica, Germany). After stained with HE staining solution (R20570-2, Yuanye, China), WAT was observed and photographed using a microscope (BX53, Olympus, Japan).

Western Blotting and FFA Determination

The four most representative rats in groups L, Z, and EC were respectively selected for western blotting and FFA determination. Epididymal WAT samples in three groups were homogenized in RIPA buffer (P0012B, Beyotime, Beijing, China) supplemented with a mixture of 100 × protease inhibitor cocktail (5871s, CST, United States) and 100 × phosphatase inhibitor cocktail (5870s, CST, United States) to obtain their protein samples. The same amounts of protein samples were subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and blotted with the following antibodies: phospho-Insulin Receptor Substrate 1 (IRS1) (Ser307) (#2381, CST, United States, 1:1,000), IRS1 (ab52167, Abcam, United Kingdom, 1:500), phospho-Protein Kinase B (AKT) (Ser473) (4058S, CST, United States, 1:1,000), AKT (9272S, CST, United States, 1:1,000), phospho-Protein Kinase A (PKA) $\alpha/\beta/\gamma$ (Thr197) (ab75991, Abcam, United Kingdom, 1: 5,000), PKA $\alpha/\beta/\gamma$ (SC-390548, Santa Cruz, United States, 1:1,000), Phospho-hormone-sensitive triglyceride lipase (HSL) (Ser563) (AF2350, Affinity, United States, 1:2000), HSL (AF6403, Affinity, United States, 1:2000), adipose triglyceride lipase (ATGL) (A6245, ABclonal, 1:1,000) and β -actin (3700S, CST, United States, 1:1,000). The membranes were incubated with secondary antibodies conjugated to HRP (BA-1054/BA1050, Boster, Hubei, China, 1: 2000). The immunoreactive bands were treated with chemiluminescence solution (ECL, Tanon, Shanghai, China) and detected by X-ray films. The blots were visualized with an Amersham Imager 600 (General Electric Company, United States).

According to the instruction of the determination kit (A042-2-1, Jiancheng, China), the concentrations of FFA in the serum samples of rats in groups L, Z, and EC were detected.

Gut Microbiota Sequencing and Data Analysis

The fecal samples of rats in L, Z, and EC groups at 5 and 9 weeks old were sequenced for the 16S rRNA gene (Shanghai Personal

Biotechnology Co., Ltd., Shanghai, China). According to the manufacturer's protocol, total microbial DNA was extracted from stool samples, and DNA was quantified by a Nanodrop. The quality of DNA extraction was detected by 1.2% agarose gel electrophoresis. The V3-V4 region of the 16S rRNA gene was amplified by polymerase Chain Reaction (PCR). The amplified products were quantified by fluorescence (Microplate reader, BioTek, FLx800), and the samples were mixed according to the corresponding proportions. The sequencing Library (TruSeq Nano DNA LT Library Prep Kit, Illumina company) was prepared, and double-ended sequencing (MiSeq PE300 sequencer) was performed with a Miseq Regent Kit V3 (600 cycles).

The analysis was carried out using Quantitative Insights into Microbial Ecology (QIIME2) and R language ggplot2 package software. The sequence denoising was performed by a DADA2 analysis process (Callahan et al., 2016). According to the distribution of amplitude sequence variables (ASVs) among the groups, the Simpson index at 5 and 9 weeks of age was evaluated to characterize alpha diversity, and a box plot was drawn using R script. The differences in beta diversity at 5 and 9 weeks of age were evaluated by principal coordinates analysis (PCoA) based on unweighted UniFrac distance, a classical multidimensional scaling (cMDScale) analysis method (Ramette, 2007). Sample two-dimensional sorting graphs of PCoA were drawn by R script, and the significance of the differences was evaluated by adonis analysis. The number of common and unique ASVs between groups was shown by a Venn diagram. At the level of taxonomic composition, species at 5 and 9 weeks of age in each group was displayed at the phylum and genus levels to understand the overall microbial composition. At the genus level, the UPGMA algorithm was carried out to perform hierarchical clustering analysis based on the Bray-Curtis distance matrix to show the similarity of the microbial composition among groups. Linear discriminant analysis (LDA) effect size (LEfSe) analysis, a nonparametric Kruskal-Wallis and Wilcoxon rank sum test combined with LDA effect size (Segata et al., 2011), was applied to explore the difference between groups at 5 and 9 weeks of age, and measure the changes in microbiota during the development of obesity and ECD treatment. An LDA value distribution histogram was used to show the species significantly enriched and their degree of importance. A cladogram was constructed to display the taxonomic hierarchical distribution of biomarkers in each group. Random forest analysis was applied to show the order of importance of biomarkers among groups at 9 weeks of age. The functional potential was predicted and analyzed based on Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt) 2. The abundance of secondary functional pathways in the KEGG pathway database (http:// www.genome.jp/kegg/pathway.html) was calculated for gut microbiota of 9-week-old rats. The functional units were identified by PCoA based on Bray-Curtis similarity, and differential metabolic pathways were predicted metagenomeSeq. Spearman correlation analysis was used to determine the correlation between biomarkers differential metabolic pathways. A heat map was constructed

to investigate the potential relationship between the biomarkers and host phenotype.

The raw sequences of Miseq sequences from 44 fecal samples of rats have been submitted to NCBI Project under accession number PRJNA686642 with NCBI Sequence Read Archive under accession number SRP298569.

SCFAs Analysis

The targeted metabolism technology, ultraperformance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS), was used to quantitatively detect SCFAs in the cecal contents of L, Z, and EC groups (Metabo-Profile, Shanghai, China). According to the manufacturer's protocol, approximately 10 mg of sample was put in a 1.5 ml tube, and 25 µL of water and 185 µL of acetonitrile:methanol (8:2) was added to extract metabolites. After high-speed centrifugation (18,000 g, 20 min), 15 µL of internal standard was added to the 135 µL supernatant, which was aliquoted and diluted. UPLC-MS/MS (Waters ACQUITY UPLC-Xevo TQ-S, Waters Corp., Milford, MA, United States) was used for SCFA detection. TargetLynx software (Waters Corp., Milford, MA, United States) was used to process the original data files generated by UPLC-MS/MS, and the peaks of each metabolite were integrated, calibrated, and quantified. Partial least squares discrimination analysis (PLS-DA) was applied to show the composition of SCFAs among groups. Integrated Metabolomic Analysis Platform v1.0 (Metabo-Profile, Shanghai, China) was used for statistical analysis. A heat map was constructed to show the potential relationship between the biomarker and host phenotype.

Statistical Analysis

The data of ZDF rat phenotypes was expressed as means \pm standard error of the mean (SEM). The statistical differences between groups were evaluated by analysis of variance (ANOVA) using GraphPad Prism 8.0 software (GraphPad, La Jolla, CA, United States), and the specific analysis method is shown in the legend of each figure. ImageJ v1.8.0 (Rawak Software Inc., Stuttgart, Germany) was used to analyze the number and cross-sectional area of adipocytes in WAT. The target protein bands were quantified with ImageQuant TL 1D software (GE Healthcare, United States). Spearman correlation analysis was conducted to evaluate correlations between the biomarkers in gut microbiota and SCFAs and host phenotype. Significant differences were accepted at p values of <0.05.

RESULTS

The Chemical Composition of ECD

A characteristic HPLC chromatogram of an ECD sample is shown in **Figure 1**. ECD contained four compounds, liquiritin, hesperidin, glycyrrhizic acid, and 6-gingerol, which are flavonoids, saponins, and phenols, and is basically consistent with the results of previous studies (Lee et al., 2020). UHPLC-ESI-Q-TOF-MS total ion chromatogram and results of ECD sample are shown in **Supplementary Figure 1** and **Supplementary Table 2**. One hundred and twenty-six compounds in the

positive ion mode and 20 compounds in the negative ion mode were detected, including naringin and 8-gingerol that were not detected by HPLC. Nobiletin was found in the positive ion mode, and five compounds were found in both the positive ion and negative ion mode. Previous studies have predicted that hesperidin, naringin, nobiletin, glycyrrhizic acid, and 6-gingerol might be the main bioactive components and medicinal material bases of ECD intervention in metabolic diseases (Lee et al., 2018).

ECD Delayed the Development of Obesity in ZDF Rats

To observe the effects of ECD on obesity in ZDF rats, we compared the changes of body weight, abdominal circumference, and food intake in the five groups. The results revealed that the difference of body weight age-dependently increased in group Z comparison to group L. ECD treatment notably reduced the body weight of rats at 8 weeks old. At 9 weeks of age, the body weight gain compared with the baseline of the ECD-treated groups was significantly lower than that of group Z (Figures 2A,B). The weekly changes in abdominal circumference showed the same trend as that of body weight, with ECD treatment at 7 weeks of age significantly reducing the enlarged abdominal circumference (Figure 2C), which illustrated that ECD had intervention effects on abdominal obesity. However, the intervention effect of ECD was not realized through the control of food intake (Figure 2D).

Insulin sensitivity was evaluated by ITT at 9 weeks of age. The results revealed a higher blood glucose level at each time point and AUC in group Z, while ECD treatment effectively improved insulin sensitivity (**Figures 2E,F**). Additionally, fasting serum insulin levels and HOMA-IR indexes increased significantly in group Z, while ECD treatment attenuated IR of ZDF rats (**Figures 2G,H**).

The fat body ratio and blood lipids were standardized at the end of the experiment. The results showed an obvious increase of fat body ratio and various indexes of blood lipids in group Z. ECD markedly reduced epididymal and total fat body ratio, serum LDL-C, and TG (Figures 2I,J), indicating that ECD could regulate abnormal lipid metabolism *in vivo*. These data illustrated that ECD could effectively prevent and treat obesity and improve IR and lipid metabolism disorders in ZDF rats as expected.

The dose used in group EC-M is a clinically effective dose, which had basically same effect while less negative impact on liver and kidney function of rats compared with group EC-H (mainly manifested in significantly elevated ALT and more notably higher Cr level in group EC-H, as shown in **Supplementary Figure 2**). Therefore, EC-M was taken as the representative of treatment groups for subsequent studies.

ECD Improved Insulin Signal Transduction and Decreased Lipolysis in WAT of ZDF Rats

WAT stores TG as an energy reserve and provides energy to tissues in the form of FFA. In pathological conditions, excessive

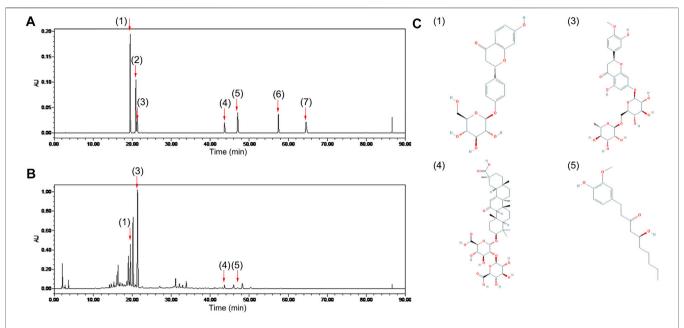


FIGURE 1 | Chemical composition of ECD. Chromatogram of (A) mixed standards and (B) ECD sample by HPLC. (C) Chemical structures of four components in ECD sample. 1) liquiritin, 2) naringin, 3) hesperidin, 4) glycyrrhizic acid, 5) 6-gingerol, 6) 8-gingerol, 7) 10-gingerol in each figure.

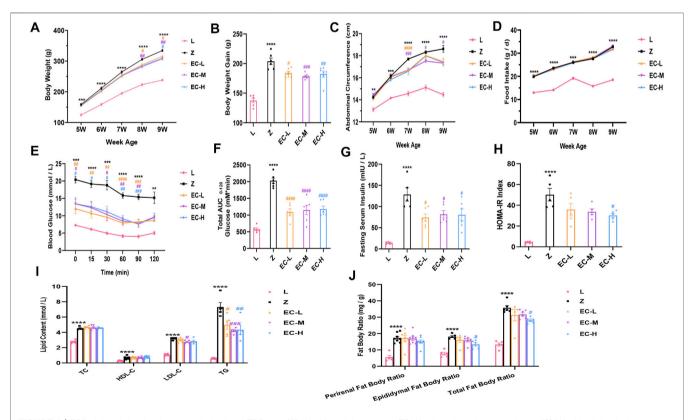


FIGURE 2 | ECD delayed the development of obesity in ZDF rats. **(A)** Weekly weight change. **(B)** Weight gain at 9 weeks of age. **(C)** Weekly abdominal circumference change. **(D)** Weekly food intake change. **(E)** Blood glucose levels during ITT. **(F)** AUC based on ITT data. **(G)** Fasting serum insulin levels. **(H)** HOMA-IR index. **(I)** Perirenal, epididymal, and total fat body ratios. **(J)** Serum TC, HDL-C, LDL-C, and TG levels at 9 weeks of age. Data are expressed as means \pm SEM (n = 5-8. Z vs. L, "p < 0.001, ""p < 0.001, ""p < 0.0001; EC-L, EC-M, and EC-H vs. Z, "p < 0.05, "#p < 0.001, "###p < 0.0001). **(A)**, **(C)**, **(D)**, and **(E)** were analyzed by two-way ANOVA, the rest were analyzed by one-way ANOVA.

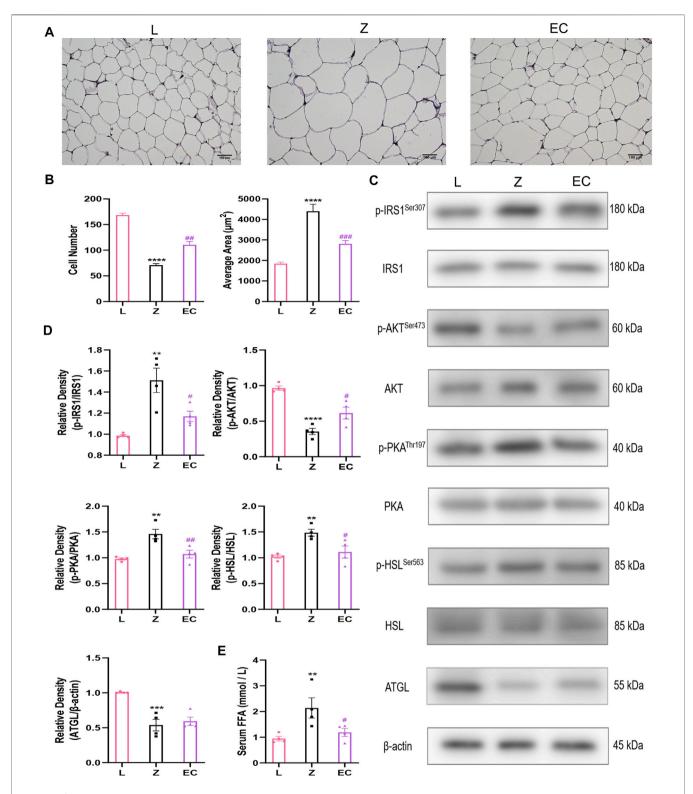


FIGURE 3 | ECD improved insulin signal transduction and decreased lipolysis in WAT of ZDF rats. **(A)** Representative image (bar: 100 μ M) and **(B)** number and average area of adipocytes of WAT HE staining (n=3. Z vs. L, ****p<0.001; EC vs. Z, *#p<0.001, *##p<0.001). **(C)** Representative bands and **(D)** relative protein expression of p-IRS1/IRS1, p-AKT/AKT, p-PKA/PKA, p-HSL/HSL, and ATGL. **(E)** Serum FFA concentration (n=4. Z vs. L, **p<0.01, ****p<0.001, ****p<0.001; EC vs. Z, *p<0.05, *#p<0.01). (B), (D), and (E) were analyzed by one-way ANOVA.

lipolysis is a characteristic pathological change of obesity. At the histological level, HE staining results showed that the adipocytes in group L were uniform in size, clear in boundary and tightly arranged. However, in the same field of vision, the number of adipocytes decreased, the diameter and cross-sectional area of adipocytes increased in group Z, while ECD treatment increased the number of adipocytes, reduced the area of adipocytes tended to be normal (**Figures 3A,B**). Insulin has an important regulatory effect on lipolysis. It activates insulin signaling by binding to receptors on adipocytes and regulates downstream PKA activity. HSL, a key enzyme in the process of hydrolyzing diacylglycerol into glycerol and FFA, is an important target for PKA control. The expressions of p-IRS1/IRS1, p-AKT/AKT, p-PKA/PKA, and p-HSL/HSL in the epididymal WAT of ZDF rats were determined by western blotting to explore the underlying effect of ECD on lipolysis. The results showed that there were no significant changes in total protein levels of IRS1, AKT, PKA, or HSL levels in the three groups. However, we observed the differences in phosphorylation with a significant increase in p-IRS1/IRS1, p-PKA/PKA, and p-HSL/HSL levels downregulation of the level of p-AKT/AKT in group Z. Compared with group Z, ECD could regulate the phosphorylation status of these molecules in the opposite direction, thereby improve significantly the activity. ATGL is the rate-limiting enzyme which decomposes triacylglycerols to diacylglycerol, which provides substrate for HSL. Contrary to HSL, its activity does not seem to be regulated by phosphorylation (Zimmermann et al., 2004). Therefore, the expression of ATGL protein was also measured. Compared with group L, ATGL protein content in group Z was notably reduced, but ECD did not modify it. These results suggested that there might be abnormal lipolysis in WAT of ZDF rats, and the effect of ECD on the lipolysis relied more on the improvement of IRS1/AKT/ PKA/HSL signaling pathway rather than on a direct regulation of HSL or ATGL (Figures 3C,D). The regulation of insulin on ATGL is not mediated by AKT (Yin et al., 2019) or PKA (Zimmermann et al., 2004), which may explain why ECD had no effect on ATGL. The level of lipolysis affects the content of FFA in the circulation. Thus, we compared the concentrations of fasting serum FFA in three groups to confirm the effect of ECD on lipolytic function of ZDF rats. Compared with group L, the FFA concentration of group Z increased, while ECD treatment significantly reduced the FFA concentration of ZDF rats (Figure 3E). The above results indicated that there were abnormal cell morphology and excessive lipolysis in WAT of ZDF rats, and ECD could possess protective effect on the morphology of adipocytes and reduce the release of FFA from excessive lipolysis of WAT by interfering with insulin signal transduction, which might be related to the improvement of IRS1/AKT/PKA/HSL signaling pathway.

ECD Modulated the Overall Structure and Composition of Gut Microbiota in ZDF Rats

To explore whether the biological effects of ECD were related to changes in gut microbiota, an important target for the development of obesity, fecal samples from rats at 5 and

9 weeks of age were collected and the 16S-V3V4 regions of the gut microbiota were pair-end sequenced using the Illumina high-throughput sequencing platform. A total of 1,610,611 sequences were gathered after denoising, and 1,113,709 high-quality sequences were obtained after quality control from 44 samples. The 17,692 sequence abundances of each sample ensured that all samples were analyzed at the same level of sequencing depth after leveling.

We first assessed the changes in the structure of gut microbiota of rats. At 5 weeks of age, the Simpson index of ZDF rats was no different from that of the control. While at 9 weeks of age, the Simpson index of group Z was significantly higher than that of L, ECD intervention significantly reduced this index and changed the alpha diversity of gut microbiota in ZDF rats (Figure 4A). PCoA based on unweighted UniFrac distance (Figure 4B) illustrated that the bacterial structure of groups Z and L were separated significantly at 5 weeks of age. With the development of obesity, the bacterial structure of group Z changed (Z-5W vs. Z-9W: $R^2 = 0.322,165$, p = 0.002), and the difference between groups Z and L was more obvious at 9 weeks of age (L-5W vs. Z-5W: R^2 = $0.127,367, p = 0.002 < L-9W \text{ vs. } Z-9W: R^2 = 0.321,536, p = 0.001).$ ECD also gradually changed the bacterial structure of ZDF rats (EC-5W vs. EC-9W: $R^2 = 0.361,867$, p = 0.002). At 9 weeks, the bacterial structures of EC and Z groups could be distinguished significantly (Z-5W vs. EC-5W: $R^2 = 0.061437$, p = 0.701 < Z-9Wvs. EC-9W: $R^2 = 0.238,092, p = 0.001$).

We further observed the changes in the composition of gut microbiota of rats. We found that from 5 to 9 weeks of age, the shared ASVs between groups L and Z decreased from 890 to 312, and those between groups Z and EC decreased from 1,237 to 689 (Figure 4C), indicating that both the development of obesity and the intervention of ECD might cause some changes in the composition of rat gut microbiota. The top 10 phyla and top 15 genera in relative abundance of fecal microbiota in each group of rats at 5 and 9 weeks old are shown in Figures 4D,E, respectively. Firmicutes and Bacteroidetes were the two main phyla, followed by Proteobacteria and Actinobacteria, which was similar to the situation of human gut microbiota. At the genus level, Lactobacillus was the dominant genus in all stages of rats in each group. Hierarchical clustering analysis of the top 10 abundant genera of gut microbiota of each group at the two stages showed that the microbial composition of the EC group was similar to that of group Z at 5 weeks of age, while at 9 weeks of age, the microbial composition of the EC group was more similar to that of group L due to the intervention of ECD (Figure 4F). These results indicated that ECD gradually regulated the overall structure and genus composition of gut microbiota in ZDF rats.

ECD Regulated the Abundance of Biomarkers at the Genus Level of Gut Microbiota in ZDF Rats

To detect biomarkers at the genus level, we compared horizontally the composition of gut microbiota among three groups at 5 and 9 weeks of age, and compared vertically the changes of gut microbiota of each group from 5 to 9 weeks of age. The gut microbiota changed significantly with the development

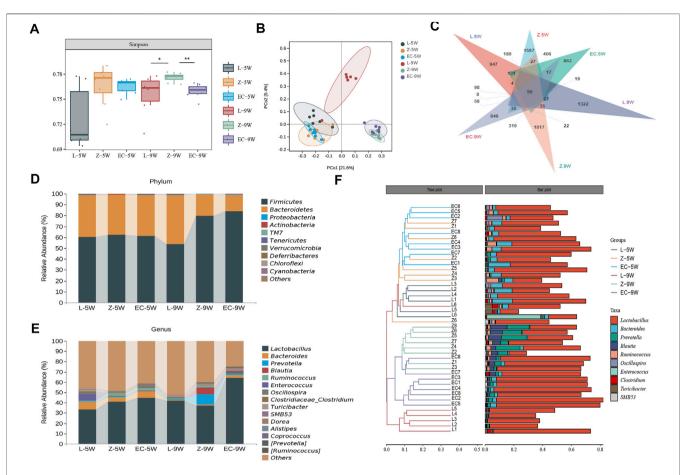


FIGURE 4 | ECD modulated the overall structure and composition of gut microbiota in ZDF rats. Gut microbiota among groups at 5 and 9 weeks of age. **(A)** Simpson diversity. The Kruskal-Wallis rank sum test and Dunnett's test were used as *post hoc* tests to verify the significance of the difference. *p < 0.05, *p < 0.01. **(B)** PCoA based on unweighted UniFrac distance. The ellipse confidence was 0.95. **(C)** ASV Venn diagram. **(D, E)** Gut microbiota composition at phylum and genus levels. **(F)** Hierarchical clustering analysis at the genus level. The left panel is a hierarchical clustering tree diagram and the right is a stacked column chart of genera.

of obesity and ECD treatment were explored. We found that the differences of gut microbiota at genus level were not significant at 5 weeks of age. However, from 5 to 9 weeks, the promotion of nine genera (Prevotella, Blautia, Dorea, SMB53, Allobaculum, Coprobacillus, [Ruminococcus], Holdemania, and Sutterella) and the reduction of five genera (Akkermansia, Oscillospira, Adlercreutzia. Dehalobacterium, f_Erysipelotrichaceae_g_Clostridium) were established during the development of obesity, which had a significant difference in group Z comparison to L at 9 weeks of age, implying the potential relevance of these genera to obesity progression (Supplementary Table 3). At the same time, ECD treatment gradually changed the relative abundance of four genera mentioned above, including decreasing Prevotella, Blautia, Coprobacillus and Holdemania, and increasing Akkermansia. In addition, ECD also gradually reduced the amount of Ruminococcus. At 9 weeks of age, the relative abundance of these genera in group EC were markedly different from group Z and tended to a normal level, which are the bacterial targets of ECD. LDA value distribution histogram and corresponding cladogram were used to show microbiota and their taxonomic

hierarchies with significant differences between groups at 9 weeks of age (**Figures 5A,B**). The relative abundances of ECD intervention biomarkers are shown in **Figure 5C**, and their LDA and *p* values are shown in **Supplementary Table 4**. The importance order of these genera is shown by random forest analysis. In particular, *Prevotella, Ruminococcus, Blautia* and *Holdemania* have a greater impact on the formation of differences among groups (**Figure 5D**).

ECD Regulated the Function of Gut Microbiota in ZDF Rats

To observe whether the changes in the composition of gut microbiota further leads to functional changes, we further carried out the prediction of the function of microbiota, and detected the changes in the content of important microbiota metabolites, SCFAs. The function of gut microbiota in 9-week-old rats was mainly focused on genetic information processing and metabolism, especially energy metabolism and the metabolism of the three major energy substances, amino acids, carbohydrates, and lipid (Figure 6A). However, PCoA showed that there was a certain

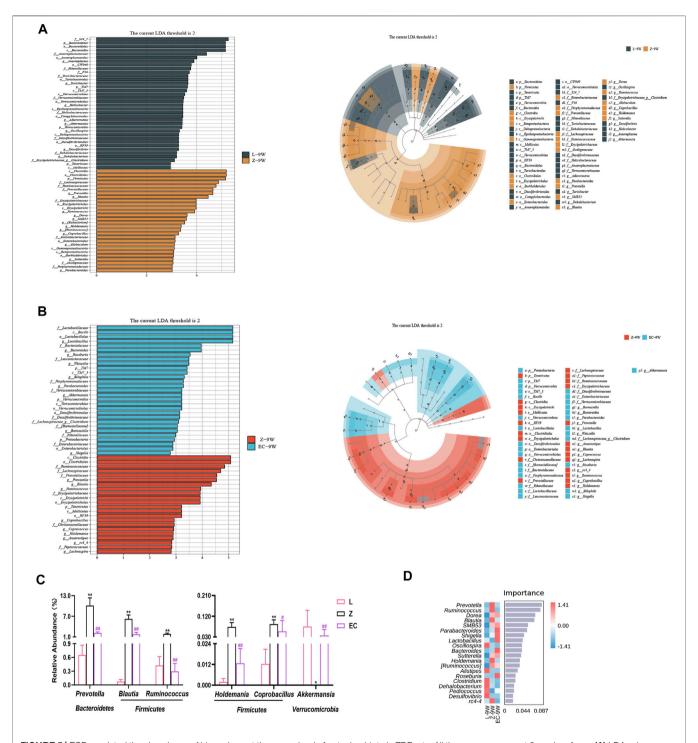


FIGURE 5 | ECD regulated the abundance of biomarkers at the genus level of gut microbiota in ZDF rats. All three groups were at 9 weeks of age. (A) LDA value distribution histogram and cladogram of biomarkers between groups L and Z. (B) LDA value distribution histogram and cladogram of biomarkers between groups Z and EC. LDA score threshold >2 in (A) and (B). (C) Relative abundances of *Prevotella*, *Blautia*, *Ruminococcus*, *Holdemania*, *Coprobacillus*, and *Akkermansia* among three groups. The *p*-value was determined by LEfSe analysis. (D) Random forest analysis of differential gut microbiota. The intensity of colors represents the abundance distribution of gut microbiota in each sample (red, the corresponding abundance was higher; blue, the corresponding abundance was lower).

separation of microbial functions among the three groups in rats. In the PC1 dimension, the functional composition of the EC group was more similar to that of group L, with a contribution rate of 51%

(**Figure 6B**). There were significant differences in eight signaling pathways, including the insulin signaling pathway (*ko04910*) (**Figure 6C**). Its abundance was significantly positively correlated

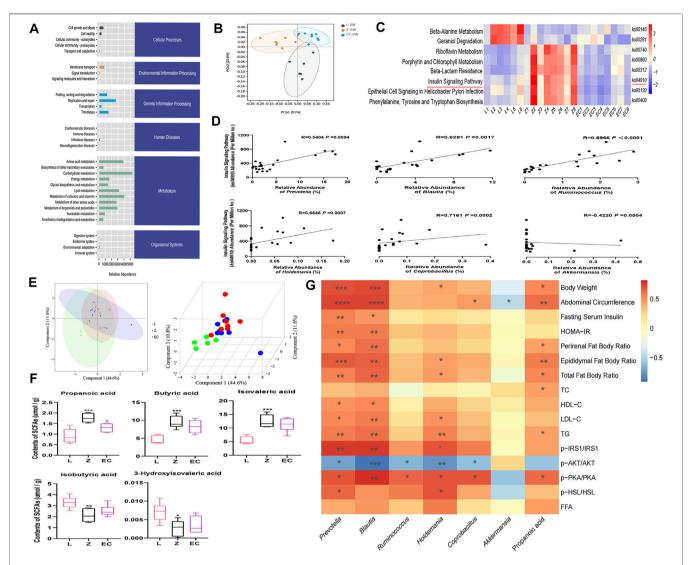


FIGURE 6 | ECD regulated the function of gut microbiota in ZDF rats. All three groups were at 9 weeks of age. **(A)** The abundance of KEGG functional pathways at the secondary classification level of gut microbiota. **(B)** PCoA of gut microbiota functional units based on Bray-Curtis similarity. The ellipse confidence was 0.95. **(C)** Different metabolic pathways of gut microbiota. The intensity of colors represents the degree of association between gut microbiota and signaling pathways in each sample (red, strong correlation; blue, low correlation). **(D)** Correlation analysis between *Prevotella*, *Blautia*, *Ruminococcus*, *Holdemania*, *Coprobacillus*, *Akkermansia*, and the insulin signaling pathway (ko04910). **(E)** 2D and 3D PLS-DA of SCFAs. **(F)** Contents of propionic, butyric, isovaleric, isobutyric, and 3-hydroxyisovaleric acid in cecal contents. The differences were analyzed by one-way ANOVA (Z vs. L, *p < 0.05, "p < 0.01, "p < 0.001; EC vs. Z, *p < 0.05). **(G)** Correlation between microbial and SCFA biomarkers and host phenotype. The panel shows the associations of six different genera and propionic acid with obesity, IR and lipid metabolism disorder phenotypes, and expression of the IRS1/AKT/PKA/HSL signaling pathway. Color intensity represents the degree of association (red, positive correlation; blue, negative correlation). *p < 0.05, "p < 0.01, "p < 0.001, "p < 0.001. Except (F) p = 5–8, the rest p = 6–8.

with the relative abundance of *Prevotella*, *Blautia*, *Ruminococcus*, *Holdemania*, and *Coprobacillus* (**Figure 6D**), implying a potential role for these ECD intervention biomarkers. The metabolites secreted, modified, and degraded by gut microbiota are important mediators of the host-microbiota dialogue, which participate in the regulation of host metabolism. SCFAs are metabolites that have a high concentration in the cecum, and mainly include acetic acid, propionic acid, and butyric acid. The metabolism of SCFAs in the cecum of groups at 9 weeks of age was analyzed. The results showed that ZDF and ZL rats were separated in their composition of SCFAs (**Figure 6E**). Compared with group L, there were significant changes

in the contents of five SCFAs in group Z, among which propionic, butyric, and isovaleric acid were notably increased, while isobutyric and 3-hydroxyisovaleric acid were obviously reduced. ECD treatment significantly reduced propionic acid and tended to reduce butyric and isovaleric acid while raising isobutyric and 3-hydroxyisovaleric acid in the cecum of rats (Figure 6F). Prevotella (De Vadder et al., 2016), Blautia (Reichardt et al., 2014) and Ruminococcus (Krautkramer et al., 2020) strains have been reported to produce propionic acid by fermentation. Therefore, ECD might reduce the abundance of these bacteria to reduce the content of propionic acid. Acetic acid is the fermentation product of

most intestinal bacteria. Butyric acid- and propionic acid-producing bacteria were almost different, which explains why there were no differences in acetic acid among the groups or a significant change in the content of butyric acid after the intervention.

ECD significantly improved IR and lipid metabolism disorders, especially in WAT of ZDF rats. Therefore, we analyzed the correlation between the six core genera and propionic acid, which changed after ECD intervention, and host phenotype (Figure 6G). We observed that Prevotella and Blautia were not only markedly correlated positively with obesity phenotypes such as body weight and abdominal circumference, but also with pathological manifestations such as IR and abnormal lipid metabolism, while Holdemania was mainly associated positively with lipid metabolism disorder-related indexes. Prevotella, Blautia, Ruminococcus, Holdemania, and Coprobacillus also showed different degrees of correlation with the expression of the IRS1/AKT/PKA/ HSL signaling pathway in WAT. In addition, the content of the gut microbiota metabolite propionic acid was significantly positively correlated with body weight, abdominal circumference, and phenotypes related to lipid metabolism disorders. These results revealed a potentially close relationship between the host phenotype and biomarkers, especially Prevotella, Blautia, Holdemania, and propionic acid. These might be important targets for ECD to improve obesity, especially lipid metabolism disorders via gut microbiota. The regulation of the insulin signaling pathway might also play an important role.

DISCUSSION

In this study, we found for the first time that ECD changes the composition and function of gut microbiota in ZDF rats, which led them towards a healthier state. Interestingly, the changes in gut microbiota induced by ECD intervention were closely related to the improvement of IR and lipid metabolism disorders, especially in WAT, indicating that the beneficial effects of ECD on obesity, especially lipid metabolism disorders, were related to the regulation of gut microbiota in ZDF rats.

ZDF rats are characterized by obesity, IR, and hyperlipidemia due to mutations in the extracellular region of the leptin receptor (Habegger et al., 2014). Compared with traditional dietary model, this animal model has a shorter time interval and is stable, which makes it ideal to study obesity. We found that ECD treatment could help the negative effects of obesity, including weight loss, improvements in IR, and the regulation of dyslipidemia, which is consistent with previous studies (Gao et al., 2015; Zhang et al., 2017; Ding et al., 2018; Zhang et al., 2020b; Lee et al., 2020) and illustrates that ECD has a regulatory effect on obesity caused by genetic factors. However, the regulatory effects of ECD on TC and HDL-C in blood lipids are not currently consistent, which might be related to the different models and drug concentrations.

Previous studies have investigated the biological effects by which ECD modulates metabolism. ECD can promote the expression of CDKAL1 and improve the function of islet cells, thereby ameliorating insulin secretion (Gao et al., 2015). Moreover, the intervention effects by which ECD improves lipid metabolism include the inflammatory response (Lee et al., 2020) and lipid

transport (Ding et al., 2018). The lipid metabolic balance is the result of a combination of lipogenesis and lipolysis. Studies have found that ECD upregulates the expression of peroxisome proliferator-activated receptor gamma (PPARy) in visceral fat and skeletal muscle and lipoprotein lipase (LPL) in skeletal muscle (Zhang et al., 2020b), and reduces the lipid accumulation caused by IR by inhibiting the expression of IRS1 phosphorylation in the liver (Zhang et al., 2017). Adipose tissue is an important target organ for the treatment of obesity (Kusminski et al., 2016), as it expands in obese individuals. Due to homeostatic regulation and continuous low-level inflammation (Shiau et al., 2019), excessive fat leads to lipolysis, resulting in FFA releases to the circulation and liver, skeletal muscle, pancreas, and other tissues, which leads to lipid toxicity and IR throughout the body. In particular, visceral adipocyte hypertrophy results in decreased insulin sensitivity, a weakened insulin anti-lipolytic effect, and enhanced lipolytic activity in adipocytes (Roden and Shulman, 2019). Studies have found that the anti-lipolytic effect of insulin can be adjusted through the AKT/PKA/HSL signaling pathway (Yin et al., 2019), and inhibiting excessive lipolysis of adipose tissue (Park et al., 2020) is an important way to treat metabolic diseases. Consistent with previous results, we found that adipocytes expanded, IRS1 phosphorylation increased, AKT activity decreased, and insulin signal transduction was impaired, while PKA-mediated HSL activity was upregulated and the ability to release FFA into the circulation was enhanced in the WAT of ZDF rats. ECD not only changed the histological morphology, but also improved lipolysis in WAT by modulating the IRS1/AKT/ PKA/HSL signaling pathway and reverting it to normal. Under the condition of basically the same food intake and calories, ECD changed the weight of ZDF rats, which might be related to the increase of energy consumption. Both previous studies and our studies have shown that ECD could improve the metabolic regulation of adipose tissue, which might be accompanied by changes in the function of mitochondria in adipose tissue, because the location (Brestoff et al., 2020) and activity (Joffin et al., 2021) of mitochondria in adipose tissue play a key role in the homeostasis of lipid metabolism.

Host genetics affect the composition of gut microbiota (Goodrich et al., 2014), and gut microbiota in turn regulate host energy homeostasis and glucose and lipid metabolism (Tremaroli and Backhed, 2012). In addition, environmental factors also importantly affect the gut microbiota (Rothschild et al., 2018). Many studies have revealed a close underlying connection between changes in gut microbiota and the occurrence and development of obesity. Targeting gut microbiota could improve insulin sensitivity (Udayappan et al., 2016), thereby regulating insulin-mediated lipid metabolism in adipocytes (Kimura et al., 2013) and improving host obesity. In our previous work, we observed the effects of fecal microbiota transplantation on the progression of obesity-susceptible diabetic mellitus (Zhang L. et al., 2020) and dynamic changes in fecal microbiota in the diabetic mellitus stage of ZDF rats (Zhou et al., 2019). We revealed a potential role for the gut microbial structure and composition in the disease progression of ZDF rats. At the same time, we found that the traditional Chinese medicine formula,

ECD could delay the development of obesity in ZDF rats. Based on this, here we investigated the intervention effect of ECD on gut microbiota in the obesity stage of ZDF rats. We found that ECD reversed the changed diversity, adjusted the overall structure, and shifted the composition of gut microbiota at the genus level to render them normal during the development of obesity, especially the relative abundances of Prevotella, Blautia, Ruminococcus, Holdemania, Coprobacillus, and Akkermansia in ZDF rats. Current studies indicate that the association of Prevotella and Blautia with host health or disease status is controversial. Some researchers believe that increased Prevotella abundance can promote glycogen storage (Kovatcheva-Datchary et al., 2015) and produce succinic acid to activate intestinal gluconeogenesis, which is related to the improvement of glucose metabolism and insulin tolerance (De Vadder et al., 2016). However, some studies have found that *Prevotella* can participate in the biosynthesis of branched-chain amino acids, which is an important risk factor for the decreased insulin sensitivity, glucose tolerance, and the occurrence of type 2 diabetes (De Filippis et al., 2019). In addition, high levels of Prevotella can activate immune and stromal cells to release more inflammatory mediators, promote chronic inflammation (Larsen, 2017), and participate in the disease process. In obese (Si et al., 2017) and non-alcoholic fatty liver disease (Zhu et al., 2013; Schwimmer et al., 2019) individuals, Prevotella is significantly enriched. We found that ECD intervention reduced the elevated Prevotella in ZDF rats, and in addition to insulin resistance, Prevotella abundance was markedly positively correlated with lipid metabolism disorders, while previous studies focused on carbohydrate and amino acid metabolic pathways (Petersen et al., 2017). Blautia is an important SCFA producing bacteria (Liu et al., 2015), with anti-inflammatory effects (Benítez-Páez et al., 2020) that aid in the recovery of intestinal mucosal damage (Zhou et al., 2017); it is inversely associated with visceral fat content (Ozato et al., 2019) and plays a beneficial therapeutic role in metabolic disorders (Rodriguez et al., 2020). However, some studies have suggested that higher Blautia is associated with increased intestinal permeability (Leclercq et al., 2014), and its abundance is positively correlated with metabolic diseases and related to cardiovascular disease predictors such as plasma glutamate and branched-chain amino acids (Ottosson et al., 2018). In metabolic diseases such as obesity (Stanislawski et al., 2017), diabetes (Egshatyan et al., 2016; Wei et al., 2018), and nonalcoholic steatohepatitis (Del Chierico et al., 2017), the abundance of Blautia is increased. This might be related to the decrease in the abundance of other SCFA producing bacteria (Becker et al., 2011), or the result of inflammatory responses in different disease stages (Tuovinen et al., 2013). Our results indicated that ECD reduced Blautia, which was remarkably enriched in ZDF rats, and its abundance was significantly positively correlated with the negative effects of insulin sensitivity and lipid metabolism. Ruminococcus can degrade resistant starches (Ze et al., 2012), thereby increasing intestinal energy absorption, which promotes weight gain in individuals (Cotillard et al., 2013). It also affects intestinal health by promoting oxidative stress (Hall et al., 2017) and

inflammatory responses (Rajilić-Stojanović et al., 2015; van den Munckhof et al., 2018), and is considered to be related to negative human health consequences (Hills et al., 2019). ECD reduced the relative abundance of this genus. Members of the Erysipelotrichaceae family are closely related to clinical indicators of impaired glucose and lipid metabolism and are important targets of metabolic diseases (Kaakoush, 2015; Lippert et al., 2017). Both Holdemania and Coprobacillus are members of the Erysipelotrichaceae family. Holdemania is related to the occurrence of inflammatory reaction (Barandouzi et al., 2020; Jang et al., 2020), elevated in patients with type 1 diabetes (Biassoni et al., 2020), and is considered to be a predictor of hypertension (Hsu et al., 2020). Coprobacillus is an important butyric acid producer and can be cross-fed with Anaerostipes, Roseburia, and Bifidobacterium to maintain butyric acid concentrations in the colon (Muthuramalingam et al., 2020). It affects intestinal function and mediates related intestinal diseases (Kassinen et al., 2007) through the inflammatory response (Shi et al., 2018; Seo et al., 2019). Its abundance is also positively correlated with the expression of immune function related genes (Elderman et al., 2018). Through the influence of lipid metabolism (Kim et al., 2018), its abundance in the intestines of obese animals and humans is increased (Wang et al., 2018; Terzo et al., 2020). ECD effectively reduced the relative abundance of these two genera of Erysipelotrichaceae in ZDF rats, and we found that the relative abundance of Holdemania was significantly and positively correlated with abnormal lipid metabolism. Akkermansia is currently one of the most widely studied probiotics, and it might be suitable for treating metabolic syndrome. It can improve metabolic disorders in obese animals and humans, including decreased insulin sensitivity and glucose and lipid metabolism disorders (Anhê et al., 2015; Dao et al., 2016; Depommier et al., 2019). It restores intestinal barrier function (Desai et al., 2016) through the immunomodulatory effect of cell membrane protein AMUC-1100 binding to toll-like receptor 2 (Plovier et al., 2017) reducing macrophage infiltration, proinflammatory cytokines, and chemokine expression, therefore reducing the risk of cardiovascular disease (Li et al., 2016). ECD increased the relative abundance of Akkermansia that was decreased in ZDF rats. The inconsistency of current research results is not only related to differences in disease states, animal models, interventions, diets, etc., but also indicates that effects of microbiota cannot be generalized simply as beneficial or harmful. Differences at the species level might lead to different results, and disease phenotypes are often only related to a small number of strains (Truong et al., 2017). Therefore, it is necessary to further explore the changes of specific strains under each genus in future research.

Gut microbiota is an important endogenous factor in regulating WAT browning (Li et al., 2017) and brown adipose tissue activity (Quan et al., 2020), and it can regulate WAT inflammation (Virtue et al., 2019) and affect WAT function. Studies have showed that intestinal barrier injury in obese individuals can lead to the translocation of intestinal flora or flora components (Anhê et al., 2020), and the

number of bacteria in adipose tissue is related to immune cell infiltration, inflammation, and metabolic indicators, which affect the metabolic health of obese individuals (Massier et al., 2020). Treatment with obesity-related harmful strains increases the hypertrophy of adipocytes in obese mice, resulting in decreased insulin sensitivity and increased lipolysis in adipose tissue (Keskitalo et al., 2018). We found that the relative abundances of Prevotella, Blautia, and Holdemania were not only clearly positively correlated with the host phenotype, but also with the expression of the IRS1/ AKT/PKA/HSL signaling pathway in WAT, suggesting that Prevotella, Blautia, and Holdemania might be important targets for ECD to enhance insulin sensitivity, thereby reducing excessive lipolysis in WAT of ZDF rats. However, the specific mechanism is still unclear, which is a direction worthy of attention in future research.

This study is the first to examine gut microbiota targets of ECD intervention. In addition to gut microbiota, their metabolite SCFAs may be an important pathway for exerting their metabolic effects (De Vadder et al., 2014). Although SCFAs are related to metabolism, the role of SCFAs in energy homeostasis is ambiguous at present (Canfora et al., 2015). Some animal and human studies have shown that obesity is associated with high levels of SCFAs (Freeland and Wolever, 2010; Kim et al., 2019). Gut microbiota ferment undigested carbohydrates (such as resistant starch and dietary fiber) and proteins in the small intestine to produce SCFAs, which increases energy absorption and then de novo synthesis of lipids and glucose in the whole body, providing about 10% of an individual's energy requirements, potentially leading to obesity (Turnbaugh et al., 2006). Consistently, propionic and butyric acid, the two most important SCFAs, increased significantly in the cecal contents of 9-week-old ZDF rats. This change might be the result of an increase in intestinal bacteria producing these two SCFAs or a decrease in bacteria utilizing them in the intestinal tract of ZDF rats. The changes may also be related to the fermentation or utilization rates of different gut microbiota, microbial cross-feeding, mucosal absorption and transport rate and other complex factors (Schwiertz et al., 2010; Fernandes et al., 2014). Studies have shown that butyric acid is the main energy source for intestinal epithelial cells and can increase lipid synthesis (Birt et al., 2013). The presence of propionic acid in feces is related to increased risk of type 2 diabetes (Sanna et al., 2019). Furthermore, both propionic and butyric acid can stimulate lipolysis in adipocytes (Rumberger et al., 2014). We found that the content of propionic acid was significantly positively correlated with the phenotypes of obesity and lipid metabolism disorders. Decreased propionic acid content could be used as an independent predictor of the improvement of insulin sensitivity (Tirosh et al., 2019). ECD administration reduced the concentration of propionic acid in ZDF rats, possibly by adjusting the gut microbiota to change the content of fermentation products. Studies have shown that Blautia strains ferment the deoxy sugars rhamnose and fucose to form propionic acid through the propylene glycol pathway (Reichardt et al., 2014). Prevotella (De Vadder et al., 2016) and

Ruminococcus (Krautkramer et al., 2020) produce succinate, an intermediate product of propionic acid, through the succinate pathway. Therefore, propionic acid might be an important medium for gut microbiota of ECD intervention and a subject for future research. Different SCFAs might exert their biological effects through synergy and antagonism (Li et al., 2020). In addition, the content of SCFAs in different intestinal segments is different (Cummings et al., 1987), and SCFAs in circulation are more closely related to peripheral insulin sensitivity, systemic lipolysis, and metabolic health (Müller et al., 2019). Therefore, the regulatory effect of ECD on SCFAs still needs to be further explored.

In conclusion, we found that ECD could regulate lipid metabolism, improve lipolysis in WAT, and modulate the composition and function of gut microbiota in ZDF rats. There was a significant correlation between biomarkers and host phenotype, suggesting that the beneficial effects of ECD on obesity, especially lipid metabolism disorders, were related to the modulation of gut microbiota. The limitations of this research were that, first of all, isoflurane anesthesia may aggravate the pre-existing IR (Fang et al., 2020), thereby affecting the judgment of the degree of IR in ZDF rats. Secondly, genetic levels and even more molecular experiments may be required to confirm the complex crosstalk among molecules for the changes in the lipolytic function of WAT. Moreover, the dietary factors cannot be ignored. The dietary components of ZL and ZDF rats were different (Supplementary Table 1), and the food intake of ZDF rats was much higher than that of ZL rats (Figure 2D), which led to different types and amounts of substrates fermented by gut microbiota, resulting in metabolic differences (Makki et al., 2018). Finally, the causal relationship between the regulation of gut microbiota by ECD and the improvement of lipid metabolism remains to be further explored.

CONCLUSION

We found that ECD delayed the development of obesity, inhibited excessive lipolysis by improving the activity of the IRS1/AKT/PKA/HSL signaling pathway in WAT of ZDF rats. In addition, ECD had an impact on the composition and function of obesity-related gut microbiota, reduced the content of *Prevotella*, *Blautia*, and *Holdemania*, and the metabolite propionic acid. These biomarkers were significantly positively correlated with host obesity phenotype, especially lipid metabolism disorders. This study provides new insights into the role of ECD in improving obesity and regulating lipid metabolism disorders via gut microbiota and helps to further clarify the mechanism of ECD in the treatment of obesity.

DATA AVAILABILITY STATEMENT

The raw sequences of Miseq sequences from 44 fecal samples of rats have been submitted to NCBI Project under accession number PRJNA686642 with NCBI Sequence Read Archive under accession number SRP298569.

ETHICS STATEMENT

The animal study was reviewed and approved by the recommendations of Guide for the Care and Use of Laboratory Animals.

AUTHOR CONTRIBUTIONS

LZ (2nd author) and SL designed and supervised the study, and provided guidance on data analysis and article writing. ZW completed the compound chemical composition test of compound. TZ, WZ, WC, and JL conducted the animal trial and sample collection. TZ performed staining and molecular experiment, conducted data analysis, figure and chart production, and completed the article writing. LZ (6th author) provided suggestions for experiment implementation and article writing. CZ provided assistance in the production of heat map. All authors approved the final article.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.647529/full#supplementary-material

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GLOSSARY

AKT protein kinase B

ALT alanine aminotransferase

ANOVA analysis of variance

AST aspartate aminotransferase

 ${\bf ASVs}$ amplitude sequence variables

ATGL adipose triglyceride lipase

AUC area under the curve

BUN blood urea nitrogen

Cr creatinine

ECD Erchen Decoction

FFA free fatty acids

HDL-C high-density lipoprotein cholesterol

HE hematoxylin-eosin

HOMA-IR homeostasis model assessment-insulin resistance

HPLC high performance liquid chromatography

HSL hormone-sensitive triglyceride lipase

IR insulin resistance

IRS1 insulin receptor substrate 1

ITT insulin tolerance test

LDA linear discriminant analysis

LDL-C low-density lipoprotein cholesterol

LEfSe LDA effect size

PCoA principal coordinates analysis

PKA protein kinase A

PLS-DA partial least squares discrimination analysis

SCFAs short-chain fatty acids

SEM standard error of the mean

TC total cholesterol

TG triglycerides

UHPLC-ESI-Q-TOF-MS ultraperformance liquid chromatographyelectrospray ionization-quadrupole-time of flight-mass spectrometry

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WAT white adipose tissue

ZDF rats Zucker diabetic fatty rats

ZL rats Zucker lean rats





Metabolomics Reveals the Mechanisms for the Pulmonary Toxicity of Siegesbeckia orientalis L. and the Toxicity-Reducing Effect of Processing

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Siegesbeckia orientalis L. (SO) is a commonly used Chinese medicinal herb. It has long been used as a remedy in traditional Chinese medicine (TCM) for symptoms that resemble inflammatory joint disorders. However, it is slightly toxic. According to the TCM theory, processing can reduce the toxicity of the herbs. Here, we performed metabolomics to determine whether processing with rice wine reduces the toxicity of raw SO, and to explore the mechanisms underlying the raw SO-induced toxicity and the toxicity-reducing effect of processing. Our results showed that raw SO has long-term toxicity in rats. It significantly elevated the serum level of LDH and caused histopathological damages in the lung tissues. It is worth noting that the LDH level in the PSO group was lower than that in the raw SO group, and the damages in lung tissues were relatively mild in PSO-treated rats, suggesting that processing reduces the pulmonary toxicity of the raw. Moreover, a total of 32 significantly changed metabolites were identified. Based on the MetaboAnalyst pathway analysis, we found that two characteristic metabolic pathways including alanine, aspartate and glutamate metabolism and glycerophospholipid metabolism were only changed in the raw SO group, while histidine metabolism was only changed in the PSO group, which suggests that induction of oxidative stress contributes to raw SO-induced pulmonary toxicity, and free radical scavenging might be responsible for the toxicity-reducing effect of processing. Our data shed new light on how raw SO induces pulmonary toxicity and how the toxicity can be reduced by processing. This study not only provides scientific justifications for the traditional processing theory of SO, but also helps to optimize the processing protocol and the clinical drug combination of SO.

Keywords: Siegesbeckia orientalis L., processing with rice wine, pulmonary toxicity, metabolomics, oxidative stress

INTRODUCTION

Siegesbeckia orientalis L. (SO), a traditional Chinese medicinal herb, was recorded to be able to eliminate the wind-dampness and soothe painful joints (the State Commission of Chinese Pharmacopoeia, 2020), and to be slightly toxic in Xinxiu Bencao (657-659 A.D., Tang Dynasty in China). SO is commonly used in managing traditional Chinese medicine (TCM) symptoms that resemble joint inflammatory disorders such as rheumatoid arthritis (RA). Chemical studies have revealed that SO contains terpenoids, glycosides, etc. Toxicological studies have demonstrated that the water extract of SO has acute toxicity in animals (Guan et al., 2007). In addition, reversible pulmonary toxicity of SO is observed in a subacute toxicity study in mice (Guan et al., 2008). SO is used as a long-term drug for treating chronic diseases such as RA and hypertension in clinical practice. However, up to now, the longterm toxicity of SO remains unknown, and the mechanisms underlying the raw SO-induced toxicity is still not fully

Raw Chinese medicinal herbs are subjected to processing before they are used for clinical prescriptions or for preparing proprietary Chinese medicines. According to the TCM theory, processing can reduce the toxicity of the herbs. As recorded in Chinese Pharmacopoeia, SO is usually processed with rice wine. In our previous study, we have demonstrated that PSO is less toxic than raw SO as demonstrated in our tested human embryonic lung cells (MRC-9) (Su et al., 2014). However, up to now, the underlying toxicity-reducing mechanisms of processing are not known.

Chinese medical herbs have multiple chemical components and the multi-target nature (Yu et al., 2012), hence, using conventional research approaches such as biochemical and histological analyses to elucidate the mechanisms for herbal toxicities and the toxicityreducing effect of processing have limitations. Metabolomics is a systematic approach for analyzing the small-molecule metabolites using various analytical methods, it can figure out the biological implications of the metabolites using bioinformatics means, and it has emerged as a powerful approach for this kind of studies (Tan et al., 2014). Here, for the first time, we explored the mechanisms underlying the raw SO-induced pulmonary toxicities and the toxicity-reducing effect of processing using metabolomics.

MATERIALS AND METHODS

Chemicals and Reagents

Raw SO (the dried aerial part of *Siegesbeckia orientalis* L.) was collected from Ganzhou (Jiangxi province, China). Rice wine was purchased from Zhejiang Tapai Shaoxing Wine Co., Ltd. (Zhejiang province, China). LC–MS grade acetonitrile, methanol, and formic acid (FA) were purchased from CNW Technologies (Germany). Kirenol was purchased from Shanghai Yuanye Bio-Technology Co., Ltd. (Shanghai,

China). Adonitol was purchased from Sigma-Aldrich (MO, United States). Milli-Q water was prepared using a Milli-Q system (Millipore, MA, United States). The commercial kits including creatine kinase (CK), lactate dehydrogenase (LDH), urea, aspartate aminotransferase (AST), and alanine aminotransferase (ALT) were purchased from Shenzhen Mindray Bio-Medical Electronics Co., Ltd. (Guangdong province, China). Malondialdehyde (MDA) was purchased from Nanjing Jiancheng Bioengineering Institute (Jiangsu province, China).

Preparation of Raw SO and PSO Extracts

The authentication of SO was confirmed in accordance with the corresponding monograph in CP 2020 (2020 edition of CP) by the corresponding author. Voucher specimens of raw SO (No. 20180510) and rice wine were deposited at the International Institute for Translational Chinese Medicine, Guangzhou University of Chinese Medicine.

PSO preparation: As shown in our previous study, 100 ml of rice wine (containing 15% ethanol): water/20:80 (v/v) was sprayed onto 100 g SO and allowed to be completely absorbed in a covered container for 1.5 h. Subsequently, the mixture was steamed for 5 h, cooled, and then dried at 40°C in a Memmert UFE500 oven (Su et al., 2014).

Raw SO and PSO extracts preparation: Raw SO or PSO (500 g) was reflux-extracted twice with water (1:10, w/v) for 2 h each. The combined extracts were filtered after cooling and then concentrated under reduced pressure to remove the water. The powdered SO (yield: 18.5%) and PSO (yield: 14.9%) extracts were obtained by lyophilizing of the concentrated samples with a VirTis Freeze Dryer (The VirTis Company, New York, United States). Powdered SO or PSO was dissolved in water to prepare raw SO and PSO solution. Detailed information of the high performance liquid chromatography (HPLC) analysis was shown in Supplementary Materials. Results showed that the contents of kirenol in raw SO and PSO were 0.13 and 0.07%, respectively (Supplementary Figure S1).

Animals and Treatments

A total of 24 male SD rats (200 \pm 20 g, 6–8 weeks) were obtained from the Laboratory Animal Center of Southern Medical University License number: SCXK (GZ)2016-0041; Guangzhou, China] and kept in the animal laboratory [License number: SYXK (GZ) 2019-0144] at the International Institute for Translational Chinese Medicine, Guangzhou University of Chinese Medicine (Guangzhou, China). Animal experiments were approved by the Guangzhou University of Chinese Medicine Animal Care and Use Committee (Guangzhou, China) and conducted according to the ethical standards and national guidelines. Every effort was made to reduce the number of animals used and minimize their pain and distress. After one week of acclimatization, rats were randomly divided into three groups (n = 8), and daily intragastrically administered an equal volume of the vehicle, raw SO or PSO extract at a dosage of 5 g/kg/day for 6 months. The experimental design was shown in Supplementary Figure S2.

Animal Sample Preparation

Blood samples were collected from the retro-orbital venous plexus each month. The blood samples were centrifuged at 3500 rpm for 10 min after standing for 2 h at 4°C. The serum was then transferred into new tubes and stored at -80°C for further analysis. A portion of the collected serum was used for routine biochemical analyses of the creatine kinase (CK), lactate dehydrogenase (LDH), urea, aspartate transaminase (AST), alanine transaminase (ALT), and plasma malondialdehyde (MDA) levels according to the manufacturer's instructions of the respective commercial assay kits. At the end of the experiment, all rats were sacrificed followed by blood collection. Fresh cardiac, hepatic, lung, and renal tissues were dissected and fixed in 10% neutral buffered formaldehyde at 4°C for paraffin embedment. Organ samples (4 µm) were sectioned and stained with H&E, and finally examined under light microscopy.

100 μ L of serum was transferred and 400 μ L extract solution (acetonitrile: methanol = 1:1) containing internal standard (adonitol, 1 μ g/ml) was added. After 30 s vortex, samples were sonicated for 5 min in an ice-water bath. Then the samples were incubated at -40° C for 1 h and centrifuged at 10,000 rpm for 15 min at 4°C. 400 μ L of supernatant was transferred to a fresh tube and dried in a vacuum concentrator at 37°C. Then, the dried samples were reconstituted in 100 μ L of 50% acetonitrile by sonication on ice for 10 min. The constitution was then centrifuged at 13000 rpm for 15 min at 4°C, and 60 μ L of supernatant was transferred to a fresh glass vial for LC/MS analysis. The quality control (QC) sample was prepared by mixing an equal aliquot of the supernatants from all the samples.

LC-TOF-MS/MS Analyses

The UHPLC separation was carried out using an ExionLC Infinity series UHPLC System (AB Sciex), equipped with a UPLC BEH Amide column (2.1 \times 100 mm, 1.7 µm, Waters). The mobile phase consisted of 25 mmol/L ammonium acetate and 25 mmol/L ammonia hydroxide in water A) and acetonitrile B). The analysis was carried with an elution gradient as follows: 0–0.5 min, 95%B; 0.5–7.0 min, 95%–65% B; 7.0–8.0 min, 65%–40% B; 8.0–9.0 min, 40% B; 9.0–9.1 min, 40–95% B; 9.1–12.0 min, 95% B. The column temperature was 25°C. The auto-sampler temperature was 4°C, and the injection volume was 2 µL (pos) or 3 µL (neg), respectively.

The TripleTOF 5600 mass spectrometry (AB Sciex) was used for its ability to acquire MS/MS spectra on an information-dependent basis (IDA) during an LC/MS experiment. In this mode, the acquisition software (Analyst TF 1.7, AB Sciex) continuously evaluates the full scan survey MS data as it collects and triggers the acquisition of MS/MS spectra depending on preselected criteria. In each cycle, the most intensive 12 precursor ions with intensity above 100 were chosen for MS/MS at collision energy (CE) of 30 eV. The cycle time was 0.56 s. ESI source conditions were set as following: gas 1 as 60 psi, gas 2 as 60 psi, curtain gas as 35 psi, source temperature as 600°C, declustering potential as 60 V, and ion spray voltage floating (ISVF) as 5,000 V or -4,000 V in positive or negative modes, respectively.

Sequence Analysis

The pooled quality control (QC) sample was analyzed at the beginning, the end, and randomly through the analytical run to monitor the stability of sequence analysis. The typical batch sequence of serum samples consisting of consecutive analysis cycles of 1 QC serum sample (at the beginning of the study) follow by 8 unknown serum samples. Meanwhile, samples were analyzed in a random order for a normal good practice. An identical sequence was repeated to complete the total set of injections (n = 28, including QCs) analyzed in less than one day per mode.

LC-MS Data Processing

Rat serum samples were analyzed by an untargeted metabolomics approach based on UPLC-Q-TOF/MS. The MS raw data (.wiff) files were converted to the mzXML format by ProteoWizard, and processed by R package XCMS (version 3.2). Principle component analysis (PCA) and orthogonal projection to latent structures discriminant analysis (OPLS-DA) were used to assess the data. Major metabolites were screened and identified using in-house libraries and the METLIN (http://metlin.scripps.edu) database, the MassBank database (http://www.massbank.jp/), the Human Metabolome Database (HMDB) (http://www.hmdb.ca/), or the LipidMaps database (http://www.lipidmaps.org) based on accurate mass measurements (mass errors <5 ppm) and MS/MS fragment information.

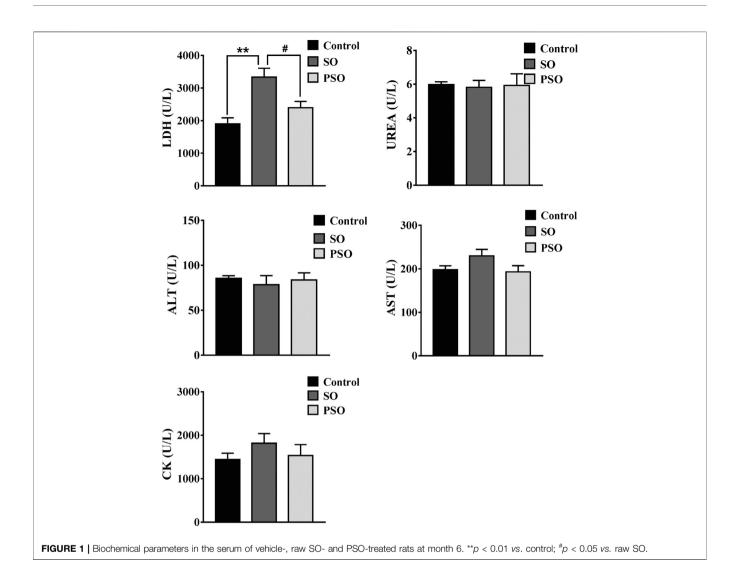
Statistical Analysis

Results of the biochemical assays were presented as Mean \pm SEM. These data were analyzed by one-way ANOVA followed by the Dunnett's multiple comparisons using GraphPad Prism version 7.0 (GraphPad Software, San Diego, CA, United States). p < 0.05 was considered statistically significant.

RESULTS

Biochemical Changes

The serum levels of AST, ALT, Urea, CK, and LDH were measured in each rat every month. ALT and AST are the markers of hepatic damage; Urea is a marker of renal damage; CK is a marker of cardiac damage. However, currently, no specific markers were used for evaluating the lung damage. It is known when an organ is damaged, LDH will be released into the circulation, which is known as a biomarker for tissue damage. Moreover, it has also been reported that the measurement of LDH activity in lung lavage fluid can assess the extent of cell damage (Gao et al., 2013). Here, we found that the serum level of LDH in raw SO group was significantly higher than that in the control group after 6-months treatment (p < 0.01). It is worth noting that, the LDH level in the PSO group was lower than that in the raw SO group (p < 0.05) (Figure 1), suggesting that processing significantly reduced the LDH level in the serum. Although raw SO increased the levels of CK and AST in the serum when compared to the control groups, they did not reach statistical significance. In addition, we also found that both



raw SO and PSO did not significantly affect the serum levels of ALT, AST, Urea, and CK in the earlier stage of the treatment, suggesting that the treatments at the early stage have no obvious liver, kidney and heart toxicities were observed in these rats (Supplementary Figure S3).

Histopathological Changes

H&E staining was used to further examine the treatment-induced toxicities in heart, liver, lung, and kidney tissues. We found that histopathological damages were observed in the lung tissues of the raw SO-treated rats as indicated by a lot of inflammatory cells infiltration, and along with the cells edema; while, the damages were relatively mild in PSO-treated rats. Liver and heart sections showed little pathological damages in the raw SO group (Figure 2), suggesting that long-term administration of raw SO may not cause obvious damages in the liver and heart when compared to the lung. Combining the pathological examination and the biochemical results, we strongly suggest that raw SO mainly causes pulmonary toxicity, which can be significantly reduced by processing.

Identification of Differential Metabolites

Total ion chromatogram (TIC) chromatograms of the serum samples were obtained from vehicle-, raw SO-, and PSO-treated rats (Supplementary Figure S4). Metabolomics chromatograms obtained through LC-Q-TOF/MS using the ESI⁺ and ESI⁻ modes revealed distinct differences. In total, 32 altered metabolites were authentically identified, including amino acids, lipids, hydrocarbons, and nucleotides. The heatmap figure showed the detailed information (Supplementary Figure S5). Based on the information obtained from LC-Q-TOF/MS, general OPLS-DA and PCA models were calculated to detect the significantly changed metabolites (VIP>1 or p < 0.05) among the control, raw SO and PSO groups. PCA scores (PC1: 14.4%, PC2: 12.4%, PC3: 9.32%) showed that the three groups were clustered (Figure 3A). The multiple pattern recognition method of partial least squares discriminant analysis was adopted based on the basis of the metabolic changes in the three groups as revealed by TIC chromatograms. As shown in the PLS-DA scores plot (**Figure 3B**, $R_2X = 0.41$, $R_2Y = 0.841$, $Q_2 = 0.388$), we found that the distribution of each group was concentrated, and the

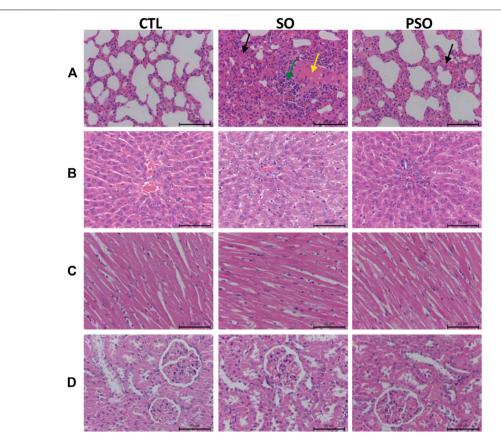


FIGURE 2 | Histopathological examinations of the lung, liver, heart, and kidney tissues in vehicle-, raw SO- and PSO-treated rats. H&E staining, 200x. (A) Lung tissue of each group: yellow arrow represents serous exudation in the alveolar cavities, green arrow represents inflammatory cell infiltration, black arrow represents the thickened alveolar septum, and the capillaries are dilated and congested; (B) liver tissue of each group; (C) heart tissue of each group; and (D) kidney tissue of each group.

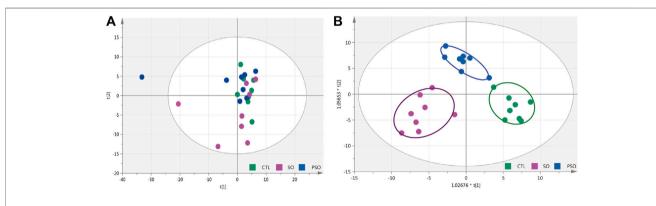


FIGURE 3 | PCA and OPLS-DA modeling were used to differentiate the rat serum metabolomic patterns after raw SO and PSO treatment. (A) PCA modeling; (B) OPLS-DA modeling. Control group (green), raw SO group (violet), and PSO group (blue).

distance between the raw SO group and control group was far, while that between the PSO group and the control group was comparatively shorter, suggesting that significant changes of the metabolites in the serum levels are shown after the administration of raw SO in rats.

As shown in **Table 1**, a total of 32 metabolites were significantly changed when compared to the control group, among them, 10 metabolites were significantly downregulated including LysoPC(20:4), LysoPC(22:6), and glucosylsphingosine, while 22 metabolites were significantly upregulated including

TABLE 1 | Significantly altered metabolites in the serum samples of vehicle-, raw SO- and PSO-treated rats. 1: upregulation; 1: downregulation; -: no significant change.

Super-pathway	Sub-pathway	No.	Metabolites	SO vs. CTL	PSO vs. CTL
Amino acid	Cysteine metabolism	1	Acetylcysteine	<u> </u>	<u></u>
	Tryptophan	2	D-Tryptophan	\downarrow	\downarrow
	Metabolism	3	L-Glutamine	1	_
	Arginine biosynthesis	4	L-Aspartic	↑	_
Lipid	Glycerophospholipid metabolism	5	Phosphorylcholine	1	_
		6	PC (16:0/16:0)	1	1
		7	PE (16:0/20:1)	1	1
		8	PE (22:5/22:6)	1	1
		9	PE (22:6/P-18:0)	↑	1
		10	PE-NMe (16:0/16:0)	↑	1
		11	PC (16:0/16:0)	1	1
		12	PC (P-18:1/18:4)	↑	1
	Lysophospholipid metabolism	13	LysoPA (18:1)	↑	_
		14	LysoPC (20:4)	\downarrow	_
		15	LysoPC (22:2)	1	1
		16	LysoPC (22:6)	\downarrow	_
		17	LysoPC (24:1)	↑	1
		18	lysoPC (26:1)	1	_
		19	LysoPE (18:1)	1	_
	Diglyceride metabolism	20	DG (20:4/18:2/0:0)	\downarrow	\downarrow
	Glycosphingolipids	21	Glucosylsphingosine	\downarrow	_
	Sphingomyelin metabolism	22	SM (d18:1/16:0)	1	1
		23	SM (d18:1/24:1)	↑	1
	Fatty acid metabolism	24	Docosahexaenoic acid	↑	_
		25	Hexadecanedioic acid	↑	_
		26	Hexadecanoic acid	↑	\downarrow
		27	Oleamide	\downarrow	1
		28	Gamma-Linolenic acid	\downarrow	\downarrow
		29	Myristic acid	\downarrow	_
Hydrocarbon	Oxidation of fatty acids	30	Vaccenyl carnitine	1	1
		31	Dodecanoylcarnitine	1	_
Nucleotide	Purine metabolism	32	Guanine	1	_

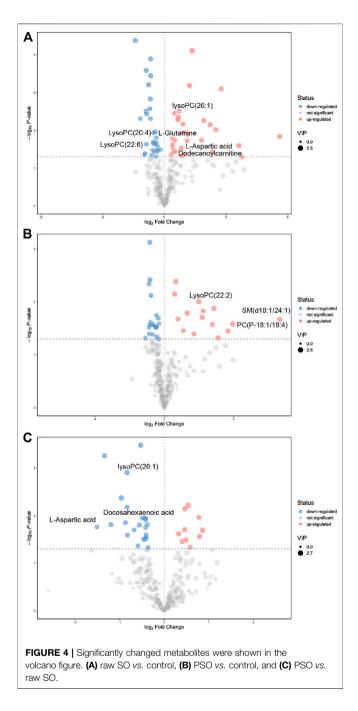
L-glutamine, L-aspartic acid, and phosphorylcholine. For the PSO group, we found that 5 metabolites were significantly downregulated including acetylcysteine, D-tryptophan, and gamma-linolenic acid, while 14 metabolites were significantly upregulated including PC (22:5/22:6). (16:0/16:0),PE(16:0/20:1), and PE Interestingly, 14 metabolites which obviously altered in the raw SO group, showed no significant differences in the PSO group, which is similar to the control group. The volcano figure can also show the metabolites fluctuation of various compounds (Figure 4). These altered metabolites may partly explain the toxicity that is caused by raw SO and the toxicity-reducing effect of processing.

Metabolic Pathway and Network Function Analyses

To further understand the correlation between the candidate metabolites and the biological association networks, we performed pathway analysis using MetaboAnalyst (https://www.metaboanalyst.ca/) pathway analysis. As shown in **Figure 5**, four significant metabolic pathways including arginine biosynthesis,

glycerophospholipid metabolism, D-glutamine, and D-glutamate metabolism, and alanine, aspartate, and glutamate metabolism were identified in the serum samples of raw SO-treated rats; while, histidine metabolism, arginine biosynthesis, and D-glutamine and D-glutamate metabolism were identified in the serum samples of PSO-treated rats.

Among them, two characteristic metabolic pathways aspartate and glutamate metabolism and glycerophospholipid metabolism were only changed in the raw SO group. It was reported that both glycerophospholipid metabolism (Wang et al., 2019) and arginine biosynthesis (Mizrahi and Warner, 2018) are closely related to oxidative stress. Therefore, we speculated that the raw SO-induced oxidative stress response may underlie the pulmonary toxicity. In addition, histidine metabolism was only changed in the PSO group. Studies suggested that histidine, an amino acid that is essential to humans, exerts favorable cytoprotective effects against oxidative stress as have been demonstrated both in vivo and in vitro, which has been shown to scavenging free radicals (Vera-Aviles et al., 2018). Hence, we speculated that free radical scavenging may be responsible for the toxicity-reducing effect of processing.



Verification of the Mechanisms Underlying the Raw SO-Induced Pulmonary Toxicity and the Toxicity-Reducing Effect of Processing

In an attempt to verify the highlighted biological functions, we examined the MDA contents in the serum samples of vehicle-, raw SO-, and PSO-treated rats. MDA, a classic biomarker of oxidative stress, is produced by free radicals in the body (Lykkesfeldt, 2007). It is also widely used as an indicator of the free radical level. As shown in **Figure 6**, we found that raw SO

treatment significantly increased the serum MDA content when compared to the vehicle control group (p < 0.05), suggesting that raw SO causes oxidative stress in the rats. While the MDA content in the PSO group was lower than that in the raw SO group (p < 0.05), and no significant difference was observed between the control and PSO groups, suggesting that processing reduces the oxidative stresscausing effects of raw SO or processing enabled the herb to possess a free radical scavenging property. These findings also suggest that free radical scavenging may be responsible for the pulmonary toxicity-reducing effect of processing.

DISCUSSION

Raw SO is toxic, studies have demonstrated that the water extract of SO has acute and subacute toxicities (Guan et al., 2007; Guan et al., 2008). However, the long-term toxicity of SO is unknown. It is worth noting that in clinical practice SO is commonly used for treating chronic diseases, such as RA and hypertension, which require long-term treatment. Therefore, it is necessary to explore the long-term toxicity of this herb. In this study, we explored the long-term toxicity of SO, and revealed the molecular mechanisms underlying the raw SO-induced toxicity. In the future, toxicity studies in the disease models will be conducted.

According to the TCM theory, processing can reduce the toxicity of the herbs. The theory has been supported by modern toxicology studies. In our previous study, PSO was demonstrated less toxic than raw SO in our tested MRC-9 cells (Su et al., 2014). However, the mechanisms of raw SO-induced toxicities and the toxicity-reducing effect of processing are still not fully understood. Here, we conducted the metabonomics study to explore the mechanisms that underlie the raw SO-induced pulmonary toxicity and the toxicity-reducing effect of processing.

In this study, a total of 32 metabolites are significantly altered including amino acids, lipids, hydrocarbons and nucleotides, they were authentically identified in the serum samples of vehicle-, raw SO-, and PSO-treated rats (**Table 1**). In the raw SO group, 22 metabolites were upregulated, while 10 metabolites were downregulated. In the PSO group, 13 metabolites were upregulated, 5 metabolites were downregulated, and the other 14 metabolites are not significantly different when compared to the healthy rats.

Among all the metabolites, 8 characteristic metabolites including L-glutamine, L-aspartic acid, phosphorylcholine, lysoPA (18:1), lysoPC (26:1), lysoPE (18:1), docosahexaenoic acid, and dodecanoylcarnitine were only upregulated in the raw SO group, and they do not show changes in the PSO group. Among them, two were amino acids. The observed changes in amino acid contents should be due to the modulation of the endogenous amino acid metabolism system, but not the loading of the exogenous amino acid. In our experiments, we had fasted the rats for 12 h before blood sample collection. The half-lives of exogenous amino acids in rats are very short (Su et al., 2016). Hence, the exogenous amino acids should have been eliminated within 12 h and cannot be detected in the serum. Glutamine is metabolized by glutaminase-1 (GLS1) to form the gas NH₃. NH₃

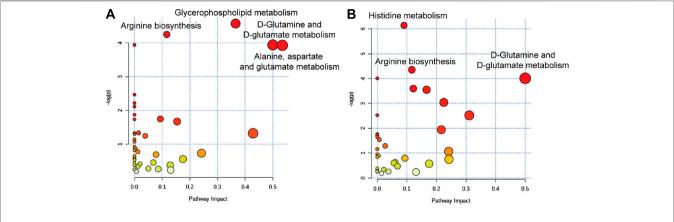
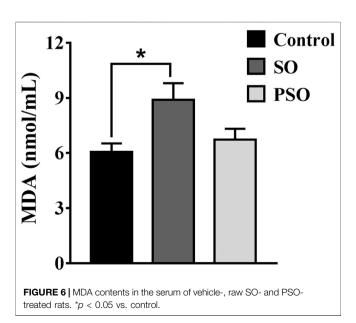


FIGURE 5 | Summary of the metabolic pathways analyzed with MetaboAnalyst software. (A) The most significantly altered pathways in the raw SO group, raw SO vs. control. (B) The most significantly altered pathways in the PSO group, PSO vs. control.

stimulated the production of mitochondrial reactive oxygen species (ROS) which causes the activation and translocation of the NF-E2related factor-2 transcription factor (Nrf2) into the nucleus, where it binds to the antioxidant responsive element (ARE) in the promoter region of the gene to trigger HO-1 transcription (Durante, 2019). It is reported that glutamine metabolism is required for collagen protein synthesis in lung fibroblasts (Hamanaka et al., 2019), and excessive proliferation of lung fibroblasts could cause lung toxicity (Huang et al., 2012). Here, in this study, we found that glutamine was only upregulated in the raw SO group, suggesting that raw SO was more toxic than PSO. Aspartic acid is an α-amino acid. The study reports that aspartic acid at high dose levels has toxicity in kidneys and salivary glands in Fischer rats (Tada et al., 2008). Docosahexaenoic acid (DHA) is a polyunsaturated ω-3 fatty acid. Some studies suggest that the elevated levels of DHA are associated with decreased risk of dementia, while, other studies reported that DHA micelles stabilized protofibrillar AB42 to prevent further fibrillization



(Hashimoto et al., 2008). Unfortunately, these protofibrils induced toxicity in PC-12 cells, suggesting that DHA may act as a double-edged sword. Depending on the context, DHA may actually exacerbate the pathology of Alzheimer's disease (Cole and Frautschy, 2006). Thus, too high or too low concentration of DHA in raw SO-treated rats may cause physiological changes. In addition, by comparing the concentration of dodecanoylcarnitine in the tissues and the urine of healthy and cancer patients, the dodecanoylcarnitine concentrations are higher in both cancer tissues (compared with the paired normal tissue) and in urine of cancer patients (compared with control urine), suggesting that dodecanoylcarnitine is highly expressed in an abnormal physiological state (Niziol et al., 2018), which also implies that raw SO treatment changes the physiological state and finally upregulated the content of dodecanoylcarnitine in the rats. Phosphorylcholine (PC), the polar headgroup of the membrane phospholipid phosphatidylcholine, which is a pro-inflammatory epitope in OxPLs and is recognized as a danger-associated molecular pattern by the innate immune system (Miller et al., 2011). Thus, elevation of this pro-inflammatory molecule in raw SO indicates that it has a strong pro-inflammatory effect, which may partly explain the toxicity that is caused by raw SO, and the reason for our observed inflammatory-cell infiltration in the lung tissues of raw SO-treated rats.

Besides the above eight metabolites that were only upregulated in the raw SO-treated group, another four metabolites were only downregulated in the raw SO group but not in the PSO group. Take glucosylsphingosine as an example, glucosylsphingosine is a key biomarker of Gaucher disease (Murugesan et al., 2016). It is believed to be responsible for macrophagic organ infiltration and the subsequent development of organomegaly, which could cause hematological and visceral changes in animals (Lukas et al., 2017). Myristic acid, is also known as tetradecanoic acid, which is a side chain of phorbol myristate acetate (PMA). It activates human polymorphonuclear leukocytes to produce oxygen radicals more potently than PMA does (Tada et al., 2009). Although the levels of these two metabolites were downregulated in the raw SO group, we know that the organism is a balanced environment, and either too high or

too low will have some effects. Whether these changes underlie the toxicity caused by raw SO deserves further investigation.

In addition, 12 metabolites including PE (16:0/20:1), PE (22:5/22:6), and PC (P-18:1/18:4) were upregulated; while, 4 metabolites including acetylcysteine, tryptophan and DG (20:4/18:2/0:0) were downregulated in both raw SO and PSO groups, which may explain the common efficacies of both raw SO and PSO.

CONCLUSION

In summary, we for the first time demonstrated that processing with rice wine significantly reduced the long-term toxicity of raw SO, which supports the TCM theory that "processing can reduce the toxicity of raw SO." Induction of oxidative stress underlies the raw SO-induced pulmonary toxicity, and free radical scavenging was, at least in part, responsible for the toxicity-reducing effect of processing. Our study sheds new light on the mechanisms underlying the raw SO-induced pulmonary toxicity and the toxicity-reducing effect of processing with rice wine. This study not only provides a scientific justification for the traditional processing theory but also should guide rational and safe clinical applications of SO by helping in optimizing its processing procedure and clinical compatibility.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**; further inquiries can be directed to the corresponding authors.

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ETHICS STATEMENT

The animal study was reviewed and approved by the Guangzhou University of Chinese Medicine Animal Care and Use Committee.

AUTHOR CONTRIBUTIONS

TJ, LL, MZ, and ZQ performed the majority experiments and analyzed the data. JS and TZ helped for the H&E examination. TS, TJ, and LL interpreted the data. GC participated in the experimental plan. TS supervised the study, drafted and finalized the manuscript. All authors have read and approved the final manuscript.

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SUPPLEMENTARY MATERIAL

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Ethnopharmacological, Phytochemical, Pharmacological, and Toxicological Review on Senna auriculata (L.) Roxb.: A Special Insight to Antidiabetic Property

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Avartaki (Senna auriculata (L.) Roxb. syn. Cassia auriculata L.; Family- Fabaceae) is a traditional medicinal plant, widely used for the treatment of various ailments in Ayurveda and Siddha system of medicine in India. Almost all the parts of the plant, such as flowers, leaves, seeds, barks, and roots have been reported for their medicinal uses. Traditionally, it has been used in the treatment of diabetes, asthma, rheumatism, dysentery, skin disease, and metabolic disorders. The principle phytochemicals in Senna auriculata (L.) Roxb. are alkaloids, anthraquinone, flavone glycosides, sugar, saponins, phenols, terpenoids, flavonoids, tannins, steroids, palmitic acid, linoleic acid, benzoic acid 2-hydroxyl methyl ester, 1-methyl butyl ester, resorcinol, α-tocopherol-β-D-mannosidase, epicatechin, ferulic acid, quercetin-3-O-rutinoside, quercetin, proanthocyanidin B1. The extracts from its different parts and their isolated compounds possess a wide range of pharmacological activities such as antidiabetic, antioxidant, anti-inflammatory, antihyperlipidemic, hepatoprotective, nephroprotective, cardioprotective, anti-atherosclerotic, anticancer, antimutagenic, antimicrobial, antiulcer, antipyretic, anthelmintic, immunomodulatory, antifertility, anti-venom, and anti-melanogenesis. The toxicological findings from preclinical studies ensured the safety of the plant, but comprehensive clinical studies are required for the safety and efficacy of the plant in humans. The current review article aimed to provide up-todate information about Senna auriculata (L.) Roxb. covering its ethnomedicinal, phytochemical, pharmacological, and toxicological aspects with special emphasis on its clinical implications in diabetes.

Keywords: Cassia auriculata L., ayurveda, antidiabetic, ethnomedicine, insulinogenic, Siddha, quercetin

INTRODUCTION

The extensive use of medicinal plants to discover new therapeutics or active pharmacological compounds is the urgent need to tackle challenging non-communicable diseases (NCDs). Around 71% of the mortality worldwide has resulted due to NCDs, including the deaths of 40 million populations worldwide per year (Naghavi et al., 2017). In India alone, 60% of the

deaths occur due to NCDs (Nethan et al., 2017). Diabetes and hypertension are the major contributory illnesses amidst the deaths caused by NCDs (Madavanakadu Devassy et al., 2020).

India has a great heritage of traditional system of medicines like Ayurveda, Siddha, and Unani, where hundreds of medicinal plants are being used to treat various diseases with their known ethnopharmacological evidence. Senna auriculata (L.) Roxb. syn. Cassia auriculata L., family Fabaceae (former Caesalpiniaceae) is one of the medicinal plants that has been used traditionally in Ayurveda, Siddha, and Unani since the 15th century. It is commonly known as Tanner's Senna/Cassia and Mature Tea Tree in English; Avartaki, Pitapuspa, Pitkalika, Manojyna, Charmaranga in Sanskrit; Tarwar, Awal, Tarval in Hindi; Tangedu, Merakatangeedu in Telagu, and Arsual, Taravada, Tarwad in Marathi. This shrub is widely spread in India, covering its southern, westerns, and central dry zones and also in Sri Lanka (Gupta and Sharma, 2007; Nille and Reddy, 2017; Win and Min, 2018).

The current review aimed to investigate the ethnomedicinal uses, phytochemical, pharmacological, and toxicological studies of the *Senna auriculata* (L.) Roxb., and endeavored to validate the experimental studies in terms of scientific data concerning the therapeutic implications of active metabolites of the plant.

METHODOLOGY

In the present review, the available literature has been explored from Ayurvedic classical texts, various published technical reports, online scientific data by accessing Scopus directory, Google Scholar, PubMed, Science Direct, EMBASE, SciFinder, Web of Science for its ethnomedicinal uses, phytochemistry, pharmacology, and biomedicinal applications. The following keywords were used: "Senna auriculata (L.) Roxb.," "Cassia auriculata L.," "Avartaki," "Avarai," "Tanner's cassia," "phytochemistry," "antihyperglycemic," "oxidative stress," "hepatoprotective," "antidiabetic," "insulinogenic," "anti-"immunomodulator," inflammatory," "antioxidant," "antihyperlipidemic," "mechanism of action" with their corresponding Medical Subject Headings (MeSH) terms using conjunctions OR/AND. The search was centered on identifying Ayurvedic claims in the available ethnomedicinal, phytochemical, pharmacological, clinical, and safety reports to understand the role of Senna auriculata (L.) Roxb. syn. Cassia auriculata L. in diabetes and other NCDs. The literature search was commenced before April 2021 and searches were limited to the English language.

BOTANICAL ASPECTS OF SENNA AURICULATA (L.) ROXB

Senna auriculata (L.) Roxb. is found in wooden grasslands up to a height of 500 m. It breeds wild in dry regions with annual precipitation of 300 mm. It grows well in areas with an annual temperature range of 15–28°C and needs full sun for its growth. It



FIGURE 1 | Flower & Leaves of Senna auriculata (L.) Roxb.

is a branched shrub with height of 1.5–5 m, trunk diameter of 20 cm and brown lenticellate bark (Kirtikar and Basu, 1918).

Leaves: Leaves are dull green in color, alternate, stipulate, paripinnate arrangement with 16–24 pairs of leaflets. Leaves are narrowly rough, pubescent and thin, with vertical and linear gland between the leaflets (Figure 1). It is short-stalked, 20–25 mm long, 10–13 mm wide; marginally overlapping, rectangular, dull-witted at both ends, and glabrous (Kirtikar and Basu, 1918; Evans, 1996).

Flowers: Flowers are bright yellow and irregular and large (50 mm) and have axillary raceme inflorescence, 2–8 flowered (Figure 1). Flowers are bisexual, zygomorphic, pentamerous, 4–5 cm; sepals are rounded at apex, imbricate; petals free, imbricate, unequal, 1.5–3 cm long; stamens 10, the 3 lower ones large stand fertile, others usually sterile; ovary superior, falcate, with 1.5 cm long, stalked, style (fruit a flattened) cylindrical pod 5–18 × 1–2 cm, transversely undulate between the 10–20 seeds, indehiscent, green turning to brown when mature (Kirtikar and Basu, 1918; Evans, 1996).

Fruits: Fruits are green or light brown, and have legume which is 7–11 cm long, 1.5 cm wide, rectangular, long style base, flat, thin, undulate crimpled (**Figure 2**). It has about 12–20 seeds per



FIGURE 2 | Fruits & Leaves of Senna auriculata (L.) Roxb.

fruit, each in its distinct cavity (Kirtikar and Basu, 1918; Evans, 1996).

TRADITIONAL AND ETHNOPHARMACOLOGICAL USES OF SENNA AURICULATA (L.) ROXB

The foremost description of the Senna auriculata (L.) Roxb. is available in Kaiyadeva Nighantu, a classical Ayurveda text (15th century), where its Pramehahara property (antidiabetic action) through different botanical parts of the plant has been mentioned. Flowers have Pramehashamana property (antidiabetic action). Tender fruits have mentioned for their Vamihara (antiemetic), Krimihara (anthelmintic), Sarvapramehahara (antidiabetic), Trishnaghna (thirst alleviating), Akshihita (eye tonic), Ruchya (appetizing) properties. Seeds are useful as Madhumehaghna (antidiabetic), Vishahara (antidote), Raktaatisaraghna (antidiarrheal). Roots are mentioned for Trishnahara (thirst alleviating), Pramehaghna (antidiabetic), Shwasaghna (antiasthamatic), Raktapittashaman (antihemorrhagic), Shukrakshayahara (sperm enhancing) properties (Sharma and Sharma, 1979). The leaf macerate of Senna auriculata (L.) Roxb. was used traditionally to treat inflammation specifically in Maharashtra, Andhra Pradesh, and Gujarat. It also effectively reduces pain and inflammation in joint disorders. The leaves of Senna auriculata (L.) Roxb. are also effective in muscle pain, irregular muscle contraction, body pain, gastritis, skin sores and ulcers. The flowers are effectively used as health beneficial agents. The crushed flowers are mixed with goat milk to cure sexually transmitted diseases. The dried powder of flowers of Senna auriculata (L.) Roxb. is used to clean the hair, and taken by diabetic patients and in fever. The root is used by chewing, and the juice is swallowed to cure abdominal complaints, vomiting, urinary discharges, tumors and diarrhea. Powder of bark is used to treat toothache by applyingit to the gums. The fruits are used in helminthic infections (Punjani, 2002; Punjani and Kumar, 2002;

Duraipandiyan et al., 2006; Pawar and Patil, 2007; Ignacimuthu et al., 2008; Kosalge and Fursule, 2009; Thirumalai et al., 2009; Patel et al., 2010; Jagatheeswari, 2012).

METABOLITES OF SENNA AURICULATA (L.) ROXB

The flower, leaves, roots and seed were investigated with advanced spectroscopic and chromatographic techniques and found various active metabolites with therapeutic implications against different diseases. The flowers of *Senna auriculata* (L.) Roxb. reported a significant amount of alkaloids, glycosides, saponins, polyphenols, tannins, phloro-tannins, terpenoids, triterpenes, carbohydrates, proteins, amino acids, anthraquinone, aloe-emodin, and sitosterols. These metabolites attributed towards the pharmacological action in diabetes mellitus and other ailments.

Leaves of Senna auriculata (L.) Roxb. shows the presence of glucose, alpha-tocopherol-beta-D 3-o-methy-d -mannosidase, n-hexadecanoic acid, resorcinol, octadecenal and carboxylic acid. The seeds of Senna auriculata (L.) Roxb. reported with presence of fatty acids content are palmitic, oleic, and linoleic acids. The ethanolic seed extract showed the presence of benzoic acid, 2-hydroxyl methyl ester, glycine, n-(trifluroacetyl), 1-methybutul ester, cupric acid ethyl ester, resorcinol, water-soluble galactomannan like beta-Dmanopyranosyl-1(1-4)-o-beta-D-manopyronosyl (1-4)-0beta-D-monopyranose. The reported metabolites have potential role in oxidative stress, microbial infections and inflammation related diseases.

Roots of *Senna auriculata* (L.) Roxb. shows the presence of anthraquinone glycosides such as 1,3-dihydroxy-2-methylanthraquinone, 1,8-dihydroxy-6-methoxy-2-methylanthraquinone-3-o-rutinoside, 1,8-dihydroxy-2-methylanthraquinone-3-o-rutinoside, flavone glycoside, and two leucoanthocyanins like leucocyanidin-3-o-

TABLE 1 | Metabolites of Senna auriculata (L.) Roxb.

No.	Name of metabolites	Isolated from a plant part	References
l.	Emodin(1)	Leaves	Nageswara Rao et al. (2000)
·.	Di-(2-ethyl)-hexylphthalate(2)	Leaves	Nageswara Rao et al. (2000)
	Phytol(3)	Leaves	Senthilkumar and Vijayakumari (2012)
	E-10- pentadecenol(4)	Leaves	Senthilkumar and Vijayakumari (2012)
	Resorcinol (5)	Leaves	Senthilkumar and Vijayakumari (2012)
	3-O-methyl-d-glucose (6)	Leaves	Senthilkumar and Vijayakumari (2012), Anandan et al. (2011)
	1,14-tetradecanediol (7)	Leaves	Senthilkumar and Vijayakumari (2012)
	3,7,11,15- tetramethyl-2-hexadecen-1-ol (8)	Leaves	Senthilkumar and Vijayakumari (2012)
	Azulene(9)	Leaves	Senthilkumar and Vijayakumari (2012)
).	1,2,3,5,6,7,8,8a-octahydro-1,4-dimethyl-7-(1-methylethenyl)	Leaves	Senthilkumar and Vijayakumari (2012)
	1,2- benzene dicarboxylic acid (10)	Leaves	Senthilkumar and Vijayakumari (2012)
	Diisooctyl ester	Leaves	Senthilkumar and Vijayakumari (2012)
3.	Squalene(11)	Leaves	Senthilkumar and Vijayakumari (2012)
	1-cyclohexylnonene (12)	Leaves	Senthilkumar and Vijayakumari (2012)
i.	1-4 - [(2- diethylamino] ethylamino[-6-methyl-2-pyrimidinyl]-3- [3,4,5- trimethoxyphenyl] guanidine (13)	Leaves	Senthilkumar and Vijayakumari (2012)
	α-tocopherol-β- d -mannoside(14)	Leaves	Anandan et al. (2011)
'. '.	n-hexadecanoic acid (15)	Leaves	Anandan et al. (2011)
3.	13-octadecenal (16)	Leaves	Anandan et al. (2011)
).).	1,2,3,4-tetrahydroisoquinolin-6-ol-1-carboxylic acid (17)	Leaves	Anandan et al. (2011)
).	Benzaldehyde (18)	Leaves	Anandan et al. (2011)
	1,6-anhydro-β-d-glucopyranose (19)	Leaves	Anandan et al. (2011)
2.	1,2-benzenedicarboxylic acid (20)	Leaves	Anandan et al. (2011)
3.	Bis (2-methylpropyl) ester	Leaves	Anandan et al. (2011)
۶. ١.	Benzenamine,2,3,4,5,6- pentamethyl (21)	Leaves	Anandan et al. (2011)
5.	13-oxabicyclo [10.1.0] tridecane(22)	Leaves	Anandan et al. (2011)
,. i.	1-tridecyne (23)	Leaves	Anandan et al. (2011)
	1- <i>E</i> ,11, <i>Z</i> -13-octadecatriene (24)	Leaves	Anandan et al. (2011)
3.	a -tocopherol (25)	Leaves	Anandan et al. (2011)
).).		Leaves	Anandan et al. (2011)
	N -acetyl tyramine(26)	Seed/Pod	
).	n -hexadecanoic acid (15)		Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
١.	Linoleic acid (27)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
	Oleic acid (28)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
2.	E, Z-1,3,12-nonadecatriene (29)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
ŀ. -	Stearic acid (30)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
5.	Benzoic acid (31)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
5.	2-hydroxyl-methyl ester (32)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
· .	β-ethoxypropionaldehyde diethyl acetal (33)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
3.	Ethyl caprylate(34)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
).	2-methoxy-4-vinylphenol (35)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
).	N -(trifluoroacetyl)-,1-methylbutyl ester	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
	2,3-dihydro-3,5-dihydroxy-6-methyl- 4 H - pyran-4-one	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
2.	Dodecanoic acid (36)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
3.	3'5'-dimethoxyacetophenone (37)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
ļ. -	Palmitic acid (38)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
5.	β-monoglyceride (39)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
3.	α-tocopherol (25)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
7.	Stigmasta-5,23-dien-3-ol (40)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
3.	Epicatechin(41)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
).	Procyanidin B1 (42)	Seed/Pod	Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011)
).	Auriculataosides-A (43)	Seed/Pod	Wang et al. (2019)
	Auriculataosides- B (44)	Seed/Pod	Wang et al. (2019)
	Rumejaposides-E (45)	Seed/Pod	Wang et al. (2019)
	Rumejaposides-F (46)	Seed/Pod	Wang et al. (2019)
	5-O-methylquercetin-7-O-glucoside (47)	Flower	Manogaran and Sulochana (2004)
5.	Propanoic acid	Flower	Venkatachalam et al. (2013)
6.	Kaempferol-3-O-rutinoside (48)	Stem	Juan-Badaturuge et al. (2011), Habtemariam (2013)
.	Rutin (49)	Stem	Juan-Badaturuge et al. (2011), Habtemariam, (2013)
3.	Kaempferol(50)	Stem	Juan-Badaturuge et al. (2011), Habtemariam (2013)
9.	Quercetin (51)	Stem	Juan-Badaturuge et al. (2011), Habtemariam (2013)
`	Luteolin(52)	Stem	Juan-Badaturuge et al. (2011), Habtemariam (2013)
Э.			
J. 1.	Glycine, N-(trifluoroacetyl)-, 1-methylbutyl ester (53)	Stem	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et a (2007), Raj et al. (2012), Puranik et al. (2011)

TABLE 1 | (Continued) Metabolites of Senna auriculata (L.) Roxb.

S No.	Name of metabolites	Isolated from a plant part	References
62.	Leucopelargonidins(54)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana, (2004)
63.	Oleanolic acid (55)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana, (2004)
64.	Chrysophanol (56)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana, (2004)
65.	1,3-dihydroxy-2-methylanthraquinone (57)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana, (2004)
66.	1,2,3,4-Tetrahydroisoquinolin-6-ol-1-carboxylic acid (58)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana, (2004)
67.	d – glucopyranoside (59)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam, (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
68.	1,6,8-trihydroxy-3-methylanthraquinone (60)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana, (2004)
69.	1-cyclohexylnonene (61)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam, (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
70.	1,8-dihydroxy-3-methoxy-6-methylanthracene-9,10-dione (62)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam, (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
71.	1,14-tetradecanediol (63)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam, (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
72.	E -10-pentadecenol (64)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
73.	3,7,11,15-tetramethyl-2-hexadecen-1-ol (65)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
74.	Sitosterol(66)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)
75.	Di-(2-ethyl) hexylphthalate(67)	Aerial Part	Juan-Badaturuge et al. (2011), Habtemariam (2013), Suresh et al. (2007), Raj et al. (2012), Puranik et al. (2011), Manogaran and Sulochana (2004)

rhamnopyroside and leucopeonidin-3-o-1-rhamanopyroside. The list of reported metabolites is enlisted in **Table 1** and **Figures 3A,B**.

PHARMACOLOGICAL ACTIONS OF SENNA AURICULATA (L.) ROXB

Antidiabetic Activity

Antihyperglycemic Activity of Plant Parts of Senna auriculata (L.) Roxb

Leaves

Antihyperglycemic activity of *Senna auriculata* (L.) Roxb. leaves extract has experimentally been proven in different diabetic animal models (Rajagopal et al., 2003; Gupta et al., 2009a; Gupta et al., 2009b; Gupta et al., 2010). The aqueous extract

of leaves of *Senna auriculata* (L.) Roxb. is reported to reduce the blood glucose levels in STZ induced diabetic rats (Gupta et al., 2011). Further, Gupta et al. (2009c) reported the potential antihyperglycemic effects of STZ induced mild and severely diabetic rats on the administration of the aqueous extract of leaves in 400 mg/kg body weight dose for 3 weeks. The 13.9% and 17.4% reduction in fasting blood glucose was observed after 5 h of dose administration in mild and severely diabetic rats respectively. The ethanolic extract of *Senna auriculata* (L.) Roxb. leaf showed significant reduction of blood glucose (p < 0.05) at a dose of 150 mg/kg of body weight for 2 weeks in alloxan induced diabetic rats. The results were compared with a standard drug, glibenclamide (Mohan et al., 2011).

The leaves of *Senna. auriculata* (L.) Roxb has various antidiabetic metabolites which are enlisted in **Table 1**. n-hexadecanoic acid, emodin (1,3,8-trihydroxy-6-methylanthracene-9,10-dione), and

squalene are evaluated for their antidiabetic potential and reported with their mechanistic pathways involved in the amelioration of diabetes (Wang et al., 2006; Wang et al., 2012; Liu et al., 2018; Tan et al., 2019). These metabolites might be responsible for the antihyperglycemic effects of leaves of *Senna auriculata* (L.) Roxb.

Flower

Aqueous extract of *Senna auriculata* (L.) Roxb. flower has shown promising antihyperglycemic activity in a dose 450 mg/kg body weight which found more significant than the doses of 150 and 300 mg/kg body weight. Similarly, the significant reduction in the urine sugar was found with aqueous extract of *Senna auriculata* (L.) Roxb. at doses of 150 and 300 mg/kg body weight whereas, at 450 mg/kg dose, sugar was absent in the urine of experimental diabetic rats. The result was more promising than glibenclamidetreated rats (Latha and Pari, 2003a; Latha and Pari, 2003b). Also, Jain and Sharma, (1997) reported the anti-diabetic potential of the aqueous flower extract of *Senna auriculata* (L.) Roxb.

The ethanol extract of *Senna auriculata* (L.) Roxb. flower possesses antidiabetic agents such as flavonoids and phenolic acids. The anti-diabetic activity of water-soluble fraction of

the ethanol extract was compared with aqueous extract of the flower where it was found that ethanol extract exhibited a more significant reduction in blood glucose level at a dose of 250 and 500 mg/kg of the body weight in alloxan-induced diabetic rats. The highly significant (p < 0.001) results of ethanol extract of the flower might be due to the metabolites present in the water-soluble fraction of the ethanolic extract (Hakkim et al., 2007). Similarly, it is observed that the ethanolic extract exhibits anti-diabetic activity and provides significant protection in streptozotocinnicotinamide induced diabetic rats (p < 0.05) and the results were statistically significant in comparison to the standard glibenclamide (Nalla et al., 2012).

Jarald et al. (2010) performed an experimental study with various extracts of flowers of *Senna auriculata* (L.) Roxb. in alloxan-induced diabetic rats to check their anti-hyperglycemic activities. Amongst different extracts, the chloroform extract was reported to have more hypoglycemic effects followed by the water-soluble fraction of ethanolic extract and ethanolic extract. The results found comparable with the standard drug, glibenclamide.

Various active compounds from the flowers of Senna auriculata (L.) Roxb. have been isolated and their potential antidiabetic activity has been reported with experimental evidence. Venkatachalam et al. (2013) reported the presence of propanoic acid, 2-(3-acetoxy-4,4,14-trimethylandrost-8-en-17yl) as an active principle of the n-butanol fraction of hydromethonolic flower extract of Senna auriculata (L.) Roxb. Propanoic acid showed potential hypoglycemic effects both in the bioassay-guided study as well as in vivo study, due to its protein tyrosine phosphatase 1B (PTP 1B) inhibitory action. The isolated phytochemical compound exerted comparable result as that of standard drug, glibenclamide. Mishra et al. (2010) and Jyothi et al. (2012) have also demonstrated the anti-diabetic potential of flowers of Senna auriculata (L.) Roxb. Oleanolic acid, a natural triterpenoid present in the aerial part of Senna auriculata (L.) Roxb. (Manogaran and Sulochana, 2004; Suresh et al., 2007; Juan-Badaturuge et al., 2011; Puranik et al., 2011; Raj et al., 2012; Habtemariam, 2013) exhibited a significant bloodglucose-lowering and weight-losing activity in STZ-induced diabetic rats (Wang et al., 2011). Further, Gao et al. (2007) reported that oleanolic acid, when administered in a dosage of 100 and 200 mg/kg body weight/day, for 40 days, showed a significant hypoglycemic effect in STZ-induced diabetic rats.

Bark

The methanolic extract of Senna auriculata (L.) Roxb. bark found effective in lowering the blood glucose level. After the administration of the bark extract to diabetic rats, it was observed that the blood glucose level reduced with a deviation of 80.9% when compared that on first day (Shiradkar et al., 2011). Moreover, Daisy and Jeeva Kani (2012) demonstrated the potent anti-diabetic effect of the methanolic extract of Senna auriculata (L.) Roxb. bark. The result was compared with hexane, ethyl acetate, and aqueous extracts where methanolic bark extract was found to be more effective in diabetic rats. Juan-Badaturuge et al. (2011) and Habtemariam (2013) reported the presence of rutin, quercetin, and kaempferol in the extracts of bark of Senna auriculata (L.) Roxb. Rutin and kaempferol have been reported to exhibit antihyperglycaemic and antioxidant activity in STZ-induced diabetic rats (Kamalakkannan and Prince, 2006; Govindasamy, 2020). Besides, quercetin has also been reported for antihyperglycemic potential due to its pleiotropic mechanisms. It showed the enhancement of insulin sensitivity, promotion of glycogen synthesis, improvement in insulin resistance by promoting its sensitization, and stimulation of pancreatic β-cell proliferation (Salehi et al., 2020). Therefore, the metabolites present in the bark may contribute to the antihyperglycemic action of the bark of Senna auriculata (L.) Roxb.

Seed

Jain and Sharma (1967) reported the antidiabetic activity of the aqueous extract of seed of *Senna auriculata* (L.) Roxb. The hypoglycemic role of the ethanolic seed extract in alloxan-induced diabetic rats has been demonstrated at a dose of 400 mg/kg body weight where the result was comparable with that of the standard drug, gliclazide. Also, the urine sugar was

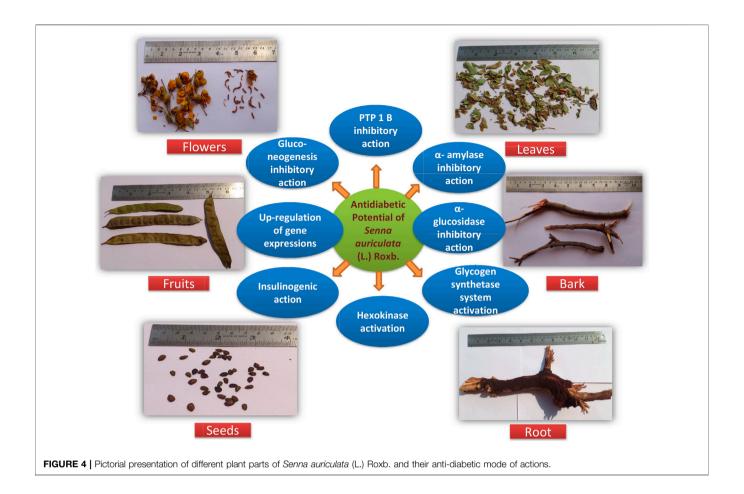
found absent in seed extract and gliclazide treated diabetic rats (Subramanian et al., 2011). Moreover, the ethanolic extract, aqueous extract, and petroleum ether fraction at a dose of 300 mg/kg body weight has reported for their significant (p < 0.001) blood-glucose-lowering activity in STZ-induced diabetic rats. The result was compared with the standard drug, metformin (250 mg/kg body weight) (Dama and Bhanoji Rao, 2011). Aruna and Roopa (2011) demonstrated the anti-diabetic potential of petroleum ether and ethyl acetate extract of Senna auriculata (L.) Roxb. seeds in alloxan-induced diabetic rats. It was found that both the extracts possess significant (p < 0.05) anti-diabetic activity when compared with the standard drug, tolbutamide (250 mg/kg body weight).

Seeds of Senna auriculata (L.) Roxb. is a rich source of antidiabetic metabolites like Linoleic acid, n -hexadecanoic acid, Oleic acid, Epicatechin, Procyanidin B1, Dodecanoic acid, Stearic acid, etc. (Suresh et al., 2007; Puranik et al., 2011; Raj et al., 2012). George et al. (2018) discussed the findings of Wu and colleagues' pooled analysis (Wu et al., 2017), where it is recommended to take increased dietary intake of linoleic acidrich vegetable foods for the prevention of diabetes. Similarly, a higher intake of linoleic acid resulted in better glycemic control and improved insulin sensitivity (Belury et al., 2018). Further, oleic acid also accounted for the prevention of Type 2 Diabetes Mellitus, where it was observed that oleic acid might have some metformin-like effects (Palomer et al., 2018). The consumption of epicatechin, a natural flavonoid found in the seeds of Senna auriculata (L.) Roxb. has been reported to reduce blood glucose levels in diabetic patients (Abdulkhaleg et al., 2017). Furthermore, procyanidin B1 (PB1) has a significant hypoglycemic action. Li et al. (2021) investigated the interaction mechanisms of PB1 with protein tyrosine phosphatase-1B (PTP1B), where a binding affinity of PTP1B to PB1 resulted in down-regulation of the expression level of PTP1B in insulin-resistant HepG2 cells. Similarly, the oral administration of graded doses of dodecanoic acid (125, 250, and 500 mg/kg) significantly reduced the fasting blood glucose level in a dose-dependent manner in hyperglycemic rats (Alex et al., 2020). Tsuchiya et al. (2013) demonstrated the role of stearic acid as a potent PTP1B inhibitor in vitro. It is suggested that stearic acid may enhance insulin receptor signaling by inhibiting the PTPB1 activity and promotes glucose uptake into adipocytes.

Although the preclinical data and pharmacological actions of various antidiabetic metabolites support each other, no clinical data is available so far. Further *in vivo* studies are expected to calibrate the antihyperglycemic role of several metabolites present in the seeds of *Senna auriculata* (L.) Roxb.

Root

Salma et al. (2021) demonstrated antihyperglycemic activity of methanolic extract of the root of *Senna auriculata* (L.) Roxb. in a high-fat diet-induced type 2 diabetes mellitus C57BL/6 mouse model. The methanolic extract (150 mg/kg body weight) could reduce the blood glucose level gradually in 8 weeks of the experiment. The results were similar when compared to a metformin-treated group of diabetic mice. The highest amount



of total polyphenols was present in the methanolic extract of root than its aqueous, ethanolic, and chloroform extracts. Further, the HPLC profile of polyphenols showed that coumaric acid is present in the methanolic extract of the root, which attributed to the antihyperglycemic activity of Senna auriculata (L.) Roxb. (Salma et al., 2021). The p-Coumaric acid, the most abundant isomer of Coumaric acid, displayed a substantial increase in the enzyme activity and improved the glucose consumption by the hepatic tissues when administered orally in STZ-induced diabetic rats. It normalizes disturbed glucose metabolism by decreasing hepatic glucose production through insulin release. Besides, it exhibited antihyperglycemic activity by protecting β-cells of the pancreas (Amalan et al., 2016). Thus, the methanolic extract of the root of Senna auriculata (L.) Roxb. may have strong antihyperglycemic effects due to the presence of coumaric acid.

Various antidiabetic metabolites present in the plant parts and their different extracts are responsible for the antihyperglycemic action. These metabolites may correct pathological changes, and further studies are needed to review their mode of action. The results were compared with available standard oral hypoglycemic agents and found significant at different levels. Altogether, all the botanical parts of *Senna auriculata* (L.) Roxb. exhibit antidiabetic activities and play a pivotal role in the correction of the

pathological mechanism by regulating the metabolic pathways, enzymatic activities, and gene expressions (Figure 4).

Insulinogenic Action

Various plant parts of *Senna auriculata* (L.) Roxb. have been reported to possess an insulinogenic action. The different extracts stimulate the insulin secretion by increasing the number of islets and β -cells and it is evidenced with the increased amount of C-peptide and histological pancreatic sections. The administration of the aqueous leaf extract of *Senna auriculata* (L.) Roxb. demonstrated the insulinogenic action in mildly and severely diabetic rats. The C-peptide level was also found increased. Pancreatic sections have confirmed the increased number of islets and β -cells. The result was similar to that of the standard drug, glibenclamide (Gupta et al., 2010).

The aqueous flower extract of *Senna auriculata* (L.) Roxb. exhibited the antihyperglycemic action by increasing the level of insulin in diabetic rats which resulted into the increased uptake of blood glucose by peripheral tissue (Pari et al., 2001). Furthermore, the water-soluble fraction of ethanolic extract of *Senna auriculata* (L.) Roxb. flower was found significantly effective (p < 0.001) than its aqueous extract (p < 0.05) in reducing the blood glucose due to its insulinogenic action in alloxan-induced diabetic rats (Hakkim et al., 2007). Kalaivani et al. (2008) reported the possibility of regeneration of β -cells in *Senna auriculata* (L.) Roxb. leaves and

flowers extracts administered diabetic rats. Moreover, oleanolic acid, an antidiabetic metabolite present in the aerial part of *Senna auriculata* (L.) Roxb. may directly improve insulin biosynthesis, secretion, and signaling by modulating the enzymes connected to insulin activities. It also protects the β -cells and preserves their functionality (Castellano et al., 2013). Similarly, Jyothi et al. (2012) reported the insulinogenic action of *Senna auriculata* (L.) Roxb. flowers.

To study insulin interaction in humans, erythrocytes have been used as a cellular model (Gambhir et al., 1978; DePirro et al., 1980; McElduff and Eastman, 1981; Ward and Harrison, 1986). Insulin binding is found to be decreased in diabetes mellitus (Kolterman et al., 1981; Olefsky and Kolterman, 1981). Pari et al. (2007) used the circulating erythrocytes to find out the insulin-receptor-binding effect of flower extract of Senna auriculata (L.) Roxb. in STZ-induced diabetic rats. It was found that the number of insulin receptors was increased on erythrocyte receptors membranes in STZ-induced diabetic control rats. The administration of flower extract resulted in increased total erythrocyte receptors membrane insulin binding sites as well as plasma insulin. Senna auriculata (L.) Roxb. flower extract stimulates insulin secretion and increases the number of insulin binding sites.

Senna auriculata (L.) Roxb. seed extract has also been reported to possess an insulinogenic action in alloxaninduced diabetic rats. The administration of seed extract resulted in increased insulin levels due to the activation of β-cells (Subramanian et al., 2011). Dodecanoic acid, also known as lauric acid, an antidiabetic metabolite, is present in the seed part of the S. auriculata. (L.) Roxb. (Suresh et al., 2007; Puranik et al., 2011; Raj et al., 2012). Alex et al. (2020) reported that dodecanoic acid (250 and 500 mg/kg body weight) stimulated the pancreatic β-cells to synthesize and secrete the insulin to maintain glucose homeostasis in a highfat diet/STZ-induced type 2 diabetic rat models. The methanolic extract of Senna auriculata (L.) Roxb. bark potentiated the levels of insulin and C-peptide in diabetic rats. The activated remnant β-cells found in histological sections of the pancreas (Daisy and Jeeva Kani, 2012). Mohan et al. (2011) also reported the insulinogenic action of ethanolic extract of S. auriculata (L.) Roxb. leaf by its insulin release stimulatory effect in alloxan-induced diabetic rats.

The various extracts of botanical parts of *Senna auriculata* (L.) Roxb. demonstrated insulinogenic action. It is due to an increased number of β -cells and regeneration and activation of remnant β -cells. Moreover, the increased level of plasma insulin is evidenced with raised C-peptide level, a part of proinsulin, and a measure of insulin secretion. The metabolites and their pleiotropic mechanisms should also be studied extensively through *in vitro* and *in vivo* studies to know the insulinogenic action of *Senna auriculata* (L.) Roxb.

Role in Carbohydrate Metabolism and Regulation of Enzymatic Activities

Liver and pancreas ailments hamper the biochemical pathways in the human body and cause deranged glucose metabolism. The liver and pancreas play a vital role in governing carbohydrate metabolism. They maintain blood glucose and also regulate blood glucose supply to other organs.

Inhibition of Alpha-Amylase and Alpha-Glucosidase Enzymes

Starch and sucrose are the main components of carbohydrates. The enzyme alpha-amylase of saliva and pancreatic juice decomposes starch into oligosaccharides. The alpha-glucosidase enzyme catalyses the cleavage of glucose from disaccharides and oligosaccharides. Hence, the use of Alpha-glucosidase inhibitors is considered one of the effective treatments of diabetes mellitus as they retard digestion of both sucrose and starch.

The alpha-amylase inhibition activity of extract of bud and flowers of *Senna auriculata* (L.) Roxb. have been revealed where the bud extract showed higher inhibition activity compared to flower extract (Nambirajan et al., 2018). Also, the hydroalcoholic extract of aerial parts of *Senna auriculata* (L.) Roxb. showed the concentration-dependent alpha-amylase inhibition activity which found better than standard drug, acarbose (Mhetre et al., 2014).

The alpha-glucosidase enzyme plays a dominant role in the digestion of the sucrose and starch and its inhibition slows down the process of carbohydrate digestion. It is reported that Senna auriculata (L.) Roxb. bud extract and Senna auriculata (L.) Roxb. flower extract possess glucosidase inhibitory activity. The concentration of the bud and flower extracts shows a direct proportion to the inhibition of α glucosidase enzyme (Nambirajan et al., 2018). Alpha-glucosidase inhibitory activity of the hydroalcoholic extract of aerial parts of Senna auriculata (L.) Roxb. was found higher than the standard acarbose (Mhetre et al., 2014). Methanol extracts of dried flowers of Senna auriculata (L.) Roxb. were found to have a potential alphaglucosidase inhibitory activity as compared to acarbose in rats. The ED₅₀ of the methanol extracts of dried flowers (4.9 mg/kg) exhibited the antihyperglycemic effect as potent as that of standard drug, acarbose (ED₅₀⁻ 3.1 mg/kg) in maltose loaded Sprague Dawley Rats (Abesundara et al., 2004).

The metabolites present in the Senna auriculata (L.) Roxb. extracts of acetone, ethanol, and water indicated the presence of flavonoids, tannins, reducing sugar, and saponins. The active components of the extracts compete with the substrate for binding to the active site of the enzyme and prevent the breaking down of oligosaccharides to disaccharides. Kwon et al. (2007a) reported that natural alpha-glucosidase inhibitors from plants inhibit alpha-glucosidase activity and can be potentially used as a safe and effective therapy for postprandial hyperglycemia. Previous studies on alpha-amylase and alpha-glucosidase inhibitors isolated from medicinal plants suggest that several potential inhibitors belong to the flavonoid class, which has features of inhibiting alpha-amylase and alpha-glucosidase activities (Kwon et al., 2007b). Senna auriculata (L.) Roxb. is a rich source of flavonoids such as kaempferol-3-O-rutinoside, kaempferol and quercetin (Juan-Badaturuge et al., 2011; Habtemariam, 2013). It was evident that kaempferol-3-O-rutinoside is a potent inhibitor of alpha-glucosidase in vitro and showed 8-folded activity than the standard drug, acarbose (Habtemariam, 2011).

Altogether, the effective inhibition of alpha-amylase and alpha-glucosidase might be due to the presence of enzyme inhibiting metabolites present in *Senna auriculata* (L.) Roxb. However, more *in vitro* and *in vivo* studies would be helpful to find out the pathways involved in the regulation of enzymatic activities.

Activation of Hexokinase

Enzymatic activity of hexokinase solely depends on insulin response and it is found affected in insulin-deficient diabetic rat liver (Gupta et al., 1997). Senna auriculata (L.) Roxb. is reported to play an important role in the activation of hexokinase in alloxan-induced diabetic rats which found resulted in increased glycolysis and glucose consumption for energy production (Krentz, 2003). The insulinogenic action of Senna auriculata (L.) Roxb. stimulates hexokinase activity which aids its role in glycolysis in all body tissues.

Inhibition of Glucose-6-Phosphatase and Fructose-1,6-Biphosphatase Enzymes

The role of Glucose-6-phosphatase and fructose-1,6-biphosphatase is also important in glucose homeostasis (Berg et al., 2001). These enzymes are known as gluconeogenic enzymes and insulin deficiency results in their activation in diabetes. It was found that the administration of *Senna auriculata* (L.) Roxb. effectively reduced the gluconeogenesis and resulted in decreased blood glucose level in diabetic rats. The augmented plasma insulin level by *Senna auriculata* (L.) Roxb. resulted in the reduced levels of glucose-6-phosphatase and fructose-1,6-biphosphatase enzymes in diabetic rats (Khader et al., 2017). Daisy and Jeeva Kani (2012) also reported the gluconeogenesis inhibitory action of *Senna auriculata* (L.) Roxb. bark extract.

Glycogen Synthesis

The healthy liver plays an important role in glycogen synthesis. It is the primary intracellular storage form of glucose and monitored by plasma insulin level and glycogen synthetase system (Garvey, 1992). The impaired capacity of the liver to synthesize glycogen was observed in diabetes due to lack of insulin. The dianthrone rich alcoholic flower extract of *Senna auriculata* (L.) Roxb. has demonstrated the increase in insulin secretion and activation of glycogen synthetase system which resulted in improved liver glycogen content (Khader et al., 2017).

Insulin deficiency in diabetes severely hampers the activities of glycolytic and gluconeogenic enzymes (Anderson and Stowring, 1973). Insulin is important for glucose uptake, phosphorylation of glucose and the glucose-6-phosphate entry into the pentose phosphate pathway in the liver (Ramachandran et al., 2003). The insulinogenic action of different extract of Senna auriculata (L.) Roxb. might be responsible for the modifications in enzymatic activities and reducing the blood glucose level (Kalaivani et al., 2008).

The flower extract of *Senna auriculata* (L.) Roxb. has also been reported for its salutary effect on hepatic enzymes involved in the carbohydrate mechanism. The flower extract (450 mg/kg body

weight) was found significant when compared with the standard drug, glibenclamide ($600 \mu g/kg$ body weight) in increasing the hexokinase activity and decreasing the gluconeogenic enzyme activity in STZ-induced diabetic rats. The increased plasma insulin level in flower extract-fed diabetic rats was responsible for the modulation of hepatic carbohydrate metabolic enzymes (Latha and Pari, 2003a; Latha and Pari, 2003b).

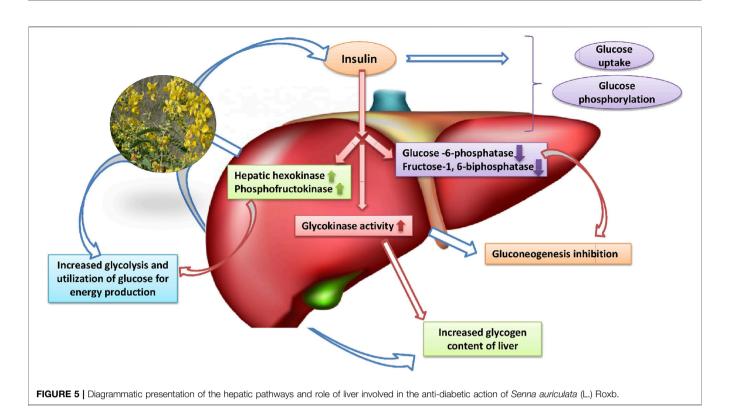
The liver glycogen level and glycogen synthetase system depend on adequate plasma insulin level. The water-soluble fraction of ethanol extract of flower of $Senna\ auriculata\ (L.)$ Roxb. significantly (p < 0.001) elevated the levels of hepatic glycogen and glycogen synthase due to its insulinogenic effects (Hakkim et al., 2007). Similarly, glucokinase, one of the key enzymes in the liver, regulate the storage and disposal of glucose. The decreased enzymatic activity of glucokinase in STZ-induced diabetic rats was found elevated with $Senna\ auriculata\ (L.)$ Roxb. bark extract treatment (Daisy and Jeeva Kani, 2012). Altogether, $Senna\ auriculata\ (L.)$ Roxb. reveals its active role in the correction of the deranged carbohydrate metabolism by regulating the various enzymatic activities in the liver (Figure 5).

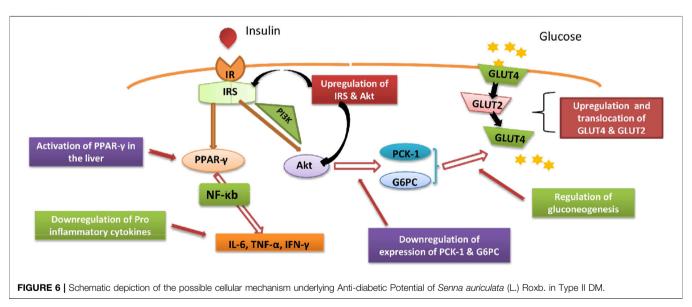
Regulation of Gene Expression in Liver

IRS-2 gene arbitrates insulin activity through the PI3K-Akt pathway in the liver (Eckstein et al., 2017). Also, IRS-2 plays a major role in suppressing gluconeogenesis and apoptosis (Valverde et al., 2004). It is found that mice lacking IRS-2 have a better chance to develop diabetes (Kubota et al., 2000). The failure in the expression of IRS-2 has observed in diabetic individuals (Gunton et al., 2005). Besides, IRS-2 gene inactivation in the human will result in peripheral insulin resistance and absence of β cell expansion which may cause hyperglycaemia, diabetes and death. Treatment with Senna auriculata (L.) Roxb. bud extract showed the upregulation of the IRS-2 gene expression in the liver (Nambirajan et al., 2018). Also, polyphenols from Senna auriculata (L.) Roxb. flowers were found able to enhance IRS-2, glucose transporters, and Akt gene expression in livers of T2DM rats (Mohd Fauzi et al., 2017) (Figure 6).

Hepatoprotective Action

The liver is a vital organ involved in the metabolism of food and drugs in the human body. The various toxicants and chemicals in the form of drugs and food result in different liver ailments. Senna auriculata (L.) Roxb. is used in liver diseases, in the traditional systems of Indian medicine. The folk claims have been validated with different experimental works. The various extracts from the leaves and root of Senna auriculata (L.) Roxb. are reported to exert a hepatoprotective role in oxidative stress-induced, ethanol and anti-tubercular-drug induced, hepatotoxicity in rats (Rajagopal et al., 2003; Jaydeokar et al., 2014), and D-galactosamine (D-GalN)-induced cytotoxicity in mouse hepatocytes (Nakamura et al., 2014). The hepatoprotective effects of methanolic extract of leaf and revertible histopathological changes in the carbon tetrachloride-induced liver damage in Wistar albino rats (Dhanasekaran and Ganapathy, 2011) have been documented. The drug

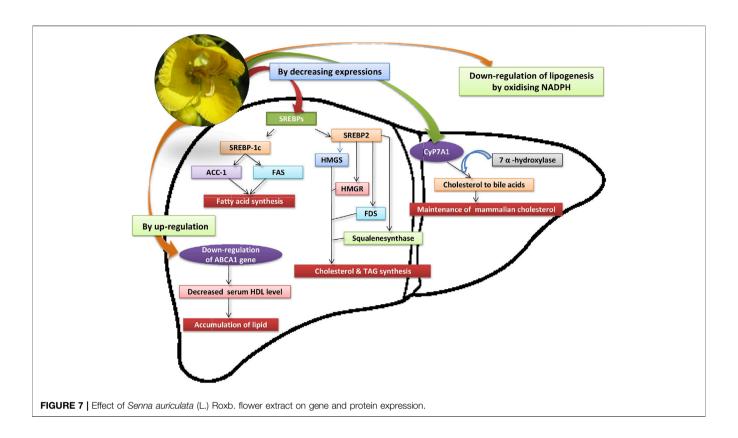




paracetamol-induced liver toxicity has also been found protected with the aqueous and methanolic extracts of the flowers of the *Senna auriculata* (L.) Roxb. (Chauhan et al., 2009).

The levels of AST and ALT were found raised in alloxaninduced diabetic rats. The oral administration of water-soluble fraction of ethanol extract of flower of *Senna auriculata* (L.) Roxb. could efficiently (p < 0.001) reduce the AST and ALT levels. Further, the increased values of acid phosphatase (ACP) and alkaline phosphatase (ALP) in alloxan-induced diabetic rats were also declined with the administration of water-soluble fraction of ethanol extract (Hakkim et al., 2007).

Taken together, these outcomes supports the traditional use of *Senna auriculata* (L.) Roxb. as a hepatoprotective agent. However, there is a need for clinical evidence to confirm and



validate the folklore claims, as human studies have not been performed so far.

Prophylactic Action on Pancreatitis

The aqueous leaf extract of Senna auriculata (L.) Roxb. demonstrated the prophylactic effect on ethanolinduced pancreatitis in a rat model. A significant reduction in the increased pancreatic enzymes such as serum α -amylase and lipase was observed at a dose of 400 mg/kg body weight. Histopathological studies also revealed normal findings in extract-treated rats (Gupta et al., 2016).

Antihyperlipidemic Action

Several phytochemical compounds have been isolated from different plant parts of *Senna auriculata* (L.) Roxb. The isolated compounds such as kaempferol-3-O-rutinoside, quercetin, rutin, and luteolin exhibit different pharmacological actions (Juan-Badaturuge et al., 2011). The antihyperlipidemic potential of crude extract and isolated compounds could be demonstrated by observing their pancreatic lipase inhibitory action. Among the isolated compounds from the aerial parts of *Senna auriculata* (L.) Roxb., kaempferol-3-O-rutinoside possesses most potential pancreatic lipase inhibitory action (IC50 = 2.9 \pm 0.50 mM) than that of rutin, luteolin and quercetin. Moreover, the crude extract of *Senna auriculata* (L.) Roxb. demonstrated inhibition of pancreatic lipase at IC50 of 6.0 \pm 1.0 mg/ml (Juan-Badaturuge et al., 2011; Habtemariam, 2013). Oleanolic acid, a metabolite present in the aerial part of *Senna auriculata* (L.)

Roxb. (Juan-Badaturuge et al., 2011), when administered in the dosage of 100 and 200 mg/kg body weight/day for 40 days, showed improved lipid profile in STZ-induced diabetic rats (Gao et al., 2007). Similarly, Vijayaraj et al. (2013) also reported the antihyperlipidemic effects of different extracts of *Senna auriculata* (L.) Roxb.

The Senna auriculata (L.) Roxb. leaves extract exhibited hypolipidemic effects by reducing cholesterol, triglycerides and LDL levels and increasing the levels of HDL in diabetic rats. The atherogenic index was also found raised indicating the cardiovascular risk preventive role of Senna auriculata (L.) Roxb. (Gupta et al., 2009c). In another study, leaves extract of Senna auriculata (L.) Roxb. has shown its reversal effects on dyslipidemia and apolipoprotein B (Gupta et al., 2011).

Furthermore, the ethanolic extract of flowers of Senna auriculata (L.) Roxb. demonstrated antihyperlipidemic effects in Triton WR 1339 (300 mg/kg body weight) induced hyperlipidemia in male albino Wistar rats. The flower extract at dose 450 mg/kg body weight/day found more significant (p < 0.001) in reducing the total cholesterol, triglyceride, and low-density lipoprotein (LDL) very-low-density lipoprotein (VLDL) levels and increasing the levels of HDL than the standard drug, lovastatin. The antihyperlipidemic effects of ethanolic extract of Senna auriculata (L.) Roxb. flowers might be exhibited due to reduced cholesterol biosynthesis by HMG-CoA reductase inhibition in the liver or by up-regulation of LDL receptors in the liver which involve in hepatic cholesterol clearance (Oh et al., 2006; Vijayaraj et al., 2013).

Similarly, in another study, the expression levels of the key genes involved in the cholesterol metabolism were examined in Triton WR-1339 induced hyperlipidemia in the male albino Wistar rats. It was found that the treatment with ethanol extract of *Senna auriculata* (L.) Roxb. flowers (300 mg/kg body weight) resulted in the reversal of altered protein and genes expression levels of HMGR, HMGS, SREBP-1c, ACC1, SREBP-2, CYP7A1, and ABCA1 to nearnormal levels (**Figure 7**). The results were comparable with the standard drug, atorvastatin (Vijayakumar and Nachiappan, 2017).

Moreover, an aqueous extract of *Senna. auriculata* (L.) Roxb. flower may also capable to oxidize the NADPH, a co-factor in the lipid metabolism. The increased activity of glucose-6-phosphatase reduces NADP⁺ to NADPH by providing H⁺ which is helpful in the fat synthesis from carbohydrates. The administration of flower extract reduced glucose-6-phosphatase activity and produced high NADP⁺ from NADPH which ultimately resulted in downregulation of lipogenesis (Pari and Latha, 2002).

Hakkim et al. (2007) compared the antihyperlipidemic potential of both aqueous extract and a water-soluble fraction of ethanol extract of *Senna auriculata* (L.) Roxb. flowers in alloxan-induced diabetic rats. It was found that the ethanol extract was exhibited significant (p < 0.001) reduction in the increased levels of triglycerides and total cholesterol than aqueous extract (p < 0.05) in diabetic rats. The restricted cholesterogenesis and reduced fatty acid synthesis were possible involved mechanism with the extracts of *Senna auriculata* (L.) Roxb. flowers in lowering of total cholesterol and triglycerides level in diabetic rats.

The seed extract of *Senna auriculata* (L.) Roxb. was also demonstrated antilipidemic activity where the significant reduction in cholesterol, triglycerides, LDL and increase in the HDL levels were observed in alloxan-induced diabetic rats (Subramanian et al., 2011). Furthermore, different extracts of seed such as aqueous, ethanolic, and pet ether and chloroform fractions were also ameliorated the altered levels of cholesterol and triglycerides in STZ-induced diabetic rats (Dama and Bhanoji Rao, 2011). Although it possesses antihyperlipidemic action, the effect in humans should be studied extensively.

Antiatherosclerotic and Cardioprotective Action

The chronic diabetic state is often associated with cardiovascular risk development by atherosclerosis due to hypercholesterolemia, oxidative damage, activation of the inflammatory cascade and associated endothelial dysfunction and defective coagulation (Esterbauer et al., 1993; Dominiczak, 1998; Rask-Madsen and King, 2005). The oral administration of aqueous extract of Senna auriculata (L.) Roxb. leaves (400 mg/kg body weight) demonstrated potential anti-atherosclerotic action in STZinduced diabetic rats. The extract suppressed lipid peroxidation and reduced the levels of oxidized LDL, soluble vascular cell adhesion molecule-1 and plasma fibrinogen. The increased serum nitric oxide level was also observed in extract-fed diabetic rats. It was also confirmed in histomorphological studies that the heart myocardium of extract-fed diabetic animals was showing normal morphology, whereas vacuolation was observed in the myocytes of the control diabetic rats (Gupta et al., 2011).

Lipid peroxidation inhibiting action, free radical scavenging activity, and anti-inflammatory action of different phytochemicals such as flavonoids, saponins, alkaloids and tannins etc. present in the aqueous extract of Senna auriculata (L.) Roxb. leaves may exhibit the significant anti-atherosclerotic and cardioprotective role in diabetic complications. For example, the leaves of Senna auriculata (L.) Roxb. is a rich source of squalene, a naturally occurring triterpenic hydrocarbon (Senthilkumar and Vijayakumari, 2012). Liu et al. (2018) demonstrated the effect of squalene on plasma and hepatic lipid levels of obese/diabetic KK-Ay mice and wild-type C57BL/6J mice. The administration of squalene was resulted in an increased HDL cholesterol level, an essential antiatherosclerotic factor, while no significant difference was found in other lipid levels. Besides, the HDL level was found raised, especially in an obese/diabetes mouse model compared with normal mice. Hence, squalene may play a crucial role behind the anti-atherosclerotic and cardioprotective action of Senna auriculata (L.) Roxb. However, more research is needed to clarify the effect of extracts of leaves of S. auriculata (L.) Roxb. on the lipid metabolism and dynamics related to atherosclerosis. Overall, the different extracts of Senna auriculata (L.) Roxb. play an important role in the prevention of atherosclerosis due to their anti-hyperlipidemic effect (Pari et al., 2001). Only a few in vivo studies are available for the antiatherosclerotic effect of Senna auriculata (L.) Roxb. Besides, more preclinical and clinical studies should be conducted to validate its promising protective effect against atherosclerosis associated with metabolic diseases.

Antifertility Action

In the early stages of pregnancy, the embryo nutrition and prevention of early abortion depend on the proper secretion of estrogen from corpus lutea. The methanolic extract of Senna auriculata (L.) Roxb. bark has demonstrated significant antifertility activity in experimental rats at doses of 100 and 200 mg/kg body weight. The oral administration of methanolic bark extract was continued for 7 days during the estrous stage of experimental rats. After dissecting the pregnant rats on day 10, it was observed that the number of corpus lutea reduced significantly, and there was an increased number of resorptions in the extract-fed rats. The effects were dose-dependent, where the extract at a dose of 200 mg/kg showed 100% antifertility activity. Senna auriculata (L.) Roxb. possesses potential antifertility activity, which may exhibit due to its antiestrogenic action (Shiradkar et al., 2011). The extract of the bark of Senna auriculata (L.) Roxb. is reported to have flavoinoids such as luteolin, kaempferol, and quercetin (Juan-Badaturuge et al., 2011; Habtemariam, 2013). Lu et al. (2012) reported luteolin, kaempferol, and quercetin as inhibitors of estrogen biosynthesis in vivo. Further studies are required to investigate the role of metabolites present in different extracts of Senna auriculata (L.) Roxb for its antiestrogenic and antifertility activity.

Cytotoxic Activity

The various isolated compounds and extracts of medicinal plants have been reported for their anticancer effects and may act as novel chemopreventive agents in the management of various

types of cancer (Aruna and Sivaramakrishnan, 1990; Graham et al., 2000; Moongkarndi et al., 2004). Many phytochemical compounds having anti-cancer effects such as flavonoids, procyanidins and triterpene glycosides have reported to be present in different parts of the Senna auriculata (L.) Roxb. plant and been isolated and evaluated for their cytotoxic actions (Ye et al., 1999; Sanghi et al., 2000; Nakamura et al., 2003; Kumaran and Karunakaran, 2007). An isolated compound, 4-(4-chlorobenzyl)-2,3,4,5,6,7-hexahydro-7-(2ethoxyphenyl) benzo[h][1,4,7]triazecin-8(1H)-one, from Senna auriculata (L.) Roxb. leaves has demonstrated cytotoxic effects on human colon cancer cell line HCT 15 and induced apoptosis mediated cell death. The cytotoxicity of the isolated compound was due to its high lipophilicity resulted in the loss of membrane integrity of the cancer cells. The compound was also found to cause membrane disintegration and it was confirmed with the significant release of lactate dehydrogenase (LDH) from damaged cell membrane as a result of its apoptosis (Esakkirajan et al., 2014). Similarly, Prasanna et al. (2009) reported the anticancer activity of ethanolic extract of Senna auriculata (L.) Roxb. leaves in human breast adenocarcinoma MCF-7 and human larvnx carcinoma Hep-2 cell lines. The extract exhibited a dose-dependent anti-cancer activity with IC₅₀ values of 400 μg in MCF-7 cells and 500 μg in Hep-2 cells. The inhibition of the growth of extract-treated MCF-7 and Hep-2 cell lines was observed due to nuclear fragmentation and condensation followed by apoptosis mediated inhibition of the proliferation of both the cells. In the same way, another isolated compound, 3-O-beta-D-xylopyranosides (triterpine glycosides), form C. dahurica (Tian et al., 2006), which also found present in Senna auriculata (L.) Roxb. (Sanghi et al., 2000) and Actaea asiatica (Gao et al., 2006), showed anti-cancer activity against HepG2 cell, and hepatoma cells (Tian et al., 2006), and MCF-7 cell line (Gao et al., 2006).

However, very few studies were undertaken to establish the cytotoxic effect of *Senna auriculata* (L.) Roxb., due to which it is pretty early to come to any conclusion for its therapeutic implications in cancer patients.

Immunomodulatory Effect

The flower extract from *Senna auriculata* (L.) Roxb. showed significant immunomodulatory effect in aged rats. The administration of extract in aged rats at different doses was found to activate T cell immunity with increased T and B cell percentage accompanied by an enhanced proliferation of splenocytes in both resting and LPS-stimulated cells. The increased number of T cells was further supported by observing the elevated counts of CD4⁺, CD8⁺, and CD25⁺ regulatory cells. Furthermore, the supplementation of polyphenols decreased ROS production by neutrophils in response to phorbol myristate acetate (PMA) and *Escherichia coli* activation that could conceivably harm multiple biological systems in aged individuals (John et al., 2011).

Rutin, the major metabolite present in flower extract of Senna auriculata (L.) Roxb. possesses therapeutic activity and shows potential as analgesic, anti-inflammatory, organ-

transplantation, and anticancer effects. A report indicated the protective effect of rutin on humoral and cellular immunity in rat model and caused a significant elevation in antibody titer and total antibody levels (Ganeshpurkar et al., 2017). Thus, we can propose the possible role of rutin and other polyphenols present in *Senna auriculata* (L.) Roxb. as immunomodulatory agent.

Nephroprotective Activity

The nephroprotective activity of ethanolic extract of *Senna auriculata* (L.) Roxb. root was evaluated in cisplatin- and gentamicin-induced renal injury in experimental rats. It was observed that the root extract reduced elevated levels of blood urea and serum creatinine effectively at a dosage of 300 and 600 mg/kg body weight in the cisplatin model and a dose of 600 mg/kg body weight in the gentamicin model (Annie et al., 2005). The ethanolic root extract could demonstrate the nephroprotective activity in cisplatin- and gentamicin-induced renal injury in male albino rats due to its antioxidant and nitric oxide free-radical-scavenging effects.

Antipyretic Activity

The fraction of ethanolic extract of *Senna auriculata* (L.) Roxb. leaves and flowers, at doses ranging from 250 to 600 mg/kg body weight, showed significant antipyretic activity in yeast-induced pyrexia in experimental rats. The effects were comparable to that of a standard drug, aspirin (Vedavathy and Rao, 1991).

Antiviral Activity

The antiviral activity of methanolic extract of flowers of Senna auriculata (L.) Roxb. was investigated in different cell lines, such as HeLa, Vero, Crandell Reus feline kidney (CRFK), and HEL cell cultures. The methanolic flower extract showed the strongest antiviral activity against herpes simplex-1 and 2, and moderate activity against vaccinia, vesicular stomatitis, coxsackie, respiratory syncytial, feline corona, feline herpes, parainfluenza, reo-1, sindbis, and puntatoro viruses (Arthanari et al., 2013). The methanolic extract of Senna auriculata (L.) Roxb. flowers could be a vital source of anti-herpetic compounds possessing antiviral activity against the double-stranded DNA enveloped Herpes simplex virus (HSV -1 and 2).

Antihelmintic Activity

The anthelmintic activity of methanolic and ethanolic extract of Senna auriculata (L.) Roxb. leaves against earthworm was investigated at the dose level of 20, 40, 60 mg/ml. The standard anthelmintic albendazole was used to compare the results. All the extracts showed the concentration-dependent anthelmintic property. Senna auriculata (L.) Roxb. leaves exhibited significant effects (p < 0.05) at the tested concentrations (20, 40, and 60 mg/ml) as determined by the paralysis and death time. Among all extracts, methanolic extract (40 and 60 mg/ml) was reported its efficacy at par in causing paralysis and death of earthworm at all concentrations (Chaudhary and Kumar, 2014). The anthelmintic property of Senna auriculata (L.) Roxb. may be attributed to the metabolites

especially tannins and phenolic compounds. Tannins act by binding to free protein in the gastrointestinal tract of the host or glycoprotein on the cuticle of the parasite and phenolic compounds by uncoupling oxidative phosphorylation hinder the energy production in helminth parasites (Sreejith, et al., 2013; Athnasiadou, et al., 2001). Further, *in vivo* and *in vitro* studies are needed to determine the role of metabolites present in different extracts of *Senna auriculata* (L.) Roxb. and to verify the antihelmintic activity.

Anti-Melanogenesis Activity

Wang et al. (2019) studied the effect of Senna auriculata (L.) Roxb. in the inhibition of melanogenesis in B16 melanoma 4A5 cells. The presence of auriculataosides A and B (phlegmacin-type anthracenone dimer glycosides) in Senna auriculata (L.) Roxb. indicated in inhibition of microphthalmia-associated transcription factor, tyrosinase, tyrosinase-related protein (TRP)-1, and TRP-2 protein expression. The methanolic extract in the concentration range of $1-100\,\mu\text{g/ml}$ exhibited significant inhibition of melanogenesis. These dimer glycosides were isolated from the methanolic fraction, and their inhibitory activity were detected in the dose range of $0.03-0.3\,\mu\text{M}$.

Antioxidant Activity

The various studies suggested the potency of *Senna auriculata* (L.) Roxb. as antioxidant agents in several assays such as ferric reducing antioxidant power (FRAP), 1,1-diphenyl-2-picrylhydrazyl (DPPH) free radical scavenging, hydroxyl radical scavenging, phosphomolybdenum reducing power, β -carotene bleaching assay, hydrogen peroxide radical scavenging, metal chelating activity, and deoxyribose degradation (Kolar et al., 2018). The antioxidant property of the *Senna auriculata* (L.) Roxb. measured by FRAP and DPPH assay was highest in flower extracts i.e. 161.5 mg AAE/g.

The methanolic and ethanolic extract of Senna auriculata (L.) Roxb. has potential free radical scavenging action in both 2,2'azinobis-(3-ethylbenzothiazoline-6-sulfonicacid) (ABTS) and 1,1-diphenyl-2-picrylhydrazyl (DPPH) assays (Kumaran and Karunakaran, 2007). Jeyashanthi and Ashok (2010) studied that flower extract of Senna auriculata (L.) Roxb. significantly lowers the TBARS (thiobarbituric acid reactive substances), hydrogen peroxide, and conjugated dienes and exert a potential antioxidant activity. The extracts also increase the important antioxidant enzymes like glutathione, catalase, superoxide dismutase, ascorbic acid, and vitamin E level in rats (Jeyashanthi and Ashok, 2010). The treatment with the leaf extract of Senna auriculata (L.) Roxb. at 400 mg/kg exhibited significant decrease in serum levels of oxidized lowdensity lipoprotein (Ox LDL) and TBARS (Gupta et al., 2009c). The alcoholic extract of the aerial part of Senna auriculata (L.) Roxb. exhibited potent antioxidant activity when assessed by DPPH radical scavenging, lipid peroxidation, and reducing power analysis (Juan-Badaturuge et al., 2011).

The phosphomolybdenum assay involves the reduction of Mo (VI) to Mo (V) in the presence of antioxidant compound and subsequent formation of a green phosphate Mo (V) complex at acidic pH. The flower extracts (63.8 mg AAE/g)

showed higher antioxidant activity of *Senna auriculata* (L.) Roxb. The highest ferrous ion chelating activity (90.05%) is reported in the extracts of flowers of *Senna auriculata* (L.) Roxb. (Kolar et al., 2018).

Oxidative stress is the main etiology behind many diseases and the antioxidant potential of *Senna auriculata* (L.) Roxb. along with above reported studies, supports its medicinal use in diabetes like metabolic diseases. The presence of polyphenols like rutin and kaempferol might be responsible for its free radical scavenging activity. Hence, these scientific evidence propose the possible therapeutic benefits of *Senna auriculata* (L.) Roxb. in various diseases.

Antimutagenic Activity

The antimutagenic activity of ethyl acetate extract of *Senna auriculata* (L.) Roxb. in cyclophosphamide induced chromosomal damage in bone marrow cells of albino mice was studied by Panigrahy et al. (2011). At dose level of 100 and 200 mg/kg, it provides a significant protection (p < 0.05) against chromosomal aberration due to presence of flavonoids in ethyl acetate extract.

The concentration-dependent inhibitory effect of the methanolic extract of *Senna. auriculata* (L.) Roxb. bark on the mutagenicity of Acridine orange (AO) was studied at the concentration of 2.3, 11.4 and 22.8 µM. The probable mechanism of antimutagenic activity of methanolic extract of *Senna auriculata* (L.) Roxb. bark, could be due to presence of excellent scavengers of reactive oxygen species (ROS) like singlet oxygen and/or superoxide anion radical whichplay a central role in multistage mutagenesis and carcinogenesis (EFSA Scientific Committee, 2011; Deshpande et al., 2013a; Deshpande et al., 2013b).

Antimicrobial Activity

Senna auriculata (L.) Roxb. exhibited the antimicrobial activity against Escherichia coli, Salmonella typhi, Proteus mirabilis, and Klebsiella pneumoniae. The studies on the antibacterial activity of alcoholic and aqueous extracts of flower of Senna auriculata (L.) Roxb. were demonstrated by using Staphylococcus aureus, Enterococcus faecalis, Bacillus subtilis, Salmonella typhi, Salmonella paratyphi A, Escherichia coli, Proteus mirabilis, Pseudomonas aeruginosa, Klebsiella pneumoniae, Vibrio cholerae, and Shigella dysentrae. The maximum activity was observed against all organisms except Pseudomonas aeruginosa and Klebsiella pneumoniae. The minimum inhibitory concentration ranged between 12.5 and 75 mg/ml depending on micro-organism and various extract. This study confirmed the antimicrobial activity of flower extract of Senna auriculata (L.) Roxb. and reported that it exhibits significant broad-spectrum activity against Bacillus subtilis and Staphylococcus aureus (Perumalsamy and Ignacimuthu, 2000).

Another study was performed to evaluate the antimicrobial activity of aerial parts of *Senna auriculata* (L.) Roxb. The chloroform extract of *Senna auriculata* (L.) Roxb. were shown to possess an antimicrobial activity against 2 g positive and 2 gnegative human pathogenic bacteria, viz. *Bacillus subtilis*,

Staphylococcus aureus, Pseudomonas aeruginosa, Escherichia coli and fungus cultures such as Candida albicans and Aspergillus niger. The extract showed antibacterial activity at all concentrations selected, but only the extract with the concentration of 300 µg/ml showed maximum antibacterial activity against all the organisms except Pseudomonas aeruginosa which were comparable with the standard control, amikacin. The antifungal activity of chloroform extract of Senna auriculata (L.) Roxb. revealed significant effect against Candida albicans and Aspergillus niger with the net inhibition zone of 14 and 14 mm, respectively, at 300 µg/ml concentration, which is almost comparable with standard control, ketoconazole used as an antifungal agent (Raja et al., 2013; Gharge et al., 2017).

The saponins rich fraction of roots of Senna auriculata (L.) Roxb. was evaluated for antimicrobial activity against P. vesicularis, Streptococcus faecalis, Aeromonas hydrophilia, Salmonella typhae, Staphylococcus cohni, Serratia ficaria, and E. coli at concentration of 12.5, 25, 37.5 and 50 mg/ml. Antimicrobial activity of Senna auriculata (L.) Roxb. was carried out by well diffusion method. The result indicates the saponins rich fraction of roots of Senna auriculata (L.) Roxb. might be exploited as natural drug for the treatment of several infectious diseases caused by these organisms (Deshpande et al., 2013a; Deshpande et al., 2013b).

Further, Win and Min (2018) evaluated the antimicrobial activities of chloroform, acetone, methanol, ethyl acetate, and ethanol extracts of leaves of *Senna auriculata* (L.) Roxb. by using the agar-well diffusion method. The acetone extract exhibited maximum antimicrobial activity against *Pseudomonas aeruginosa*, *Bacillus pumalis*, and *Escherichia coli*, whereas the ethanol extract showed more antimicrobial activities against *Bacillus subtilis* and *Candida albicans*.

Thus, above data suggested that plant possess a good antimicrobial activity against various strains of pathogenic bacteria and fungus. The ethno-pharmacological utility of Senna auriculata (L.) Roxb. has been proven by cited studies but future prospects about the identification of active metabolites for the same is highly suggested, as their mechanism of action will determine its further therapeutic implications.

Anti-Ulcer Activity

The anti-ulcer activity of methanolic extract of *Senna auriculata* (L.) Roxb. leaves (300 mg/kg body weight) was evaluated against pylorus ligation induced gastric ulcers, and the results were compared with the standard drug famotidine (10 mg/kg body weight) (Ahmed et al., 2010). It was observed that the *Senna auriculata* (L.) Roxb. leaf extract decreased the number of ulcers in pyloric ligated rats with a significant reduction in the gastric volume, free and total acidity, and ulcerative index.

Anti-Inflammatory Activity

Mali et al. (2012) reported the role of *Senna auriculata* (L.) Roxb. leaf extracts viz. methanolic, ethyl acetate aqueous, and hydroalcoholic extracts in inflammation by using carrageenan

induced paw edema. The highest inhibitory action in inflammation was exerted by methanolic extract. The methanolic extract showed significant anti-inflammatory potential at 6 h with percentage inhibition of 37% at 250 mg/kg and 31.63% at 500 mg/kg. This effect was attributed due to presence of alkaloids, flavonoids, tannins, and steroids. The ethyl acetate extract of Senna auriculata (L.) Roxb. at 250 & 500 mg/kg showed significant activity in second phase of inflammation induced by carrageenan with percentage inhibition of 34.16 and 30.79% respectively. The aqueous extract of Senna auriculata (L.) Roxb. (250 & 500 mg/kg) showed significant activity at 6 h with percentage inhibition of 31.06 and 30.62% respectively. The hydroalcoholic extract of Senna auriculata (L.) Roxb. in 250 & 500 mg/kg exerted significant activity at 6 h with percentage inhibition of 23.73 and 30.95% respectively. The standard indomethacin showed significant activity maximum at 6 h with percentage inhibition of 42.56%.

The presence of polyphenols in flower viz. rutin is responsible for the suppression of pro-inflammatory mediator's release and expression of the inflammatory proteins such as adhesion molecules, COX, and NOS (Lilian et al., 1998; Habtemariam and Belai, 2018). Hence, the anti-inflammatory potential of *Senna auriculata* (L.) Roxb. has been proven its traditional uses in inflammation and needs further studies involving clinical subjects for its scientific and regulatory approval.

HERBAL DRUG-DRUG INTERACTIONS

The concurrent use of an herbal tea prepared from the flowers of the Senna auriculata (L.) Roxb. and theophylline performed a significant drug interaction. Their concurrent administration resulted in an increased steady-state level (32.5%) of drug theophylline (Thabrew et al., 2004). Similarly, they have also reported the potential drug interaction between Senna auriculata (L.) Roxb. tea and antiepileptic drug carbamazepine in experimental rats. The concurrent administration of herbal tea and carbamazepine in rats elevated (47.1%) the blood levels of the carbamazepine significantly than the levels in animals treated with carbamazepine alone. Therefore, the patients who have advised theophylline or carbamazepine should avoid the concurrent use of herbal tea prepared from Senna auriculata (L.) Roxb.flowers to influence the bioavailability of theophylline.

Puranik et al. (2011) reported safety pharmacology and pharmacokinetic herb-drug interaction studies of a hydro-alcoholic and supercritical extract of *Senna auriculata* (L.) Roxb. with metformin. Both these extracts were found safe at tested doses. However, the co-administration of technology-based supercritical extract (1,000 mg/kg) and metformin showed a significant decline (60%) in the absorption of metformin. The traditionally prepared hydro-alcoholic extract did not show any change in the pharmacokinetics of metformin. Furthermore, Elango et al. (2015) demonstrated the pharmacodynamic and pharmacokinetic interactions on

TABLE 2 | List of formulations in which Senna auriculata (L.) Roxb. is used as principal ingredient.

Sr. No.	Name of formulation	Ingredients	Indications	References
	Diasulin	Senna auriculata (L.) Roxb., Curcuma longa Linn., Gymnema sylvestre R. Br., Coccinia indica W. & A., Momordica charantia Linn., Scoparia dulcis Linn., Syzygium cumini Linn., Trigonella	Diabetes mellitus	Srivastava et al. (2012), Saravanan and Pari (2005)
2.	Sugnil	foenumgraecum Linn., Tinospora cordifolia Willd Miers. Aristolochia bracteata Retz., Shorea roxburghii G. Don, Senna auriculata (L.) Roxb., Casearia esculanta Roxb., Coscinium fenestratum (Gaertn) Colebr, Curcuma longa Linn., Eugenia jambolana Lam., Gymnema sylvestre R. Br., Triphala (three myrobalans)	Microvascular complications in Diabetes mellitus	Karthikeyan et al. (2011a), Karthikeyan et al. (2011b).
3.	Kalpa harbal taa	Senna auriculata (L.) Roxb.	Diabetes mellitus	Nille et al. (2016a)
4.	Kalpa herbal tea Avarai panchanga choornam	Equal quantities of fruits, leaves, roots, flowers, and bark of Senna auriculata (L.) Roxb.	Diabetes mellitus, Obesity	Latha and Pari, (2003a), Latha and Pari (2003b)
5.	Avarai kudineer	Senna auriculata (L.) Roxb., C. fistula Linn., Syzygium cumini Linn., Olax scandens Roxb., Saussurea lappa C.B. Clarke, Terminalia arjunaRoxb., Cyperus rotundus Linn.	Diabetes mellitus, Microbial and fungal infection	Rajalakshmi et al. (2018), Kumar et al. (2019), Prakash et al. (2014)
6.	Talapotaka churna	Senna auriculata (L.) Roxb., Emblica officinalis Gaertn, Berberis aristata DC., Curcuma longa Linn.	Diabetes mellitus, Obesity	Nille et al. (2016b)
7.	Avaram Poo	Senna auriculata (L.) Roxb. flower water extract	Diabetes mellitus	Sankhari (2019)
8.	Diazen	Gymnema sylvestre R. Br., Momordia charantia Linn, Eugenia jambolana Lam., Tinospora cordifolia Willd Miers, Trigonella foenumgraecum Linn., Withania somnifera Linn., Senna auriculata (L.) Roxb., Aegle marmelos Corr., Azadirachta indica	Diabetes mellitus	Mishra and Mishra (2012)
9.	Hyponidd	A. Juss, Curcuma longa Linn. Pterocarpus marsupium Roxb., Gymnema sylvestre R. Br., Syzigium cumini Linn., Momordica charantia Linn., Enicostemma littorale Blume, Emblica officianale Gaertn, Curcuma longa Linn., Melia azadirachta Linn., Tinospora cordifolia Willd Miers, Senna	Diabetes mellitus, Polycystic ovarian syndrome	Poongothai et al. (2002), Babu and Stanely Mainzen Prince (2004)
10.	Dia Sakthi	auriculata (L.) Roxb., Trivang Bhasma and Shilajit. Centella asiatica Linn., Curcuma longa Linn., Senna auriculata (L.) Roxb., Phyllanthus amarus Schumach. &Thonn., Tinospora cordifolia Willd Miers, Syzygium cumini Linn., Abrega	Diabetes mellitus	Nille and Reddy (2015)
11.	Dianex	Chendooram, Linga Chendooram, Triphala Choorna Aegle marmelos Corr., Gymnema sylvestre R. Br., Eugenia jambolana Lam., Momordica charantia Linn., Azadiracta indica A. Juss, Senna auriculata (L.) Roxb., Withania somnifera Linn.,	Diabetes mellitus	Mutalik et al. (2003), Mutalik et al. (2005) Sudha et al. (2005)
12.	Diakyur	Curcuma longa Linn. Senna auriculata (L.) Roxb., Cassia javanica Linn., Gymnema sylvestre R. Br., Mucuna pruriens Linn., Salacia reticulate Linn.,	Diabetes mellitus	Joshi et al. (2007)
13.	Diamed	Syzygium cumini Linn., Terminalia arjuna Roxb. Azardirachta indica A. Juss, Senna auriculata (L.) Roxb., Momordica charantia Linn.	Diabetes mellitus	Pari et al. (2001)
14.	Mersina	Gymnema sylvestre R. Br., Momordica charantia Linn., Syzium cumini Linn., Phyllanthus emblica Linn., Trigonella foenumgraceum Linn., Coccinia indica W. & A., Tinospora cordifolia Willd Miers, Melia azadarichta, Javakhar, Senna auriculata (L.) Roxb.	Diabetes mellitus	Belemkar and Veeranjaneyulu (2009)
15.	Byesukar	Senna auriculata (L.) Roxb., Eugenia jambolana Lam., Thespesia populnea Soland ex Correa	Diabetes mellitus	Guruvayoorappan and Sudha (2008)
16.	Diabkil	Azardirachta indica A. Juss, Momordica charantia Linn., Tinospora cordifolia Willd Miers, Senna auriculata (L.) Roxb., Curcuma longa Linn., Terminalia arjuna Roxb., Piper nigrum Linn., Shilajit, Chlorophytum borivilianum Sant., Trigonella foenumgraecum Linn., Gymnema sylvestre R. Br.	Diabetes mellitus	Grover and Bafna (2013)

co-administration of metformin and aqueous extract of *Senna auriculata* (L.) Roxb. leaves. The reduced dose of metformin (45 mg/kg) when combined with *Senna auriculata* (L.) Roxb. leaf extract (500 mg/kg) exhibited a similar blood-glucose-lowering effect of metformin (90 mg/kg) alone.

Further studies are needed to discover the possible pharmacodynamic and pharmacokinetic interactions between *Senna auriculata* (L.) Roxb. and various oral hypoglycemic agents to avoid serious adverse events in diabetic patients upon their concurrent use.

FORMULATONS OF SENNA AURICULATA (L.) ROXB

Senna auriculata (L.) Roxb. is one of the main ingredients of many Ayurvedic and Siddha formulations available in the market. These formulations are commonly being used in diabetes, hyperlipidemia, obesity, and diabetic-associated co-morbidities. The formulations available in the market are enlisted in **Table 2**.

Toxicity Profile of Senna auriculata (L.) Roxb

Sabu and Subburaju (2002) carried out an acute toxicity study on aqueous extract of *Senna auriculata* (L.) Roxb. (leaf) on normal healthy albino Wistar rats at different doses (500, 1,000, 2,000, 5,000 mg/kg body weight). They showed that the extract did not produce any mortality up to the highest dose tested i.e. 5,000 mg/kg body weight. Also, animals did not exhibit any toxic signs like restlessness, respiratory depression, convulsion or coma.

In an acute toxicity study on albino Wistar male rats using ethanol extract of Senna auriculata (L.) Roxb. root suspended in acacia up to a dose 3,000 mg/kg body weight per oral observed that the alcoholic extract of Senna auriculata (L.) Roxb. did not produce any significant changes in the autonomic or behavioral changes including death during the observation period (Annie et al., 2005). Deshpande et al. (2013a) also carried out an acute toxicity study (OECD 423 guideline) at different dose levels of 5, 50, 300, and 2,000 mg/kg of ethyl acetate extract of roots of Senna auriculata (L.) Roxb. The rats did not show any toxic effects as well as any significant variation in their behavior. Acute toxicity studies of ethanol and aqueous extract of Senna auriculata (L.) Roxb. flowers on healthy adult male albino rats at a dose of 100, 500, 1,000, and 3,000 mg/kg body weight indicated the non-toxic nature of extracts in terms of mortality (Hakkim et al., 2007).

Gupta et al. (2009a) studied the toxicity of aqueous extract of *Senna auriculata* (L.) Roxb. leaves at a dose of 1,000 and 2,000 mg/kg body weight per oral once a daily for 3 weeks. The rats treated with 1,000 and 2,000 mg/kg doses of extract did not show any drug-induced physical signs of toxicity during the complete experimental period and no mortality was noted.

CLINICAL STUDIES

Nille et al. (2018) evaluated the antidiabetic potential of *Talapotaka churna* (4 g TID), a polyherbal formulation containing *Senna auriculata* (L.) Roxb. as a major ingredient, in Type II Diabetes Mellitus patients. The results were compared with the standard drug, glimepiride (1 mg BD). In the 2 months of the clinical trial, *Talapotaka churna* improved the symptoms of diabetes such as polyurea, polyphagia, and polydipsia with effective reduction (p < 0.05) in fasting and postprandial blood glucose levels. Further, a significant (p < 0.01) improvement was reported in disturbed biochemical parameters such as serum creatinine, SGOT, SGPT, and lipid profile.

Similarly, the aqueous extract of *Senna auriculata* (L.) Roxb. flowers demonstrated a potential anti-hyperglycemic effect in

pre-diagnosed type-2 diabetes mellitus subjects. A significant result (p < 0.001) was observed in 30 days of oral administration of flower extract with the effective reduction in fasting as well as postprandial blood glucose level (Sankhari, 2019).

Very little clinical data is available, and further extensive clinical studies are needed to support the experimental outcomes of *in vivo* studies and propose the antidiabetic potential of *Senna auriculata* (L.) Roxb. in human participants.

PERSPECTIVES AND FUTURE DIRECTIONS

The present review provides comprehensive data, relevant ethnomedicinal uses, details of metabolites, pharmacological activities of crude and various extracts along with pure compounds, marketed formulations, and its safety profile. Investigations on extracts and metabolites of Senna auriculata (L.) Roxb. provides a scientific evidences to explore the clinical implications as antidiabetic, antioxidant, anti-inflammatory, antihyperlipidemic, hepatoprotective, nephroprotective, anti-atherosclerotic, cardioprotective, anticancer, antimutagenic, antimicrobial, antiulcer, antipyretic, anthelmintic, immunomodulatory, antifertility, and antimelanogenesis potentials with different underlying signaling pathways. The biological potential and mechanisms of action of many metabolites are need to be scientifically investigated for their molecular modes of action and bioactivities. It could provide a lead for further advancement into therapeutics. Well-organized, well-designed, and multicentric clinical studies should be warranted to evaluate the clinical efficacy and safety of the standardized extracts of Senna auriculata (L.) Roxb. carrying pharmacologically active metabolites. There are limited data from clinical reports on diabetes and associated complications. Based on available evidence data, it is advised that Senna auriculata (L.) Roxb. could be used as an adjunct to the current therapy for diabetes and other metabolic disorders.

CONCLUSION

Though the available experimental evidence insinuates the therapeutic potential of *Senna auriculata* (L.) Roxb., to date, it's an unexploited plant species in clinical practice. The reason is the scattered experimental data and scarcity of clinical evidence. The present review focuses on addressing the safe pharmacological actions of *Senna auriculata* (L.) Roxb. on multiple pathways involved in the pathogenesis of diabetes and various other diseases, which also indulges its ethnomedicinal uses in diabetes mellitus. Also, the extensive animal studies involved different extracts of all the botanical parts of *Senna auriculata* (L.) Roxb., which provides the limelight for the traditional claims and its medicinal uses in various ailments in folkloric practices. The metabolites present in the *Senna auriculata* (L.) Roxb. provide an ultimate scope for its wide acceptance in the scientific community to discover and

produce synthetic molecules as an adjunct to the current therapy in NCDs. Its commercial cultivation and safety pharmacology aspects will contribute to the national economy and would be helpful to reduce the burden of NCDs with its medicinal uses.

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AUTHOR CONTRIBUTIONS

SM and GN worked on literature search, wrote and edited the manuscript while AC and KR gave ideas and proof-read the manuscript.

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Supercritical Carbon Dioxide Extracts of *Cordyceps sinensis*: Chromatography-based Metabolite Profiling and Protective Efficacy Against Hypobaric Hypoxia

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Mishra J, Khan W, Ahmad S and Misra K (2021) Supercritical Carbon Dioxide Extracts of Cordyceps sinensis: Chromatography-based Metabolite Profiling and Protective Efficacy Against Hypobaric Hypoxia. Front. Pharmacol. 12:628924. doi: 10.3389/fphar.2021.628924 The toxicity and disposal concerns of organic solvents used in conventional extraction purposes has entailed the need for greener alternatives. Among such techniques, supercritical fluid extraction (SFE) has gained popularity by yielding extracts of high purity in a much faster manner. Carbon dioxide (CO₂) is generally preferred as a supercritical solvent because of its lower temperature requirements, better diffusivity and easy removal. The present study describes the characterization of supercritical CO2 extracts of Indian variety of Cordyceps sinensis (CS)- a high-altitude medicinal mushroom widely revered in traditional medicine for its extensive anti-inflammatory, anti-proliferative and energy-enhancing hypercholesterolemic, properties. Experimental parameters viz. 300 and 350 bar of extraction pressure, 60°C of temperature, 0.4°L/h CO₂ of flow rate and use of 1% (v/v) of ethanol as entrainer were optimized to prepare three different extracts namely, CSF1, CSF2 and CSF3. Highperformance thin-layer chromatography (HPTLC) was used for assessing the quality of all the extracts in terms of cordycepin, the pivot biomarker compound in CS. Characterization by HPTLC and GC-MS confirmed the presence of flavonoids and nucleobases and, volatile organic compounds (VOCs), respectively. The chromatographic data acquired from metabolite profiling were subjected to chemometric analysis in an open source R studio which illustrated interrelatedness between CSF1 and CSF2 in terms of two major principal components, i.e. Dim 1 and Dim 2 whose values were 40.33 and 30.52% in variables factor map plotted using the HPTLC-generated retardation factor values. The factor maps based on retention times of the VOCs exhibited a variance of Dim 1 = 43.95% and Dim 2 = 24.85%. Furthermore, the extracts demonstrated appreciable antibacterial activity against Escherichia coli and Salmonella typhi by generation of reactive oxygen species (ROS), protein leakage and efflux pump inhibition within bacterial pathogens. CSFs were elucidated to be significantly cytoprotective (p < 0.05) in a simulated hypobaric hypoxia milieu (0.5% oxygen). CSF2 showed the best results by effectively improving the viability of human embryonic kidney (HEK 293) cells to 82.36 ± 1.76% at an optimum dose of 100 µg/ml. Levels of hypoxia inducible factor-1 alpha (HIF-1a) were modulated four-fold upon supplementation with CSF2. The results collectively evinced that the CSF extracts are substantially bioactive and could be effectively utilized as mycotherapeutics for multiple bioeffects.

Keywords: Cordyceps sinensis (Berk) Sacc., GC-MS, HPTLC, metabolomics, supercritical fluid extract, hypobaric hypoxia (HH)

INTRODUCTION

The increasing popularity of alternative healthcare has opened new dimensions for extraction of high value-added products from natural sources like medicinal plants and mushrooms. Though conventional extraction techniques like maceration, Soxhlet extraction, hydro-distillation, pressurised liquid extraction, etc. have been adopted for product development, however, certain disadvantages such as high operational energy requirements, use of expensive and toxic organic solvents, disposal concerns of the solvents, lesser selectivity in extraction and loss of volatile compounds have entailed the search for an efficient, environment friendly extraction approach (Malaman et al., 2011). One such approach is "supercritical fluid extraction" that utilizes supercritical fluids that above their critical points exhibit dual liquid-like and gas-like nature. In this manner, supercritical fluids are capable of solvent power with negligible surface tension as well as excellent mass transfer properties (Pronyk and Mazza, 2009). Although supercritical water and carbon dioxide (CO₂) have garnered major attention amongst researchers for extracting superior quality cosmeceuticals, essences, fragrances, pharmaceuticals from medicinal herbs, CO₂ happens to be advantageous in industrial bioprocessing owing to its comparatively moderate supercritical temperature, better diffusivity, low viscosity and easy recovery in addition to being an economical solvent, nonflammable and recyclable gas (Montesantos and Maschietti, 2020). Previous literature evidence that CO₂ is contemplated to be a better supercritical fluid than other solvents like water (Kumoro et al., 2010). In case of water, the temperature requirement is relatively much higher than that for CO2. For instance, in a study describing the preparation of tumuji oil, a temperature of 500°C was used (Meng et al., 2006). Similarly, for extracting Huadian oil shale using water in supercritical state, the temperature required was 373°C (Hu et al., 1999). Such higher temperatures are not suitable for extraction of bioactive compounds from natural sources because of their thermolabile properties. In this perspective, CO₂ is preferred as a solvent especially in the areas of functional food and pharmacological products because of its moderate supercritical points (Norodin et al., 2016; Bittencourt et al., 2021). Therefore, in the present study, supercritical CO₂ extraction was employed to prepare bioactive extracts from Indian high-altitude variety of medicinal mushroom, Cordyceps sinensis, popularly known as "keera jhari" in the Kumaon region of Indian Himalayas, from where the particular variety used in current study is sourced (Pal and Misra, 2018).

C. sinensis has been extensively revered as "ethnomedicine" in ancient medicinal systems like Ayurveda and traditional Chinese

medicine, due to its multitude of health benefits like antiinflammatory, antioxidant, cardioprotective, enhancing, hepatoprotective, etc. effects. Recent research has established evidence-based pharmacological effects demonstrating the potential of C. sinensis as anti-proliferative, immunomodulatory, cardiostimulant and the like (Holliday and Cleaver, 2008). It has been widely acclaimed in previous literature for its efficacy in modulating physiological systems including the circulatory, immune, hematogenic, cardiovascular, respiratory and glandular systems of the human body under various stressful conditions (Koh et al., 2003; Yi et al., 2004; Jordan et al., 2008; Ahmed et al., 2012; Nie et al., 2013; Yan et al., 2013; Rajput et al., 2021). The substantial therapeutic value of C. sinensis can be attributed to its rich chemical composition encompassing glycosides, lipids, phenolics, proteins and peptides, sterols and so forth (Rajput et al., 2020).

Although the restorative potential of C. sinensis has been harnessed for formulation of numerous medicinal products and supplements, however its role in the management of highaltitude-induced maladies namely, acute mountain sickness (AMS), chill blains, high-altitude cerebral edema (HACE), high-altitude pulmonary edema (HAPE) and hypothermia are relatively untapped. Only few researchers have reported the considerable potential of C. sinensis in amelioration of adverse effects brought about by high-altitude hypoxia. For instance, aqueous alcoholic extracts of C. sinensis have restorative effects to treat hypoxic pulmonary hypertension by downregulating the expression of PCNA, c-fos and c-jun (Gao et al., 2010). Chen et al. (2014) have shed light on the vital role of a supplement composed of Rhodiola crenulata and C. sinensis in augmenting aerobic performance of healthy male subjects during a 2-wk highaltitude training regime where significant normalization of parasympathetic nervous system action and a prolonged exhaustive run time was observed. In studies carried out by our group, it has been observed that aqueous extracts and phenolic rich fractions of Indian Himalayan variety of C. sinensis have substantially averted the debilitating impact of hypobaric hypoxia in vitro in various mammalian cell lines namely, A549, HT22, HEK 293 cell lines and, in vivo in male Sprague Dawley rat models (Singh et al., 2013; Pal et al., 2015; Rajput et al., 2020). To further establish the promising adaptogenic potential of C. sinensis in a hypobaric hypoxia milieu, supercritical fluid extracts were prepared from C. sinensis ("CSF extracts") using supercritical CO2 as main solvent and ethanol as entrainer. The extracts were well characterized by high-performance thin layer chromatography (HPTLC) in terms of cordycepin, flavonoids and nucleobases and in terms of volatile organic compounds (VOCs) by gas chromatography-mass spectrometry (GC-MS).

Chromatography-based metabolomics using principal component analysis was carried out to group the extracts based on their metabolite content. Cognate bioactivities viz., free radical scavenging, ferric ion reduction and bactericidal action against Escherichia coli (E. coli) and Salmonella typhi (S. typhi) were revealed. These are common pathogenic bacteria whose invasion in human host cells is reportedly aggravated under hypoxia conditions (Ding et al., 2001; Jennewein et al., 2015). Since the main objective of the present study was to establish the efficacy of supercritical CO₂ extracts of C. sinensis for recuperation in low oxygen tension, hence the selection of the abovementioned bacterial strains was considered relevant. Furthermore, the protective role of the fractions in resolving hypoxia-instigated concerns were thoroughly studied in vitro in HEK 293 cell lines where CSF extract significantly recuperated cellular viability under oxygen deficient conditions and also modulated levels of major hypoxia transcription factor, i.e., hypoxia inducible factor-1 alpha or, "HIF-1a."

The novelty of the present manuscript resides in the fact that the protective action of supercritical CO2 extracts of C. sinensis against hypobaric hypoxia has been addressed for the very first time. Reports pertaining to hypoxia protective action are not available for supercritical extracts of any species of Cordyceps genus. In our earlier studies, anti-hypoxia effects of phenolic fractions and aqueous extracts (prepared by accelerated solvent extraction) of Indian Himalayan variety of C. sinensis were confirmed (Singh et al., 2013; Rajput et al., 2020). However, this is the very first time that supercritical carbon dioxide extracts of this variety have been researched. This is the first study of its kind that provides a detailed insight into the protective role of *C*. sinensis supercritical CO2 extracts against a hypobaric hypoxia milieu. These observations, along with metabolomics performed on chromatography profiling can further be taken up as a lead for value-added product development, especially against highaltitude malaises.

MATERIALS AND METHODS

Chemicals and Reagents

Ultra-pure, molecular grade chemicals from Sigma-Aldrich (St. Louis, MO, United States) were used in the entire study. Solvents were purchased from Merck (Rahway, NJ, United States). Water used throughout was of Millipore grade (Merck, United States). Powder of C. sinensis was commercially procured from Aryan Mushroom (Batch No. CO-1601; Delhi, India). The average particle size of C. sinensis powder was 300 µm, as determined using Supra scanning electron microscope (Carl Zeiss, Germany). Bacterial strains used were E. coli (ATCC 9837) and S. typhi (clinical isolate from All India Institute of Medical Sciences, Delhi, India). HEK 293 cell line was procured from National Centre for Cell Science (Pune, India). Nutrient agar, nutrient broth and antibiotic solutions used were from HiMedia (Mumbai, India). Dulbecco's minimal essential medium (DMEM) used in cell culture studies was procured from HiMedia" (Mumbai, India).

Preparation of *C. sinensis* Supercritical Extracts

The supercritical fluid extracts of *C. sinensis* collectively referred to as "CSF extracts" were prepared in SFE-500R system (Thar, Pittsburgh, United States), by modifying a methodology reported earlier (Miao et al., 2010). The instrument had two separate feed lines for CO2 and the entrainer (here, ethanol). The optimum pressure and temperature for preparing CSF extracts in the current study were finalized after evaluating the yields (%, w/w) obtained from a combination of four extraction pressures viz., 200, 250, 300 and 350 bar and three temperatures of 40, 50 and 60°C. The afore stated pressures and temperatures were selected by keeping in consideration the type of bioactive molecules (flavonoids, nucleobases and VOCs) being targeted putatively in the extracts (He et al., 2005; Liza et al., 2010; Shan et al., 2012). CO2 flow rate was maintained at 0.4 L/h. Ethanol 1% (v/v) was used as an entrainer/ co-solvent. Amongst all the combinations of extraction pressures and temperatures tested, the ones giving extracts of highest yields ("CSF1" followed by "CSF2") were selected as the optimum extraction conditions. Maintaining the same extraction parameters as "CSF1," but without the use of entrainer, resulted in extraction of "CSF3." In the experimental procedure, CO2 from the cylinder was released via a cooling bath in order to hold a constant temperature for ensuring a constant feeding rate of the pump. Subsequently, the mixture of C. sinensis powder, supercritical CO₂ and ethanol for CSF1 and CSF2 and C. sinensis powder and only supercritical CO₂ in case of CSF3 were contacted in a mixer. The temperature of the reaction mixture was controlled by a heating jacket. At extraction pressure of 300 bar, an extraction time of 2 h was maintained for acquiring CSF1 and CSF3. For CSF2, the extraction pressure was higher i.e., 350 bar, hence the time was reduced to 1.5 h. After an extraction time period of 2, 1.5 and 2 h for CSF1, CSF2 and CSF3 separately, the ensuing extracts were collected in the separation vessel. All the procedural parameters were regulated by the instrument console.

Characterization of the CSF Extracts by HPTLC

Chemical characterization of the CSF extracts in terms of cordycepin, nucleobases and flavonoids was accomplished by HPTLC. The entire HPTLC analysis was accomplished on a CAMAG system (Muttenz, Switzerland) consisting of a Linomat 5 sample applicator, TLC Scanner 3 and Reprostar 3 documentation system. The samples were applied by means of a Hamilton microsyringe (100 μ L) on 20 \times 10 cm glass backed silica gel 60 F_{254} HPTLC plates (Merck, Billerica, MA, United States). Spectral scanning was done using winCats software (version 1.4.4.6337).

HPTLC Analysis of Cordycepin

Quality assessment of the supercritical CO₂ extracts was performed by characterizing them in terms of the major biomarker metabolite of *C. sinensis*, i.e. "cordycepin" or 3'-

deoxyadenosine. Here, 0.5 mg of cordycepin was dissolved in 1 ml of methanol to form the cordycepin standard solution. For sample preparation, 20 mg of each CSF extract was dissolved in 10 ml of methanol thus, forming final sample concentration of 2 mg/ml. Three different application volumes (0.5, 1 and 2 μl) of cordycepin standard solution and 20 µl of each sample was applied onto separate lanes of uniform band thickness of 6 mm on a silica gel plate. The plate was developed using a mobile phase comprising chloroform, methanol and water in a ratio of 52: 7: 0.5 (v/v/v) (Sari et al., 2016). The plate was developed in a CAMAG twin-trough vertical development chamber, pre saturated with mobile phase. The solvent front was maintained till 85 mm. Thereafter, the plate was subjected to densitometric scanning at 254 nm in absorption mode, with deuterium as the light source. Slit width was $6 \times 0.3 \,\mu\text{m}$. Quantities of cordycepin in the three CSF extracts were computed from the corresponding peak areas generated by winCats software.

HPTLC Analysis of Nucleobases

For quantification of nucleobases, specifically, thymine, uracil, adenine, cytosine, guanine and guanosine present in CSFs by HPTLC, stock solutions of the standard nucleobases were prepared by dissolving 0.5 mg of each standard in 1 ml of methanol and vortexing the same for 10 min. A standard mixture comprising equal volume from each of these six standard nucleobase solutions was prepared. CSF samples were prepared as mentioned in previous paragraph. Then, 6, 7 and 8 μl of the standard mixture and 20 µl of individual CSF extract were applied on silica gel plates as mentioned above. The constituent nucleobases were identified by developing the plate in a solvent system composed of dichloromethane, methanol and formic acid in a ratio of 8: 2.25: 0.8 (v/v/v) (Mishra et al., 2018b). All the analytical parameters for separation and quantification of nucleobases were retained as described in the previous section for cordycepin.

HPTLC Analysis of Flavonoids

A standard mixture of flavonoids containing equal volume of quercetin, gallic acid, ascorbic acid and rutin was made up in a similar manner as that for nucleobases. Flavonoids present in the CSF samples were separated and quantitated using a mobile phase constituted of ethyl acetate: dichloromethane: formic acid: glacial acetic acid: methanol in a ratio of 10:10:1:1:2 (v/v/v/v/v) (Bhardwaj et al., 2015). Rest analytical and detection parameters were maintained as described in the previous sections.

Characterization of the CSF Extracts by GC-MS

Detection of VOCs present in CSFs was carried out upon a fused silica stationary phase Rtx-5MS, having dimensions 30 m \times 0.25 mm, 2 μ m. GC-MS analysis was conducted using a Shimadzu QP2010 system (Kyoto, Japan), equipped with an AOC-20i autosampler. The following analytical parameters were set: sample injection volume: 1 μ l; injection temperature: 260°C; purge rate: 3 ml/min; gas flow rate: 1.21 ml/min; column

temperature: initial at 60°C for 2 min, then ramped at a rate of 10°C/min till 280°C; total run time: 27 min. An electron beam of 70 eV was used for ionization of samples. VOCs detected in the supercritical extracts were confirmed by matching their respective mass spectra and retention times with existing entries in NIST library (Cui et al., 2017).

Metabolomics Studies by Principal Component Analysis

The metabolite profiling acquired from HPTLC and GC-MS analyses were utilized as input data to derive relatability patterns among the CSF extracts by means of chemometrics. Here, principal component analysis (PCA) for data reduction was realized in an open source R studio: A Language and Environment for Statistical Computing (R Foundation for Statistical Computing, Vienna, Austria (http://cran.r-project. org/). The entire datasets comprising retardation factors and peak areas of various nucleobases and flavonoids in CSF extracts in case of HPTLC, and the retention times and area percentages of constituent VOCs from GC-MS output were represented in terms of two principal components denoted as "Dim1" and "Dim2" in separate variables factor maps generated from PCA. This facilitated drawing interrelatedness patterns among the CSF extracts while ensuring data compression (Bhardwaj et al., 2017).

Antioxidant Potential of the CSF Extracts

The antioxidant potency of C. sinensis supercritical CO_2 extracts was adjudged by evaluating their free radical scavenging potential for 2,2'-azinobis-3-ethylbenzothiazoline-6-sulphonic acid (ABTS) and 2,2-diphenyl-1-picryl-hydrazyl-hydrate (DPPH) radicals as well as by determining the ferric ion reducing antioxidant power (FRAP), as detailed below.

DPPH Assay

Various concentrations viz., 10, 5, 2.5, 1.25 and 1 mg/ml of the supercritical fluid extracts were prepared. 24 mg of DPPH powder was dissolved in 100 ml of ethanol. 10 ml of this solution was mixed well with 45 ml of methanol. Absorbance was adjusted to 1.1 \pm 0.02 units at 515 nm to form the working solution. Then, 10 μ l of sample was added to 190 μ l of this working solution and left undisturbed for 2 h to allow proper reaction with the stable DPPH radical. A change in colour from deep violet to light yellow was measured at 515 nm. Results were represented in terms of micromole Trolox equivalent per gram of extract (μ M TE/g of extract) (Mishra et al., 2018a).

ABTS Assay

ABTS free radical scavenging assay was determined as reported elsewhere (Sharma et al., 2015). Trolox ranging from 800 to 50 μM were taken as standards to plot the standard curve. Different concentrations viz., 10, 5, 2.5, 1.25 and 1 mg/ml of all the CSF extracts were prepared. ABTS free radical scavenging values of CSF extracts were expressed as μM TE/g of extract. Absorbances were recorded at 734 nm.

FRAP Assay

FRAP values of CSF extracts were determined using a method described previously (Mishra et al., 2018b). Various concentrations of Trolox over a range of 400–12.5 μ M were taken as standards. Different concentrations (10, 5, 2.5, 1.25 and 1 mg/ml) of all the CSF extracts were prepared. Results were expressed as μ M TE/g of extract. Final absorbances were recorded at 593 nm.

Antibacterial Efficacy of the CSFs Screening of CSF Extracts for Antibacterial Activity

Glycerol stocks of two bacterial strains: *E. coli* and *S. typhi* were revived in nutrient broth for 16–18 h at 37°C, in an incubator-cum-shaker (Orbitek, Chennai, India), at 90 rpm. The pure cultures obtained were streaked on nutrient agar medium. Antibacterial action of CSF1, CSF2 and CSF3 against *E. coli* and *S. typhi* was determined by Kirby Bauer disk diffusion technique (Mishra et al., 2018a). Briefly, 100 µg/ml of each CSF extract dissolved in nutrient broth was applied onto spherical disks made out of Whatman No.1 filter paper. The dried disks were placed on nutrient agar medium plates swabbed with bacterial pathogens under study. Thereafter, these plates were incubated at 37°C for 16–18 h at a shaking speed of 90 rpm. Prominent zones of inhibition formed around the disks were indicative of antibacterial activity. Kanamycin and nutrient broth were taken as the positive and negative controls, respectively.

Determination of Minimal Inhibitory Concentration

Bacterial colonies approximately, $16-18\,h$ old, cultured on nutrient agar medium were diluted in 0.8% physiological saline to prepare a $0.1\,$ McFarland suspension. The bacterial cultures were inoculated in test tubes containing 5 ml nutrient broth. To these tubes, the specific CSF extracts were added in concentrations over a range of $10-100\,\mu\text{g/ml}$ and incubated at 37°C for $16-18\,h$ at $90\,\text{rpm}$. The lowest concentration of an extract demonstrating inhibition of bacterial growth was determined to be its minimal inhibitory concentration (MIC) for a given bacterial pathogen (Zhang et al., 2015). Kanamycin and pure nutrient broth medium were used as the positive and negative controls, respectively.

Generation of Reactive Oxygen Species Within Bacterial Cells

Reactive oxygen species (ROS) generation in a bacterial cell upon treatment with a specific CSF extract as a potential antibacterial mechanism was investigated by a method described previously (Zhang et al., 2015). Various concentrations of the CSF samples were added to nutrient broth tubes containing bacterial cells at density of 10^5 CFU/ml and incubated at 37° C for 3 h. The cultures were then centrifuged at 4° C for 15 min at a speed of $500 \times g$, and the resultant supernatant was treated with $50 \, \mu M$ of $2^{\circ},7^{\circ}$ -dichlorofluorescein diacetate (DCFDA), for 1 h at 37° C, in dark. A control group untreated with DCFDA was taken as control. The level of ROS generated in the bacterial cultures was recorded in triplicates using a fluorescence

spectrophotometer (Cary Eclipse, Santa Clara, CA, United States) at an excitation wavelength of 485 nm and emission wavelength of 528 nm.

Protein Leakage in Bacterial Cells

Protein leakage instigated within the bacterial pathogen's cellular environment triggered by particular CSF extracts as yet another antibacterial mechanism was examined (Zhang et al., 2015). Here, 16–18 h old cultures of bacteria in nutrient broth were centrifuged at 10,000 rpm for 20 min, followed by resuspension in 0.8% physiological saline. After this, the bacterial cells were treated with CSF extracts of varied concentrations. Following an incubation period of 3 h, each bacterial suspension was centrifuged at 12,000 rpm for 15 min and the supernatant was analysed for protein content by Bradford method. Protein concentration at 595 nm was determined using bovine serum albumin (BSA) as standard.

Inhibition of Efflux Pumps in Bacterial Cells

Bacterial cultures inoculated in nutrient broth were incubated overnight for 24 h at 37°C at 95 rpm. The culture was then centrifuged for 5 min at 4000 rpm. Discarding the supernatant, the pellet collected was suspended in nutrient broth. A 500 μ g/ml sample of each CSF extract was prepared in nutrient broth. To individual wells of a 96 well microtiter plate, 150 μ l nutrient broth containing bacterial inoculum, 20 μ l ethidium bromide (EtBr) and 50 μ l of the respective CSF sample was added and incubated for 10 min at room temperature. Thereafter, fluorescence was recorded using a fluorescence spectrophotometer over 30 min with interims of 5 min, at an excitation wavelength of 530 nm and emission wavelength of 600 nm. In this study, 5 μ l of carbonyl cyanide 3-chlorophenylhydrazone or, "CCCP" known to be an effective efflux pump inhibitor was taken as the positive control and water served as negative control (Kumar et al., 2016).

Protective Action of CSF Extracts Against Hypobaric Hypoxia in Human Embryonic Kidney Cell Line

The protective effects of the *C. sinensis* supercritical fluid extract in recuperating human embryonic kidney cells (HEK 293) from hypoxic stress was evaluated by segregating the experimental cells into four groups for every dose (50/75/100/125 µg/ml) of each CSF extract. The groups were: normoxia control (N), normoxia supplemented with CSF extract (N+sample), hypoxia control (H) and, hypoxia supplemented with CSF extract (H+sample). Initially, the cells were cultured in high glucose DMEM (Dulbecco Minimal Essential Medium), (pH 7.2, 37°C, 5% CO₂) supplemented with antibiotics gentamycin sulphate (100 mg/L) and penicillin (100 mg/L) and enriched with foetal bovine serum (FBS) (10%, v/v) as described in a previous study (Kirar et al., 2017). Cells were grown in 96-well microtitre plates (Nunc, Roskilde, Denmark), maintaining a cell density of 10⁵ cells/cm², and placed in incubator (New Brunswick, Galaxy 170R, Hamburg, Germany) with 21% O2 i.e., normoxic condition. Experiments were conducted only on cells that were at least 80% confluent.

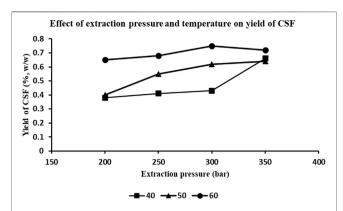


FIGURE 1 | Effect of extraction pressure and temperature on the yields of *C. sinensis* supercritical fluid (CSF) extracts. Combination of various pressures (200, 250, 300 and 350 bar) and temperatures 40, 50, and 60° C were used for the optimization protocol. 1% (v/v) ethanol was used as entrainer. CO₂ flow rate was 0.4 L/h.

For hypoxia stress, cells were cultured for 24 h in a low oxygen environment (0.5% $\rm O_2, 5\%$ $\rm CO_2$ and 94.5% $\rm N_2)$ in New Brunswick Galaxy 48R hypoxia incubator (Hamburg, Germany). Cellular viability of the cells was determined using MTT assay (Mosmann, 1983). Different concentrations (50, 75, 100 and 125 µg/ml) of CSF extracts were supplemented to the growth medium, according to the aforementioned grouping. Dose of each CSF extract demonstrating maximum restoration of cellular viability under hypoxic conditions was inferred as its corresponding optimum dose.

Western Blotting for Assessing Effect of CSF Extract on HIF-1 α Levels

Post hypoxia exposure, cells were de-adhered from the T25 flask by trypsinization (0.1%, v/v in PBS) for about 5 min. Cells were homogenized in radioimmunoprecipitation assay buffer (50 mM/ L Tris-HCl, 150 mM/L NaCl, 0.1% sodium dodecyl sulfate, 1% NP-40, 0.5% deoxycholate, and protease inhibitor cocktail 5 µl/ml (MP Biomedicals, Ilkirch, France) and centrifuged at $12,000 \times g$ at 4°C for 30 min. The supernatant collected contained cytosolic fractions. Total protein was estimated by Lowry's method (Nehra et al., 2015). For Western blotting, 25 µg of cytosolic protein was resolved in 10% SDS-PAGE (sodium dodecyl sulphatepolyacrylamide gel electrophoresis) and transferred onto nitrocellulose (Millipore, membrane Bedford, MA, United States) via semi-dry trans-blot system (BioRad, Hercules, CA, United States) at 15-20 V for 60 min. Membranes were blocked in blocking buffer composed of 3-5% bovine serum albumin in 0.5% Tris-buffered saline-Tween (TBST), for 2 h and incubated with primary antibody i.e., polyclonal HIF-1α antibody (1:1000 dilution, E-AB-31662; Elabscience Biotechnology Inc., Houston, TX, United States) for 2 h. After washing in TBST, the membranes were incubated with appropriate secondary antibodies (1:20,000-30,000) (Santa Cruz Biotechnology, Dallas, TX, United States) at room temperature for 1 h, on dancing shaker. HIF-1α being probed was visualized

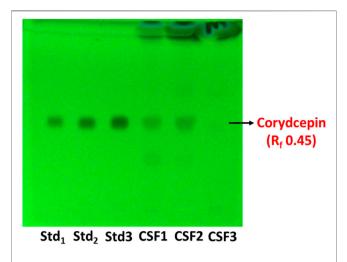


FIGURE 2 | HPTLC chromatogram at 254 nm shows bands distinctive of cordycepin, the main marker metabolite used for quality assessment of *Cordyceps* spp. The retardation factor (R_1) was determined to be 0.45. Lanes labelled Std_1 , Std_2 and Std_3 contain 0.25, 0.5 and 1 μg of standard cordycepin.

using $H_2O_2/3,3',5,5'$ -tetramethylbenzidine (TMB) (Sigma-Aldrich, St. Louis, MO, United States). Quantitation was done by densitometric analysis using ImageJ software (Kirar et al., 2017).

Statistical Analysis

Quantitation in all the HPTLC experiments were performed in triplicates. Data from antioxidant, antibacterial and *in vitro* cell culture assays were acquired in triplicate manner for all the CSF extracts in order to determine reproducibility. Results have been expressed as mean \pm SD. All the statistical analyses viz., computation of mean and standard deviations were performed using Statistical Package for the Social Sciences (SPSS) software version V 2.21 (IBM, Chicago, IL, United States). One way analysis of variance (ANOVA) was applied to check the level of significance by Bonferroni *post hoc* tests. In all the tests, p < 0.05 was taken as a criterion for statistical significance.

For construction of variables factor maps by PCA, data acquisition and processing including generation of covariance matrices and proportion of variances were generated by R, version 4.0.3 (http://cran.r-project.org/).

RESULTS

The different combinations of four extraction pressures and three extraction temperatures resulted in acquisition of 12 supercritical $\rm CO_2$ extracts, of varying yields. The effect of extraction pressures and temperatures on the yields of extracts is depicted in **Figure 1**. It is observed that the yields incremented with a combination of rising pressure and temperature, except for 350 bar and 60°C, which displayed lesser yield than that at 300 bar and 60°C. The maximal yields were achieved with combination of 1) extraction pressure of 300 bar and temperature of 60°C (extract labelled

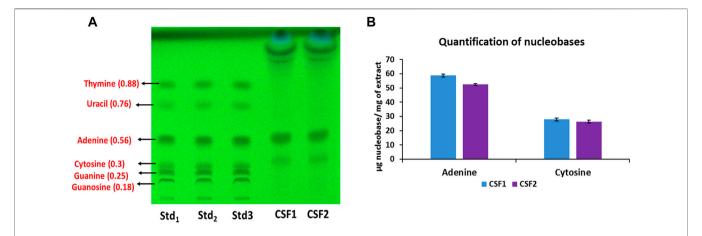


FIGURE 3 | HPTLC chromatogram at 254 nm confirms the presence of adenine and cytosine in CSF1 and CSF2 extracts. Respective retardation factor values are written in parentheses (A). Quantities detected from densitometric scanning are also given (B). Lanes labelled Std₁, Std₂ and Std₃ contain 0.5, 0.58 and 0.66 μg of each standard nucleobase. Values for quantification are represented as mean ± SD (*n* = 3).

"CSF1") and, 2) extraction pressure of 350 bar and temperature of 60°C (extract labelled "CSF2"). Keeping the former condition intact but without the use of entrainer wielded the third extract "CSF3." These three *C. sinensis* supercritical CO₂ extracts, were collectively referred to as "CSF extracts." The yields were 0.75, 0.72 and 0.53% (w/w), for CSF1, CSF2 and CSF3, correspondingly. The physical properties of all the *C. sinensis* supercritical extracts were viewed to be sticky in nature and dark brownish in colour.

HPTLC Characterization Confirmed the Presence of Cordycepin, Flavonoids and Nucleobases in the CSF Extracts

HPTLC fingerprinting given in **Figure 2** illustrated distinct bands indicative of cordycepin, the main marker metabolite of *C. sinensis* in CSF1 and CSF2, but not in CSF3. Cordycepin was quantitated to be fairly more in CSF1 with 296.6 \pm 15.3 μg/mg of extract than CSF2 (267.1 \pm 9.2 μg/mg of extract).

Figure 3A represents the HPTLC chromatogram for identification of nucleobases in *C. sinensis* supercritical extracts. Among the nucleobases under consideration, adenine and cytosine were detected in CSF1 and CSF2. **Figure 3B** denotes the quantities of these nucleobases as calculated from densitometric scanning. It was perceived that CSF1 consisted of a marginally higher content of adenine (58.85 \pm 0.24 µg/mg of extract) and cytosine (27.94 \pm 1.81 µg/mg of extract) than that in CSF2, where adenine content was 52.43 \pm 0.68 µg/mg of extract and cytosine was 26.35 \pm 1.07 µg/mg of extract.

Figure 4A represents the HPTLC profiling for flavonoids detected in *C. sinensis* supercritical extracts. Here, presence of ascorbic acid, gallic acid and quercetin was confirmed in CSF1 and CSF2. **Figure 4B** denotes the quantities of these flavonoids as measured using densitometric scanning. It was clearly seen that CSF1 possessed the highest quantity of all three aforesaid flavonoids having ascorbic acid, gallic acid and quercetin in amounts of 15.2 ± 0.6 , 3.8 ± 0.48 and $10.63 \pm 0.26 \,\mu\text{g/mg}$ of

extract. Corresponding values of CSF2 were 14.48 \pm 0.5, 3.18 \pm 0.19 and 8.55 \pm 0.28 µg/mg of extract. CSF3 was found to have only quercetin (2.31 \pm 0.27 µg/mg of extract). The identification and quantification of bands corresponding to standard nucleobases or flavonoids has been performed within the permissible evaluation window of winCATS software.

Presence of Putative Bioactive VOCs Verified by GC-MS Analysis

The CSF extracts were observed to comprise various VOCs inclusive of alcohols, esters, stearates, terpenes, etc. The major VOCs detected in the supercritical CO2 extracts with their respective retention times, peak areas and area percentages are depicted in Tables 1-3 for CSF1, CSF2 and CSF3, respectively. Results based on the area percentages of individual VOCs established that 9,12-octadecadienoic acid (Z,Z)- or, α-linoleic acid was the most abundant VOC in CSF1; 9,12-octadecadienoic acid (Z,Z)-, trimethylsilylester i.e., linoleic acid trimethylsilyl ester was the most abundant VOC in CSF2 whereas hexadecanoic acid, trimethylsilyl ester (palmitic acid TMS) was the most abundant VOC in CSF3. Total ion chromatograms of the aforesaid most abundant VOCs are represented in Figure 5. All the three supercritical extracts individually had certain VOCs which are unique to each of them, thus proving that every individual sample had its own distinct characteristics in terms of bioactivity, as discoursed later.

Metabolomics by PCA Based on Chromatographic Data Verified Inter-relatedness Between CSF1 and CSF2

The chromatographic data acquired from metabolite profiling were subjected to chemometric analysis in an open source R studio, to carry out data reduction and pattern recognition. In case of both HPTLC and GC-MS data, two major principal components, represented as Dim1 and Dim2 depicted the overall variance over

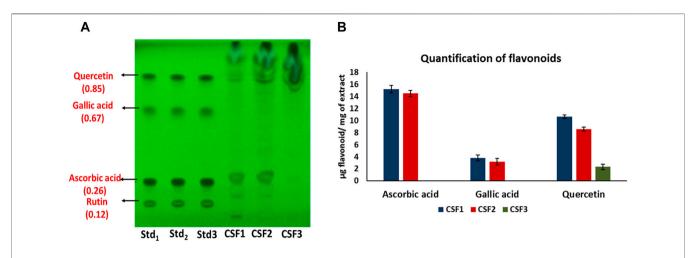


FIGURE 4 | HPTLC chromatogram at 254 nm confirms the presence of ascorbic acid, gallic acid and quercetin in CSF1 and CSF2 extracts, and only quercetin in CSF3 extract. Respective retardation factor values are written in parentheses **(A)**. Quantities detected from densitometric scanning are also given **(B)**. Lanes labelled Std₁, Std₂ and Std₃ contain 0.75, 0.875 and 1 µg of each standard flavonoid. Values for quantification are represented as mean ± SD (n = 3).

TABLE 1 | List of major volatile organic compounds detected in CSF1 extract by GC-MS.

Peak	Retention time (R_t), min	Area	Area%	Name
1	26.121	419,928	0.29	1-TETRADECANOL, ACRYLATE
2	29.466	444,072	0.30	TETRADECANOIC ACID, TRIMETHYLSILYL ESTER
3	29.803	1,550,751	1.07	PENTADECANOIC ACID
4	31.056	858,623	0.59	HEXADECANOIC ACID, METHYL ESTER
5	31.596	2,185,882	1.50	n-PENTADECANOIC ACID, TRIMETHYLSILYL ESTER
6	32.152	20,965,594	14.40	PENTADECANOIC ACID
7	32.673	1,888,914	1.30	HEXADECANOIC ACID, ETHYL ESTER
8	33.776	2,952,332	2.03	HEXADECANOIC ACID, TRIMETHYLSILYL ESTER
9	34.165	1,824,254	1.25	9-OCTADECENOIC ACID (Z-)
10	34.609	6,324,673	4.34	9,12-OCTADECADIENOIC ACID (Z,Z)-, METHYL ESTER
11	35.484	56,200,296	38.60	9,12-OCTADECADIENOIC ACID (Z,Z)-
12	35.650	10,256,586	7.04	ETHYL (9Z,12Z)-9,12-OCTADECADIENOATE #
13	36.364	2,484,453	1.71	LINOSAEURE, TRIMETHYLSILYL ESTER
14	37.597	1,243,151	0.85	OCTANAMIDE, N-(2-HYDROXYETHYL)-
15	38.138	1,785,300	1.23	METHYL OCTADECA-9,12-DIENOATE
16	39.930	759,375	0.52	1,2-BENZENEDICARBOXYLIC ACID
17	42.270	679,937	0.47	13-DOCOSENAMIDE, (Z)-
18	42.475	592,267	0.41	DECANEDIOIC ACID, BIS (2-ETHYLHEXYL) ESTER
19	43.567	790,657	0.54	TETRACONTANE
20	45.138	9,853,510	6.77	9(11)-DEHYDROERGOSTERYL BENZOATE
21	45.618	1,157,108	0.79	9(11)-DEHYDROERGOSTERYL BENZOATE
22	45.936	1,053,723	0.72	HEXADECANOIC ACID, METHYL ESTER
23	46.907	537,691	0.37	TETRACONTANE
24	47.115	717,398	0.49	PYRAZINE, TETRAKIS (1-METHYLETHYL)-
25	49.081	1,162,320	0.80	ERGOSTA-5,7,9(11),22-TETRAEN-3-OL, (3.BETA.,22E)
26	50.015	6,610,013	4.54	ERGOSTEROL
27	51.612	3,491,024	2.40	16-HENTRIACONTANONE
28	55.315	6813,607	4.68	10,13-DIMETHYL-17-(1,4,5-TRIMETHYL-HEX-2-ENYL
		145,603,439	100	V · · · ·

The retention times, peak areas and area percentages are indicated.

the entire dataset. The primary axis, i.e., the first principal component describes majority of the variance in a factor map.

For HPTLC data, all the retardation factors from analysis of both nucleobases as well as flavonoids were taken into account to form data matrix. Information pertaining to retardation factor values and peak areas of 98 metabolites were compressed to manifest the entire data in form of Dim 1 and Dim 2, whose values were 40.33 and 27.91% in variables factor map (**Figure 6A**). Data compression in PCA ensures that there is no loss in variances while describing the dataset.

TABLE 2 | List of major volatile organic compounds detected in CSF2 extract by GC-MS.

Peak	Retention time (R_t), min	Area	Area%	Name
1	14.800	145,752	0.36	TETRADECANOIC ACID, TRIMETHYLSILYL ESTER
2	15.609	2,388,227	5.84	HEXADECANOIC ACID, METHYL ESTER
3	15.811	1,402,036	3.43	n-PENTADECANOIC ACID, TRIMETHYLSILYL ESTER
4	16.270	322,754	0.79	HEXADECANOIC ACID, ETHYL ESTER
5	16.594	312,992	0.76	cis-9-HEXADECENOIC ACID, TRIMETHYLSILYL ESTER
6	16.816	9,859,447	24.09	HEXADECANOIC ACID, TRIMETHYLSILYL ESTER
7	17.290	1,431,582	3.50	9,12-OCTADECADIENOIC ACID (Z,Z)-, METHYL ESTER
8	17.339	1,803,748	4.41	9-OCTADECENOIC ACID, METHYL ESTER
9	17.383	353,836	0.86	9-OCTADECENOIC ACID (Z-), METHYL ESTER
10	17.500	253,523	0.62	9,12-OCTADECADIENOIC ACID (Z,Z)-, TRIMETHYLSILYL ESTER
11	17.549	765,219	1.87	METHYL STEARATE
12	17.611	176,041	0.43	METHYL 15-HYDROXY-9,12-OCTADECADIENOATE
13	17.701	933,283	2.28	HEPTADECANOIC ACID, TRIMETHYLSILYLESTER
14	17.897	9,004,280	22.00	9,12-OCTADECADIENOIC ACID (Z,Z)-
15	18.377	10,633,336	25.99	9,12-OCTADECADIENOIC ACID (Z,Z)-, TRIMETHYLSILYL ESTER
16	19.726	192,583	0.47	CYCLOPROPANEOCTANOIC ACID,2-[(2-ETHYLCYCLOPROPYL)METHYL ESTER]
17	20.580	134,002	0.33	1,3,5-TRISILACYCLOHEXANE
18	22.057	194,423	0.48	1,3-DIOXOLANE, 2-METHOXY-4-HEXADECENYL ESTER
19	23.841	150,386	0.37	SQUALENE
20	26.263	462,562	1.13	9(11)-DEHYDROERGOSTERYL BENZOATE
		409,200,002	100	

The retention times, peak areas and area percentages are indicated.

TABLE 3 | List of major volatile organic compounds detected in CSF3 extract by GC-MS.

Peak	Retention time (R_t), min	Area	Area%	Name
1	14.802	28,836	0.21	TETRADECANOIC ACID, TRIMETHYLSILYL ESTER
2	15.607	1,519,042	11.10	HEXADECANOIC ACID, METHYL ESTER
3	15.809	192,622	1.41	n-PENTADECANOIC ACID, TRIMETHYLSILYL ESTER
4	16.595	75,701	0.55	OCTADECANOIC ACID, METHYL ESTER
5	16.784	3,575,513	26.14	HEXADECANOIC ACID, TRIMETHYLSILYL ESTER
6	16.924	45,600	0.33	ANDROST-1-EN-3-ONE, 17-HYDROXY (5.α., 17.β.)-
7	16.980	157,023	1.15	17-OCTADECEN-14-YNOIC ACID, METHYL ESTER
8	17.284	463,156	3.39	9,12-OCTADECADIENOIC ACID (Z,Z)-, METHYL ESTER
9	17.334	1,503,058	10.99	9-OCTADECENOIC ACID, METHYL ESTER
10	17.380	240,987	1.76	9-OCTADECENOIC ACID (Z-), METHYL ESTER
11	17.436	51,640	0.38	METHYL OCTADECA-9,12-DIENOATE
12	17.547	647,472	4.73	METHYL STEARATE
13	17.608	142,648	1.04	METHYL 15-HYDROXY-9,12-OCTADECADIENOATE
14	17.697	210,047	1.54	HEPTADECANOIC ACID, TRIMETHYLSILYL ESTER
15	17.813	60,642	0.44	4-BROMOBUTANOIC ACID, DODEC-3-YNYL ESTER
16	17.891	78,198	0.57	OXACYCLOHEPTADEC-8-EN-2-ONE, (8Z)
17	18.127	65,294	0.48	9,12-OCTADECADIENOIC ACID, METHYL ESTER
18	18.347	3,477,306	25.42	9,12-OCTADECADIENOIC ACID (Z,Z)-, TRIMETHYLSILYL ESTER
19	18.570	102,810	0.75	OCTADECANOIC ACID, TRIMETHYLSILYL ESTER
20	19.094	30,316	0.22	DOCOSANOIC ANHYDRIDE
21	19.272	28,802	0.21	2, PYRROLIDINONE, 1-[2-(4-PIPERIDINYL)ETHYL]-
22	19.322	24,106	0.18	EICOSANOIC ACID, METHYL ESTER
23	20.582	149,004	1.09	1,3,5-TRISILACYCLOHEXANE
24	21.266	59,380	0.43	HEXADECANOIC ACID, 4-TRIMETHYLSILYL ESTER
25	22.062	249,823	1.83	5,5-DIMETHYL-1,3-DIOXANE-2-ETHANOL, TERT-BUTYLDIMETHYLILYL ESTER
26	22.865	95,494	0.70	9-OCTADECENOIC ACID (Z)-,2-TRIMETHYLSILYL ESTER
27	26.257	851,928	0.62	9(11)-DEHYDROERGOSTERYL BENZOATE
28	27.678	91,601	0.67	STIGMASTA-4,7,22-TRIEN-3.BETAOL
29	32.549	229,002	1.67	16-HENTRIACONTANONE
		13,680,321	100	

The retention times, peak areas and area percentages are indicated.

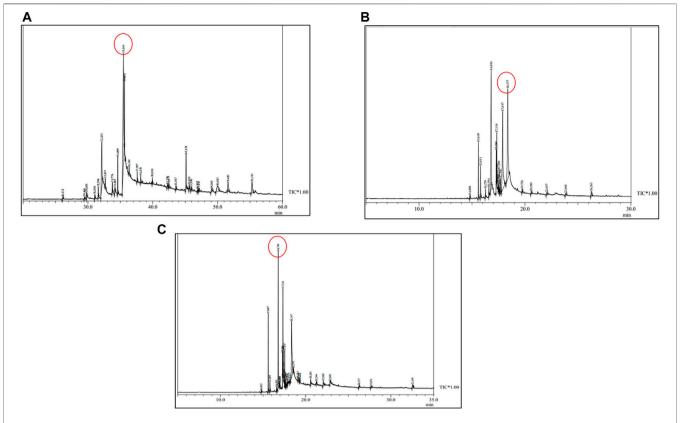


FIGURE 5 | Total ion chromatograms obtained after GC-MS analysis of *Cordyceps sinensis* supercritical carbon dioxide extracts. Based on area percentages, the most abundant volatile organic compounds in CSF1, CSF2 and CSF3 were revealed to be 9,12-octadecadienoic acid (Z,Z)- (A); 9,12-octadecadienoic acid (Z,Z)-, trimethylsilyl ester (B) and hexadecanoic acid, trimethylsilyl ester (C), respectively.

Similarly, the factor map constructed on basis of retention times of 67 constituent VOCs exhibited a variance of Dim 1 = 43.95% and Dim 2 = 24.85% (**Figure 6B**).

It can be clearly seen that CSF3 was present in separate quadrants, distinctive from CSF1 and CSF2, in case of both HPTLC as well as GC-MS profiling. This can be linked to the difference in metabolome owing to variation in extract preparation protocol. Moreover, the presence of CSF1 and CSF2 in the same quadrant and their proximity to each other illustrated their obvious interrelatedness (**Figure 6**).

CSF Extracts Exhibited Substantial Free Radical Scavenging and FRAP Activities

All the CSF extracts were capable of antioxidant power by virtue of free radical scavenging as well as ferric ion reduction. DPPH radical scavenging activities were 25.39 \pm 1.48, 18.82 \pm 3.42, and 11.65 \pm 1.44 μ M TE/g of extract, in that order for CSF1, CSF2 and CSF3. Similarly, ABTS assays brought out an activity of 15.05 \pm 0.91, 14.12 \pm 0.65, and 10.64 \pm 0.72 μ M TE/g of extract, correspondingly for CSF1, CSF2 and CSF3. FRAP results of the three supercritical CO₂ extracts explicated the antioxidant potential as 20.22 \pm 0.82, 16.47 \pm 0.44 and 11.14 \pm 0.43 μ M TE/g of extract. Overall, it can be verified from

above results that CSF1 had the highest antioxidant potency over the rest supercritical fluid extracts (Figure 7).

CSF Extracts Were Observed to Be Potent Antibacterial Leads Against *E. coli* and *S. typhi*

The significant presence of bioactive metabolites in the CSF extracts and their effective antioxidant abilities stimulated exploration of further bioeffects. In this context, evaluation of antibacterial activities clearly exhibited the efficacy of all three CSF extracts as potential antibacterial agents against pathogenic strains of *E. coli* and *S. typhi*.

For CSF1, agar disc diffusion studies brought out distinct zones of inhibition of diameters 7.0 ± 0.5 mm and 8.5 ± 0.7 mm against *E. coli* and *S. typhi*. Likewise, CSF2 wielded zones of inhibition of 7.5 ± 0.7 mm and 8.2 ± 1.0 mm averting *E. coli* and *S. typhi*. For these two pathogens, CSF3 exerted comparatively lesser antibacterial action wherein the zones of inhibition were 6.5 ± 0.5 mm and 6.5 ± 1.5 mm. The positive control, kanamycin gave distinct zones of inhibition of 30 ± 2 mm against *E. coli* and 35 ± 1.5 mm against *S. typhi*. The zones of inhibition and MIC values of all CSF extracts are noted in **Table 4**. Representative figure illustrating discrete zones of inhibition of CSF1 and CSF2 against *S. typhi* is given in **Figure 8A**.

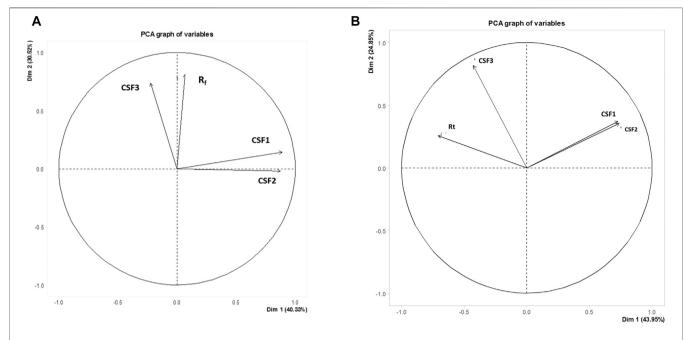


FIGURE 6 | Variables factor map depicting variances among CSF1, CSF2 and CSF3 extracts on basis of HPTLC (A) and GC-MS (B) metabolite profiling. Similarities were observed between CSF1 and CSF2, the supercritical extracts prepared using ethanol as co-solvent, owing to their close presence in same quadrant. CSF3 occurred on a separate quadrant from the former. R₁, retardation factor value of metabolites detected by HPTLC; R₁, retention time of VOCs identified by GC-MS.

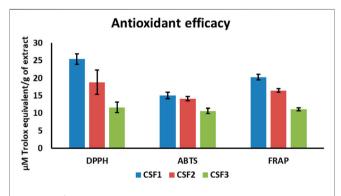


FIGURE 7 | Among all the supercritical CO_2 extracts of *Cordyceps sinensis*, CSF1 was discerned to have the highest *in vitro* free radical (DPPH, ABTS) scavenging activity and ferric ion reducing power (FRAP). Values are represented as mean \pm SD (n=3).

Owing to promising insights of CSF extracts being prospective antibacterials, certain typical mechanisms of inhibitory action were examined. Generation of ROS, induction of protein leakage and inhibition of efflux pumps were confirmed to be the modes of antibacterial action.

ROS generated in bacterial microenvironment after exposure to CSF extracts were measured using DCFDA. A linearly upward trend was indicated in levels of ROS formed with increasing doses of CSF1, CSF2 and CSF3 over 50–125 µg/ml, against both *E. coli* (**Figure 8B**) and *S. typhi* (**Figure 8C**). The bactericidal action was also analysed by probing concomitant leakage of intracellular proteins upon treatment with the CSF extracts. Results portrayed

TABLE 4 | Inhibitory action of *Cordyceps sinensis* supercritical carbon dioxide extracts on bacterial pathogens, *Escherichia coli* and *Salmonella typhi*.

Extract Zone of inhibition (mm)		MIC (μg/n		
CSF1:				
E. coli	7.0 ± 0.5	50		
S. typhi	8.5 ± 0.7	35		
CSF2:				
E. coli	7.5 ± 0.7	40		
S. typhi	8.2 ± 1.0	45		
CSF3:				
E. coli	6.5 ± 0.5	60		
S. typhi	6.5 ± 1.5	65		
Kanamycin:				
E. coli	30 ± 2	5		
S. typhi	35 ± 1.5	5		

Values for diameters of zones of inhibition (in mm) are given as mean \pm SD (n = 3). Values in μ g/ml indicate the specific minimal inhibitory concentrations (MIC). Kanamycin antibiotic was taken as the positive control against both pathogenic strains.

that incremented doses of these extracts resulted in higher amount of protein leakage from the bacterial pathogens–*E. coli* as seen from **Figure 8D** and *S. typhi* (**Figure 8E**). This observation was consonant with those obtained for ROS generation that the extent of bactericidal action was proportionate to CSF extract doses. **Figures 8B–E** also depict that CSF2 showed the most potent abilities in generation of ROS and eliciting protein leakage in the bacterial pathogens.

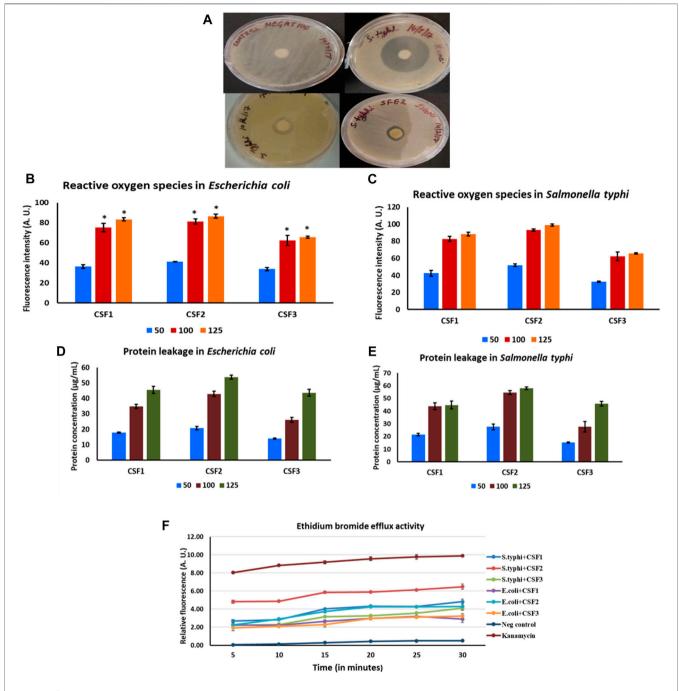


FIGURE 8 | Distinct zones of inhibition after treatment with CSF1 and CSF2 extracts, against pathogenic *Salmonella typhi* can be clearly seen **(A)**. Generation of reactive oxygen species after treatment with different doses (50, 100, 125 μ g/ml) of *Cordyceps sinensis* supercritical fluid extracts within *E. coli* **(B)** and *S. typhi* **(C)** was deduced as a potential antibacterial mode of action. Induction of protein leakage of aforesaid extracts against *E. coli* **(D)** and *S. typhi* **(E)** was confirmed to be yet another inhibitory mechanism. The supercritical fluid extracts also led to inhibition of efflux pump activities in the bacterial cells **(F)**. Nutrient broth and kanamycin acted as negative and positive controls, respectively. Data are expressed as mean \pm SD (n = 3). * represents significant change at level of p < 0.05.

Besides, it was also proven that CSF2 followed by CSF1 and finally, CSF3 effectually displayed EtBr efflux pump inhibitory activity against *E. coli* and *S. typhi*, thus revealing yet another essential mode of bactericidal action. The results are indicated in **Figure 8F**.

CSF Extracts Conferred Protective Action in HEK 293 Cells Against Hypobaric Hypoxia

Previous literature has sufficient evidence to testimony that hypoxic stress noticeably damages the normal functioning of kidney, thus leading to renal failure (Fu et al., 2016). Thus, it is

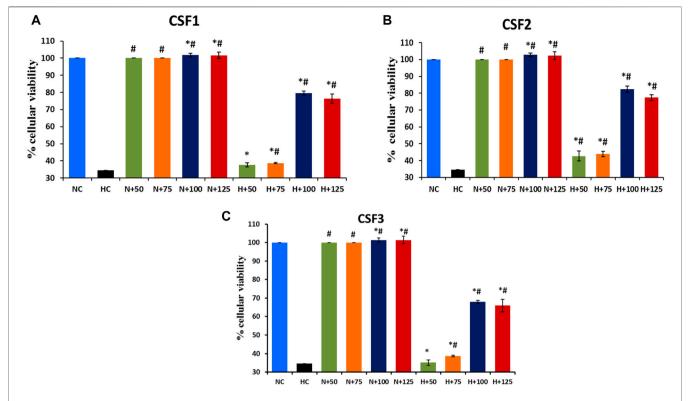


FIGURE 9 | Restoration of cellular viability by *C. sinensis* supercritical CO_2 extracts. At an optimum dose of 100 μ g/ml, CSF1, CSF2 and CSF3 improved HEK 293 cellular viability to 79.53% **(A)**, 82.36% **(B)** and 68% **(C)**, under hypoxia. N, normoxia; H, hypoxia; N+x, supplementation of various doses (x = 50/75/100/125 μ g/ml) of CSF in normoxia; H+x, supplementation of various doses (x = 50/75/100/125 μ g/ml) of CSF in hypoxia. Results are expressed as mean \pm SD (n = 3). * represents significant change at level of p < 0.05 with respect to N, # represents significant change at level of p < 0.05 with respect to H.

imperative to develop therapeutics for recuperating the detrimental effects of hypobaric hypoxia. With this perspective, the proficiency of *C. sinensis* supercritical CO₂ extracts as protective leads against hypoxia in human embryonic kidney, HEK 293 cells was probed.

Exposure to hypoxia in culture conditions significantly reduced the viability of HEK 293 cells to 37.5%, in contrast to 100% cell viability under normoxia. Significant restoration (p < 0.05) of cell viability under hypoxic milieu was brought about by the addition of CSF extracts. The effect of *C. sinensis* supercritical extracts in efficaciously countering the debilitating impact of hypoxia milieu is shown in **Figure 9**. Out of all the different doses that is, $50/75/100/125~\mu g/ml$ of the subject extracts being studied, $100~\mu g/ml$ was ascertained to be the optimal dose. The best cytoprotective action against hypoxia was conferred by CSF2 whose optimum dose of $100~\mu g/ml$ revived cell viability to $82.36~\pm~1.76\%$ (**Figure 9B**). This was followed by CSF1 and then CSF3 that improved cellular viability to $79.53~\pm~1.33\%$ (**Figure 9A**) and $68~\pm~0.75\%$ (**Figure 9C**), in that order.

CSF2 Efficiently Modulated HIF-1α in HEK-293 Cells, as a Predominant Protective Mechanism Against Hypobaric Hypoxia

The effect of the CSF extract showing highest protective potential, i.e, CSF2 was studied on modulation of HIF-1α, the main marker

of cell survivability under low oxygen tension. Western blotting experiments brought out that level of HIF-1 α , which was otherwise heightened in hypoxia conditions, was visibly diminished after supplementation with CSF2. β -Actin served as the loading control (**Figure 10A**). Densitometry by ImageJ revealed that CSF2 influenced a four-fold downregulation in the levels of HIF-1 α , as verified from **Figure 10B**.

DISCUSSION

The use of supercritical fluids is gaining ground as a "green technology" for faster production of bioactive extracts of higher purity, with the use of non-toxic solvents like water or CO₂. It is worth mentioning here that water has a critical temperature of 374°C and critical pressure of 22.1 MPa whereas CO₂ has parallel values of 31.2°C and 7.3 MPa. These moderate operational requirements of CO₂ make it a preferred choice over water in supercritical fluid extraction. The major advantages of using supercritical CO₂ from a pharmacological viewpoint is that, since the process parameters i.e., supercritical conditions are moderate, there is no risk of extract degradation. In addition, by bringing about slight variations in temperature or pressure, the selectivity of target compound can be varied. Moreover, CO₂ as a solvent is categorized as GRAS ("generally regarded as safe"), hence end products are not harmful or toxic. Also, the products

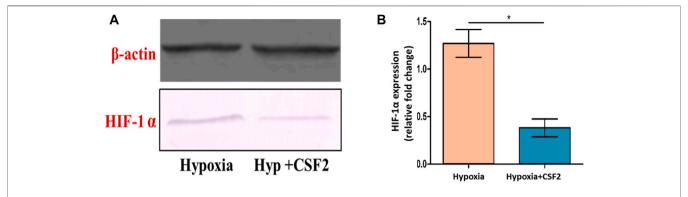


FIGURE 10 | Western blot showing level of hypoxia inducible factor-1 alpha (HIF-1 α) (**A**), which otherwise elevated under hypoxia stress, was decreased after supplementation with CSF2 (**B**). Hypoxia+CSF2 indicates supplementation of 100 μ g/ml of CSF2 extract in HEK 293 cells being cultured in low oxygen tension (0.5% O₂). Results are expressed as mean \pm SD (n = 3). * represents significant change at level p < 0.05.

are almost residue free; even if co-solvents like ethanol are added, they are easily removed (Bhusnure et al., 2015). Also, carbon dioxide has low viscosity and better diffusivity capacity in solid matrices owing to its dual gaseous and liquid-like properties, thus efficiently solubilizing the desired bioactive compounds (Capuzzo et al., 2013). Supercritical CO₂ has been reportedly used for separation of alkaloids, carotenoids, essential oils, flavones, preparation of several value-added pharmaceuticals, cosmetics, nutraceuticals, food additives, etc. (Machmudah et al., 2006; Takeuchi et al., 2010; Rahimi et al., 2011; Kagliwal et al., 2012).

The only shortcoming linked to the usage of supercritical CO₂ is its low polarity index that obstructs efficient extraction of polar compounds. This limitation is overcome with the addition of entrainers or co-solvents like methanol, ethanol, or water. Use of co-solvents indirectly enhances the solute contact with solvent, thus, offering an augmented overall solubility and optimum mass transfer, especially of bioactive polar compounds in the extract (Walsh et al., 1987; Pronyk and Mazza, 2009). Previous reports cite that the usage of co-solvents result in efficient extraction of polar compounds (Antunes-Ricardo et al., 2017; Wrona et al., 2017). It is always ensured that the co-solvent is added temperately, mostly ranging from 1 to 5% (w/w) so as to minimize time taken for its removal or recovery, per se. Ethanol being a food grade modifier is often used as the cosolvent for choice while preparing supercritical extracts for pharmacological or nutraceutical purposes (Sovová et al., 2001; Macías-Sánchez et al., 2009; Capuzzo et al., 2013; Nagavekar and Singhal., 2018) including separation of bioactive compounds from various traditional Chinese medicinal sources (Li, 2007).In this outlook, supercritical CO₂ along with ethanol as an entrainer was used for preparing supercritical extracts from the Indian high-altitude variety of "keera jhari" or C. sinensis.

Previous studies have established that an increase in extraction pressure enhances the fluid density, thus, increasing the solvating power, hence resulting in higher extraction yield. However, the effect of temperature in supercritical fluid extraction is not always linear. The influence of temperature on extraction is a lot more difficult to predict than that of pressure due to the above stated counter effects. An increase in temperature might lead to increase or decrease in yield, or even not affect the yield at all, depending

on the competing effect between fluid density and solute vapor pressure (Shao et al., 2014; Danlami et al., 2015; Hamid et al., 2018).

The results in our study were in agreement with the aforesaid observations where the higher yields were obtained with the highest extraction pressures, i.e., 300 and 350 bar. Also, the yields incremented with a combination of rising pressure and temperature, except for 350 bar and 60°C, which displayed lesser yield than that at 300 bar and 60°C (**Figure 1**). Since the major objective of our study was to establish the bioefficacy of the *C. sinensis* supercritical CO₂ extracts rather than an elaborate response-based analysis, we selected only those extracts of maximal yields, i.e., CSF1 (300 bar, 60°C) and CSF2 (350 bar, 60°C) for further analyses. For preparation of CSF3, i.e., without entrainer, the best yielding combination of pressure of 300 bar and temperature of 60°C was maintained.

With respect to the flow rate, certain studies have reported that higher solvent flow rate raises the operational and capital costs. Moreover, efficiency of the column is compromised with increased $\rm CO_2$ flow rate, since the HTU (height of a transfer unit) increases with increasing $\rm CO_2$ loading. Also, a high flow rate may cause decrease in the yield either by increasing analyte loss during fluid decompression or by increasing the pressure drop across the extraction cell. On the other hand, a very low flow rate might not facilitate ideal extraction at all (Mendiola et al., 2013; Shao et al., 2014). Keeping these factors in consideration, a moderate flow rate of 0.4 L/h was maintained in this study.

The three final extracts - CSF1, CSF2 and CSF3 had yields 0.75, 0.72 and 0.53% (w/w), respectively. Akanda et al. (2012) have cited that pressure, temperature and time can influence the supercritical extraction procedure, in turn, affecting the yields. The manner in which the above parameters affect the actual extraction depends on the type of the raw material and also on the target metabolite. In the present study, the extraction temperature was kept constant at 60°C. A pressure of 300 bar was applied over 2 h for CSF1. A higher pressure i.e., 350 bar was applied for a shorter time to obtain CSF2. The better yield of CSF1 than CSF2, despite a marginally higher extraction pressure, can be ascribed to the longer extraction time in the former. The noticeably lower yield of CSF3 highlighted the significant procedural impact of

ethanol as a co-solvent, which at a volume as low as 1%, enhanced the overall yield, and also the content of metabolites in CSF1 and CSF2, as discussed in subsequent paragraphs. The yields in current study were lower than conventional extraction methods wherein the yield of aqueous extract obtained by hot water extraction was reportedly 25.4% (Zheng et al., 2008). The yield as observed in case of accelerated solvent extraction was 33.3% (Rakhee et al., 2016). Despite lower yields, the supercritical $\rm CO_2$ extracts prepared here were rich in bioactive metabolites as discussed in following paragraphs.

The supercritical extracts were quantitatively characterized by HPTLC in terms of cordycepin, nucleobases and flavonoids. High throughput, ease of workflow and efficient automation in HPTLC procedure makes it an ideal tool for identification and quantification of bioactive molecules in natural extracts (El-Gindy et al., 2001). Cordycepin or 3'-deoxyadenosine, the predominant functional marker of Cordyceps spp. was quantified by HPTLC for quality assessment of the CSFs. It was found that CSF1 and CSF2 exhibited distinct bands suggestive of cordycepin, at quantities 296.6 ± 15.3 μg/g extract and 267.1 ± 9.2 μg/g extract, respectively. As depicted in Figure 1, there was a directly proportionate effect of extraction pressure on the extract yield, except the decrease at 350 bar, 60°C. Thus, CSF1 had better yield than CSF2. This lesser overall yield of CSF2 than CSF1 possibly influenced the lesser amount of cordycepin in CSF2, in comparison to CSF1. In addition, the longer extraction time period also contributed to the higher quantity of cordycepin detected in CSF1. CSF3, whose preparation was bereft of ethanol as co-solvent did not display any band specific to cordycepin, thus, indicating that ethanol was essential to extract out polar compounds. Cordycepin has been noted to exert anti-proliferative activity on cancerous cell lines like human colorectal adenocarcinoma, HT-29 and human colorectal carcinoma, HCT 116 (Lee et al., 2013; Jeong and Choi, 2014). Cordycepin has also been seen to elicit apoptosis in human leukemia cells via ROS-mediated caspase pathway. In line of this, presence of cordycepin in CSF1 and CSF2 indicated their potential bioactive properties.

Nucleobases identified in CSF1 and CSF2 extracts were adenine and cytosine, as seen in **Figure 3**. The markedly better content of these two nucleobases typically coincided with the higher yield and longer extraction time for procuring CSF1, in comparison to CSF2. Adenine plays key role in cellular respiration in higher organisms and cytosine is essential for energy transport (Hasan et al., 2019). Hence, availability of these nucleobases suggested their prospective bioeffects, especially from a hypoxia-protective standpoint.

Flavonoids encompass a class of bioactive compounds occurring in medicinal plants and mushrooms that have established benefits towards improvement of human health (Nijveldt et al., 2001). Specifically, quercetin, gallic acid, ascorbic acid and rutin were selected as the standard flavonoids for identification in *C. sinensis* supercritical extracts due to their reported anti-carcinogenic, anti-mutagenic and anti-oxidative modes of actions. In addition, supplementation of flavonoids in diet of human volunteers has been cited to induce free radical scavenging, blood viscosity lowering and

enhancement of function of vital organs (Hoensch and Kirch, 2005). Similar to cordycepin and nucleobases, even flavonoids namely, quercetin, gallic acid and ascorbic acid were quantitated to be more in CSF1 than CSF2 (**Figure 4**). These being polar compounds were not extracted efficiently in CSF3, which contained only quercetin.

HPTLC analysis clearly revealed that CSF1 had an overall higher content of all the aforementioned bioactive compounds than CSF2. This was possibly due to the fact that at a constant temperature, a rise in pressure increased the density of solvent, thus, solubilizing more quantities of flavonoids and nucleobases (Miao et al., 2010). A further increase in extraction pressure resulted in decreased vapour pressure which restricted solubility, hence the marginally lower quantities of compounds in CSF2. Nonetheless, presence of bioactive metabolites was confirmed in CSF1 and CSF2 which prompted investigation of their multifarious bioactivities as elaborated later.

VOCs have been extensively studied for diverse bioeffects. The types of VOCs expected in the supercritical CO₂ extracts in this study were fatty acids, fatty acid methyl esters and trimethylsilyl esters. Similar compounds have been reported in many medicinal plants and fungi (Dey and Chaudhuri, 2016; Adeoye-Isijola et al., 2018). As instance, hexadecanoic acid methyl ester, 9,12-octadecadienoic acid and 11-octadecenoic acid, methyl ester are known to impart anti-inflammatory, hypocholesterolemic and antimicrobial effects (Kalpana et al., 2012). Methyl stearate influences intestinal lipid metabolism regulation and also leads to antinociceptive, antioxidant, antifungal effects and so forth (Adnan et al., 2019). GC-MS analysis of supercritical extracts from *C. sinensis* have unveiled the presence of 9-octadecenoic acid, 9,12-octadecadienoic acid and hexadecanoic acid as the chief VOCs (Jianya et al., 2006).

In the current study, similar VOCs were perceived in CSF extracts (Tables 1-3 and Figure 5). 9,12-octadecadienoic acid (Z,Z)- was the most abundant VOC in CSF1 which is known to possess substantial antimicrobial, antioxidant, diuretic and hepatoprotective properties (Adeove-Isijola et al., 2018). Also, it is capable of anti-arthritic, anti-histaminic hypocholesterolemic activities (Kalaivani et al., 2012). In CSF2, 9,12-octadecadienoic acid (Z,Z)-, trimethylsilylester was major VOC which presumedly has diuretic, hypocholesterolemic and skin protectant properties in addition to anti-androgenic and anti-histaminic abilities (Sudha et al., 2013; Abubakar and Majinda, 2016). Finally, CSF3's most abundant VOC was seen to be hexadecanoic acid, trimethylsilyl ester which has antioxidant and contraceptive-like effects along with antimicrobial and free scavenging activities (Jain et al., 2012; Patil et al., 2013). These well recognized curative properties of constituent VOCs in all three CSF extracts motivated exploration of varied bioactivities of these extracts.

Metabolomics has emerged as an effective approach, especially while standardizing the pharmacological implications of the vast metabolome of natural extracts (Khan et al., 2017). Application of metabolomics by principal component analysis to the chromatographic profiling obtained from HPTLC and GC-MS, deliberated relatedness between the various supercritical extracts. Peak areas and retardation factor values in HPTLC, and area

percentages and retention times from GC-MS acted as input data for plotting the variables factor map. PCA works by decomposition of the eigenvector. Mean centring of data and data normalization are integral in this analysis. The primary axis representing the first principal component ("PC") or Dim 1 is responsible for describing maximum variance in the dataset. The next PC defines rest of the major variance as Dim 2. In present context, an overall variance of 70.85% in terms of metabolites detected by HPTLC was established. For GC-MS, summative variance with respect to metabolites detected, identified or otherwise, was 68.8%. Similarities in metabolite profiling between CSF1 and CSF2, as discussed in "Results" section, was corroborated by the proximal presence of these two extracts in same quadrant of variables factor map (Figure 6).

Extracts from medicinal mushrooms like Coprinopsis atramentaria, Xerocomus chrysenteron, Ganoderma lucidum and Cordyceps sinensis possess remarkable antioxidant abilities which is often accredited to their noteworthy content of flavonoids, phenolics, nucleobases and also VOCs (Pal et al., 2015; Bhardwaj et al., 2017). Supercritical CO₂ fractions from C. sinensis have been proven to possess excellent antioxidant effects (Wang et al., 2005). In line of this, the current study brought out efficient free radical (ABTS and DPPH) scavenging and FRAP of all three CSF samples. As reported earlier, flavonoids and VOCs are powerful antioxidant agents and often play key roles in antiviral and anti-proliferative features of natural extracts (Agati et al., 2012; Abubakar and Majinda, 2016). This validated the distinctive antioxidant efficacy of CSF1 followed by CSF2, which was much higher than that in CSF3 (Figure 7). This was plausibly because of higher amount of component polar compounds like flavonoids and nucleobases in the former two extracts due to use of co-solvents (Oman et al., 2013).

Incidence of increased bacterial resistance to synthetic antibiotics and related drugs has set the foreground to survey antibacterial candidates from natural sources (Alves et al., 2012). Supercritical fluid extracts from medicinal sources like *Gingko biloba* and palm are already known to have effective antibacterial and antifungal properties (Akanda et al., 2012; Oman et al., 2013). Concomitant to this, CSF1, CSF2 and CSF3 exerted bactericidal action against *S. typhi* and *E. coli*.

In addition to this, the prevalence of *E. coli* infection has been deemed to be more severe in uropathogenic infections. A study by Lin et al. (2015) had pointed out the importance of transcriptional regulator HIF-1α in innate defense against uropathogenic E. coli urinary tract infection. This was relevant to our study since we have used HEK 293 as cell culture model and have elaborated the modulation brought about by CSF extract on HIF-1a. Thus, the concerted effect of C. sinensis supercritical CO2 extracts in hindering the growth of E. coli while normalizing the adverse effects of hypoxia conditions in kidney cell line could be correlated here. As seen in Table 4, CSF1 and CSF2 displayed much better deterrent action with lower MIC values. The antimicrobial property of the C. sinensis supercritical extracts can be attributed to the presence of flavonoids like ascorbic acid and gallic acid (Pal et al., 2015). Besides, the constituent VOCs certainly contributed to the noticeable antibacterial activity. In the endeavour to deduce probable modes of antibacterial action,

ROS generation within the bacterial cells was observed as a primary mechanism. Amount of ROS generated and hence the degree of bactericidal action, incremented in a dose dependent manner for all the extracts (**Figure 8**). Recent literature has evidenced the effect of herbal extracts on cellular membrane damage by generating ROS formation in multidrug-resistant *Acinetobacter baumannii* (Zhang et al., 2015; Tang et al., 2016). The dose dependent increase in ROS generation is in accord with previous papers stating that natural compounds act as ROS producers to evoke antimicrobial response (Jiang et al., 2007).

As yet another inhibitory mode, protein leakage in pathogenic bacterial cells was confirmed. The effectiveness of *C. sinensis* supercritical extracts in inducing dose dependent protein leakage is probably indorsed to the richness of these samples in constituent mycoconstituents like flavonoids, nucleobases and bioactive VOCs, as proven from HPTLC and GC-MS experiments. These results are in concurrence to previous reports that flavonoids and VOCs are capable of conferring antimicrobial resistance against pathogenic microorganisms (Abubakar and Majinda, 2016; Singh et al., 2016).

Efflux pumps have been manifested to be major defensive components in Gram negative bacteria by causing active extrusion of antibiotic or related interventions from the periplasm and/or cytoplasm. In this manner, efflux pumps are discerned to render such bacterial pathogens resistant against antibacterial drugs. This type of resistance is often fathomed by the degree of EtBr efflux since viable bacterial cells curb uptake of EtBr via active efflux pump inhibitors. As a result, EtBr accumulates in bacterial cells with compromised membranes only, consequently emitting a strong fluorescence. In current study it was seen that CSF2, followed by CSF1 and finally CSF3 revealed efflux pump inhibitory activity against S. typhi and E. coli, designating their potency against these strains. Relative fluorescence suggesting EtBr accumulation is given in Figure 8F. A study by Lechner et al. (2008) portrays that plant phenolic compounds and flavonoids act as efflux pump inhibitors in Mycobacterium smegmatis. Also, secondary metabolites in herbal sources exhibit similar effect (Kumar et al., 2016). Hence, in concurrence to above observations and similar to ROS generation and protein leakage, the bioactive constituents detected in CSF1, CSF2 and CSF3 contributed to the efflux pump inhibition. Afore stated results attest the overall better antibacterial properties of CSF2, trailed closely by CSF1, corroborating the importance of ethanol as a co-solvent while preparing bioactive supercritical extracts.

Various restorative abilities of the medicinal mushroom under consideration have been well elaborated in evidence based medicinal systems. However, there are only few reports that describe the efficacy of *C. sinensis* in countering hypoxia-induced maladies. For instance, treatment with *C. sinensis* aqueous extracts imparted tolerance in adenocarcinoma human alveolar basal epithelial, A549 cell lines against hypoxia by declining ROS generation and lipid peroxidation. Cellular viability was restored up to 52% in the A549 cells. Expression of HIF-1 α , NRF-2 and NF- κ B were duly tempered, thus, proving the effectiveness of *C. sinensis* in hypoxia tolerance (Singh et al., 2013). Similarly, hydroethanolic extracts of *C. sinensis* endorsed

defence against hypoxia in neuronal hippocampal cells HT22, by accentuating cell viability to about 72% and also by enhancing anti-inflammatory cytokines and deterring pro-inflammatory cytokines (Pal et al., 2015). Phenolic fractions from C. sinensis conferred appreciable protective action against hypobaric hypoxia milieu in HEK 293 cell lines by recuperating cellular viability up to 79.5%. Additionally, these phenolic fractions catalysed a reduction in levels of superoxide dismutase and oxidized glutathione in experimental male Sprague Dawley rats, within a simulated hypobaric hypoxic setting (Rajput et al., 2020). Owing to above promising results, the C. sinensis supercritical CO₂ extracts were explored for hypoxia protective action in HEK 293 cell line. It was established that CSF2 proved to be a more prospective lead than the other supercritical CO₂ extracts as well as the aforesaid extracts (aqueous, hydroethanolic and phenolic) to overcome the loss in cellular viability in mammalian cells in vitro under low oxygen tension by reviving cellular viability to 82.36% (Figure 9). Bioactive constituents namely, ascorbic acid, rutin as well as adenine atone reduction of cell death in vitro under low oxygen stress conditions and therefore, possibly aided the role of CSF2 as therapeutic lead against hypobaric hypoxia (Winter et al., 2016; Patil et al., 2017).

Furthermore, in order to elucidate the mechanism by which CSF2 extract confers protection against hypoxia *in vitro*, its effect in modulating HIF- 1α was investigated. HIF- 1α , the subunit of HIF-1 transcription factor, is the most important functional component of cellular homeostasis under low oxygen stress that regulates cellular redox status (Nehra et al., 2015). In stark contrast to normoxia conditions, the level of HIF- 1α gets overexpressed manifold in oxygen deficient milieu. However, treatment with appropriate therapeutic candidates leads to downregulation of this transcription factor. Congruent results were obtained in current study, where Western blotting analyses explicated that supplementation with optimal dose of CSF2 extensively downregulated the levels of HIF- 1α by four-fold thus, establishing its prominent protective role against hypoxic insult in HEK 293 cells (**Figure 10**).

The major objective of the present study was to establish *C. sinensis* supercritical CO₂ extracts as prospective therapeutic in a holistic manner. Extracts prepared from medicinal plants and mushrooms consist of a plethora of bioactive compounds. Bioeffects imparted from such extracts are a result of synergistic and/ or additive action of various molecules (Zhao et al., 2015; Segneanu et al., 2017; Gupta et al., 2018; Das et al., 2020). This study has confirmed varied activities viz., antioxidant, antibacterial and

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hypoxia protective action of the supercritical extracts in consideration which largely is because of their richness in terms of different metabolites e.g. flavonoids, nucleobases and VOCs.

CONCLUSION

The present research highlighted multifarious pharmacological properties of the well revered medicinal mushroom, *Cordyceps sinensis*. Supercritical fluid extraction using CO₂ yielded three distinct extracts of superior quality. Elaborate chromatographybased metabolite profiling by HPTLC and GC-MS signposted the rich chemical composition of *C. sinensis*. Application of metabolomics on the chromatographic data by principal component analysis helped in confirming similarities between CSF1 and CSF2. Overall, the results strongly indicate that *C. sinensis* supercritical fluid extracts can be projected as candidates for mycotherapeutics development, especially for recuperation against hypobaric hypoxia. Furthermore, determination of bioprocess efficiency in terms of product quality and yield needs to be addressed to materialize the use of above extracts on an industrial scale.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

AUTHOR CONTRIBUTIONS

JM performed the chromatographic, metabolomics, microbiological and cell culture procedures and also, wrote the manuscript. WK conducted the extraction experimentation and its data interpretation. SA contributed to conceptualization and data investigation. KM planned the overall work and critically evaluated all the data and manuscript.

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Dose-Effect/Toxicity of Bupleuri Radix on Chronic Unpredictable Mild Stress and Normal Rats Based on Liver Metabolomics

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Wang P, Gao X, Liang M, Fang Y, Jia J, Tian J, Li Z and Qin X (2021) Dose-Effect/Toxicity of Bupleuri Radix on Chronic Unpredictable Mild Stress and Normal Rats Based on Liver Metabolomics. Front. Pharmacol. 12:627451. doi: 10.3389/fphar.2021.627451 Depression, one of the most prevalent psychiatric diseases, affects the quality of life of millions of people. Studies have shown that the lower polar fraction of Bupleuri Radix (PBR) elicited therapeutic effects in chronic unpredictable mild stress (CUMS) rats. In contrast, comparatively mild liver injury was observed in normal rats administered a high PBR dose. It is essential to clarify the effective and safe dose of PBR and its dose-effect/toxicity relationship. In this study, we used the CUMS model to evaluate the effects and toxicities of PBR and to decipher the dose-effect/toxicity relationship and mechanism using the liver metabonomics combined with multivariate statistical analysis. In CUMS rats, PBR improved the depression-like behaviors including reduced body growth rate, anhedonia, and locomotor activities, and markedly reduced the contents of alanine aminotransferase (ALT) and aspartate aminotransferase (AST). In control rats, PBR treatment altered ALT and AST from typical levels. Moreover, the effective dose range for CUMS rats was 12.6–163 g (herb)/kg, the median toxicity dose for CUMS and normal rats were 388 and 207 g (herb)/kg. The toxicological results showed that the cytokeratin-18 fragment level was increased significantly in CUMS rats given with 100 g (herb)/kg PBR. After a comprehensive analysis, the use of PBR dose was determined to be 12.6-50 g (herb)/kg. In CUMS rats, PBR could reverse amino acid metabolism, energy metabolism, sphingolipid metabolism, and β-oxidation of fatty acids to produce an antidepressant effect in a dose-dependent manner. In control rats, two additional metabolic pathways were significantly perturbed by PBR, including glycerophospholipid metabolism and bile acid metabolism. Moreover, the comprehensive metabolic index including dose-effect index (DEI) and dose toxicity index (DTI) had a remarkable ability (ROC = 0.912, ROC = 0.878) to predict effect and toxicity. The DEI and DTI were used to determine the dose range of effect and toxicity which was shown high concordance with previous results. Furthermore, the CUMS rats possessed a higher toxicity tolerance dose of PBR which was consistent with the theory of "You Gu Wu Yun" in traditional Chinese medicine. The metabonomics techniques combined with correlation analysis could be used to discover indicators for comprehensive evaluations of efficacy and toxicity.

Keywords: bupleuri radix, anti-depression, dose- effect/toxicity, UHPLC-MS, CUMS, liver metabolomics

INTRODUCTION

Depression, a complicated psychiatric disorder, leads to low morale, weight loss, and anhedonia (Fabricatore and Wadden, 2006; Paykel, 2006). It is considered the fourth leading cause of disability worldwide and the third leading cause of global disease burden (Sayers, 2001; Mathers and Loncar, 2006). The current clinical anti-depressant drugs are ineffective on at least a quarter of patients and produce side effects such as psychomotor impairment, dependence and hepatotoxic reactions (Sarko, 2000; Ishino and Park, 2013; Voican et al., 2013). Traditional Chinese medicines (TCMs) might offer here new options for depression therapy (Liu et al., 2021). Therefore, research studies have paid increasing attention to the TCMs in treating depression.

Bupleuri Radix, the root of Bupleurum chinense DC. or Bupleurum scorzonerifolium Wild., and is one of the most popular traditional Chinese medicines (TCMs) over the past 2,000 years. The main pharmacological effects of Bupleuri Radix are soothing the liver and relieving depression, evacuating fever, and elevating "Yang Qi" (The Pharmacopoeia Commission of the PRC, 2020). Clinical studies have shown that Bupleuri Radix has also been used for anti-virus infection, antiacute radiation injury, anti-ulcer effect, reducing blood lipid, inducing serum interferon, enhancing immune function, etc. (Xing, et al., 2017; Jiang et al., 2020). Along with the steadily increasing use of Bupleuri Radix, safety has been highlighted. The effect of "robbing liver yin" of Bupleuri Radix had been widely reported since the Ming and Qing Dynasties (Teo et al., 2016). Modern studies have shown that Bupleuri Radix caused acute liver injury, hepatocyte apoptosis, and acute hepatitis following overdose or long-term, unrestricted and unjustified use (Wang and Song, 2014). Some components in the sibling species of Bupleuri Radix including bupleurotoxin, acetylbupleurotoxin, and saikosaponin D have been reported neurotoxic effect and hepatotoxicity, respectively (Zhang et al., 2014; Zhang F. et al., 2015). In our previous study, the Bupleuri Radix improved depression-like behaviors in chronic unpredictable mild stress rats (CUMS, a depression model of depression, Zhou et al., 2011; Liu et al., 2013). The lower polar fraction of Bupleuri Radix (PBR) had the strongest antidepressant activity than other parts of Bupleuri Radix (Meng et al., 2020). However, comparatively mild liver injury was observed in normal rats administered high doses (Gao et al., 2017).

The liver is the center of material metabolism and energy metabolism. It plays diverse biological roles in oxidative stress and glycogen storage. In traditional Chinese medicine (TCM), the liver has become the main target organ of depression treatment (Jia et al., 2016; Jia et al., 2017). Depression is considered to be "liver qi stagnation", and relieving "liver qi stagnation" is regarded as an effective method for treating depression in TCM theory (Li, et al., 2020; Chen, et al., 2020a). Xiaoyao San and Radix Bupleuri were the well-known TCM formula for the treatment of depression by relieving "liver qi stagnation" (Liu, et al., 2021; Zhang, et al., 2020). In addition, modern pharmacological studies have shown that chronic stress might cause liver injury by disturbing hepatic function indices (Chen, et al., 2020b), hepatic metabolic profile (Gao, et al., 2017), and the

genes expression in phospholipid and primary bile acid biosynthesis pathways (Jia, et al., 2016; Tian, et al., 2017). Furthermore, clinical studies have shown that chronic and acute liver disease patients exhibited different degrees of depression reversely (Nardelli et al., 2013; Suh, et al., 2013; Youssef et al., 2013). Therefore, the liver was selected as a primary target organ of efficacy and toxicity for PBR. Metabonomics is widely used to discover biomarkers and recognize key pathways involved in biological processes (Medina et al., 2014). Currently, Liquid chromatography with mass spectrometry (LC-MS) is becoming the mainstream platform for metabonomics research because of its rapid analysis, high resolution, and high sensitivity (Theodoridis et al., 2012). Advanced analytical techniques of LC-MS and computational methods of metabonomics technologies can provide unique and fundamental insights into disease and therapeutic progression.

In this study, liver metabonomics combined with correlation analysis was applied to characterize the metabolic profile of CUMS rats and the dose-effect/toxicity relationship of PBR in the physiological and pathological conditions of rats (**Figure 1**). This study provides an objective reference for the evaluation of the safety and effectiveness of PBR.

MATERIALS AND METHODS

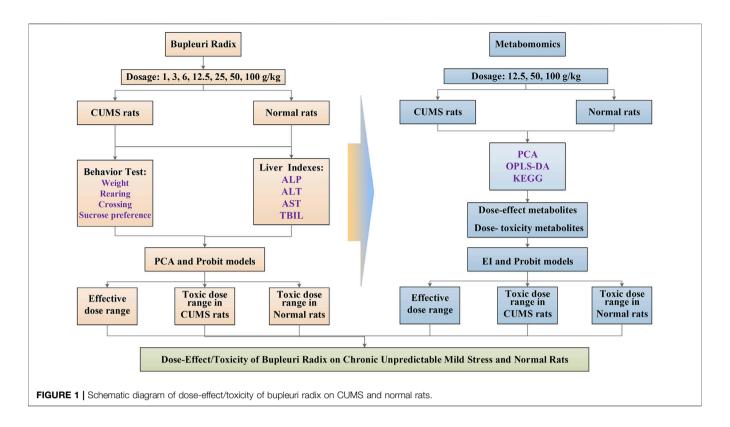
Instruments, Chemicals and Reagents

An UltiMate 3,000 ultrahigh performance liquid chromatography (UHPLC, Thermo-Fisher, United States) in tandem with a Q Exactive Orbitrap-MS (Thermo-Fisher Scientific, United States) was used. Xcalibur workstation (Thermo Fisher Scientific, United States), IKA T10 tissue homogenizer (Ningbo Xinzhi Biotechnology Co., Ltd, China), Neofuge13R high-speed freezing centrifuge (Likang Biotechnology Company, China), and MX-S Adjustable mixer (Scilogex, United States) were used. LC-MS grade acetonitrile and HPLC grade formic acid were obtained from Thermo-Fisher (United States).

Preparation of PBR

The preparation of PBR was briefly described in our previous study (Gao et al., 2017). Five kilograms of Bupleuri Radix (Shanxi Huayang Pharmaceutical Co., Ltd., China) were extracted three times with 95% fresh ethanol, each extraction was performed for 2 h. The mixture was filtered, and the filtrate was concentrated under reduced pressure to obtain an aqueous solution. For further extraction, the aqueous solution was extracted three times with an equal volume of petroleum ether by using 30 min ultrasonication. The petroleum ether fraction (approximately 128.5 g, with an extract yield of 2.57%) was obtained after concentration and drying (60°C).

To assure the quality of PBR, eight polyacetylene compounds from PBR were detected by UPLC Photodiode Array (PDA) analysis in our previous study (Zhang et al., 2017). In this study, the contents of the main active compounds of (2Z, 8E, 10E)-pentadecatriene-4,6-diyn-1-ol and bupleurynol in PBR were 3.62 mg/g and 1.88 mg/g detected by UPLC-PDA. Polyacetylenes accounted for approximately 30% of the total components in PBR, using a quantitative analysis of multiple



components by a single marker (QAMS, Xie et al., 2010; Supplementary Figure S1, 2).

PBR extract and venlafaxine was dissolved in distilled water containing 0.5% CMC-Na and 0.5% Tween-80 at seven concentrations of 0.1, 0.3, 0.6, 1.25, 2.5, 5.0, and 10.0 g (herb)/mL for PBR and 3.5 mg/ml for venlafaxine for administration of animal experiments. Among them, the 12.5 g (herb)/kg PBR was regarded as the medium dose, which was based on the effective dose reported in previous research (Gao et al., 2013).

Animals

136 healthy, adult, 6 weeks old male Sprague-Dawley (SD) rats, 200 \pm 20 g weight, license NO. SCXK (JING 2012–0001) were purchased from the Experimental Animal Center of Beijing Weitong Lihua Technology Co. Ltd. (China). The rats were acclimatized for 1 week and maintained on a 12 h light/dark cycle (lights on from 6:00 a.m to 6:00 p.m.), 30–70% relative humidity and temperature (23–27°C) with a commercial diet and water available. All animal experiments were performed under the NIH Guidelines for Care and Use of Laboratory Animals (United States) and the Prevention of Cruelty to Animals Act (1986) of China, and the experiments were approved by the Animal Ethics Committee of Shanxi University (ethical batch number: SXULL2019004).

Drug Administration and Experimental Design

After 1 week of adaptation, the animals were randomly divided into 17 groups (n = 8): [CM] CUMS rats, [K] control rats,

[C1] \sim [C7] CUMS rats given PBR (7 different dosages), [Z1] \sim [Z7] control rats administered PBR, and [CY] CUMS rats administered venlafaxine hydrochloride as a positive control (**Table1**). The different oral doses of PBR were 1, 3, 6, 12.5, 25, 50, and 100 g (herb)/kg, and the oral dose of venlafaxine was 35 mg/kg. All rats were administered agents by gavage at a dose of 10 ml/kg body weight once daily for 21 days, 1 h before modeling.

The control rats were housed together, while the CUMS rats were housed alone and exposed to nine mild stressors randomly every day including swimming in 4°C cold water for 5 min, foot shocking for 2 min (36 V, one shock/2 s, 10 s duration), tail clamping for 2 min, noise for 3 h (60 dB), day-night reversal (12 h/12 h), exposure to an experimental room at 45°C for 10 min, constraint for 3 h, food deprivation for 24 h, and water deprivation for 24 h (Supplementary Table S1; Gao et al., 2017).

Behavioral Tests and Measurement of Liver Function

During the experiment, all the behavioral tests were measured in day 0 (served as the baseline) and day 21. The rats were weighed and this index reflected the basic survival state of the rats. The open-field test was conducted to measure the number of rearings (defined as standing upright on the hind legs) and the number of crossings (grid lines crossed by the rat with at least three paws). The different forms of activity were used to assess the rats' mobility. Sucrose preference values were calculated as the percentage of 1% sucrose solution consumed relative to the total liquid intake within 4 h. This test was used to assess

TABLE 1 | Animal grouping and processing.

Group	Animal model	Drug	Dosage (g/kg)	Administration	
K	_	Solvent	_	Intragastrical	
CM	CUMS	Solvent	_	Intragastrical	
CY	CUMS	Venlafaxine hydrochloride	0.035	Intragastrical	
C1	CUMS	PBR	1	Intragastrical	
C2	CUMS	PBR	3	Intragastrical	
C3	CUMS	PBR	6	Intragastrical	
C4	CUMS	PBR	12.5	Intragastrical	
C5	CUMS	PBR	25	Intragastrical	
C6	CUMS	PBR	50	Intragastrical	
C7	CUMS	PBR	100	Intragastrical	
Z1	_	PBR	1	Intragastrical	
Z2	_	PBR	3	Intragastrical	
Z3	_	PBR	6	Intragastrical	
Z4	_	PBR	12.5	Intragastrical	
Z5	_	PBR	25	Intragastrical	
Z6	_	PBR	50	Intragastrical	
Z7	_	PBR	100	Intragastrical	

Note: [CM] CUMS rats, [K] control rats, [C1] ~ [C7] CUMS rats given PBR (7 different dosages), [Z1] ~ [Z7] control rats administered PBR, and [CY] CUMS rats administered venlafaxine hydrochloride. The solvent was water containing 0.5% CMC-Na and 0.5% Tween-80. All the rats were given agents at a dose of 10 ml/kg body weight.

anhedonia-like behavior. The growth rate (Δ %) of body weight, rearings, crossings, and sucrose preference values were calculated using the formula (F_{21} – F_0)/ F_0 , where F_{21} were the body weight, rearings, crossings, and sucrose preference values on the day 21, and F_0 were the body weight, rearings, crossings, and sucrose preference values on the day 0. The growth rate was used to reflect the behavioral changes in CUMS and control rats between day 0 and 21.

The rats were anesthetized with 10% chloral hydrate at 8:00 a.m. on day 21. Blood was collected from rats 1 h after administration from the abdominal aorta. After 30 min incubation, the serum was separated by centrifugation at 3,500 rpm for 15 min, and then stored at -80° C. Then, the rats were sacrificed by cervical dislocation, and the liver was quickly removed, frozen in liquid nitrogen, and stored at -80° C.

A portion of the serum was used for quantification of alanine aminotransferase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP), and total bilirubin (TBIL) using an automated biochemical analyzer (Konelab PRIME 7.2.1, Finland). Cytokeratin-18 fragment (CK-18F) was quantitatively measured in the serum and liver using the M30 Apoptosense ELISA kit (Shanghai Enzyme-linked Biotechnology Co., Ltd., China). These biochemical indices were examined to assess hepatic function.

Sample Preparation

To extract metabolites, each liver tissue sample (250 mg) was thawed, and 1,500 μL of chilled acetonitrile containing 0.2% formic acid was added. The sample was homogenized in an ice bath and centrifuged at 13,000 rpm for 15 min at 4°C. The supernatant was transferred to a fresh tube and dried in a refrigerated vacuum centrifugal dryer. The dried residue was dissolved in 500 μL of the solvent containing 0.1% formic acid water-acetonitrile (9:1, ν/ν) and centrifuged at 13,000 rpm for 15 min at 4°C. A 5 μL supernatant was injected for UHPLC-MS analysis.

LC-MS Analysis

UHPLC Q Exactive Orbitrap-MS conditions for liver analysis were the same as those described in our previous study (Gao et al., 2017). UHPLC was performed using a Thermo-Fisher UHPLC coupled to a Q Exactive Orbitrap-MS (Thermo-Fisher, United States). Chromatographic separation was achieved on a Waters ACQUITY UPLC HSS T3 column $(2.1 \times 100 \text{ mm}, 1.8 \mu\text{m})$ maintained at 40°C. The mobile phase consisted of 0.1% formic acid in water (A) and 0.1% formic acid in acetonitrile (B), respectively, and operated under the following program with a flow rate of 0.2 ml/min: 0-2 min, 2% B; 2-3 min, 2-35% B; 3-17 min, 35-70% B, 17-18 min, 70% B; 18-29 min, 70-98% B; 29-31 min, 98% B; 31–33 min, 98–2% B; 33–35 min, 2% B. The sample injection volume was 5 µL. The mass spectrometer was fitted with an electrospray ionization source, and the ESI source was used in both positive and negative ion modes at a temperature of 320°C. Nitrogen was used as the sheath and auxiliary gas at flow rates of 35 and 10 arb. The heater gas temperature was 300°C, and MS data were collected in the full-scan mode in the m/z range of 100-1,500.

Quality control (QC) samples were processed in the same way as the analytical samples and injected throughout the run to monitor the LC/MS platform's stability.

Behavioral Regulation Index (BRI) and Liver Composite Index (LCI)

The behavioral findings and liver biochemical indexes were regarded as the primary evaluation metrics to determine the effect and toxicity dose range of PBR. The behavioral regulation index (BRI) and liver composite index (LCI) were presented as composite scores by combining behavioral indexes and liver biochemical indexes. In this study, principal component analysis (PCA) was used to calculate BRI and LCI, with the formula:

$$f_1 = k_1 z x_1 + k_2 z x_2 + k_3 z x_3 + k_4 z x_4 \tag{1}$$

$$f_2 = k_5 z x_1 + k_6 z x_2 + k_7 z x_3 + k_8 z x_4 \tag{2}$$

$$f = \frac{\lambda_1}{\lambda_1 + \lambda_2} f_1 + \frac{\lambda_2}{\lambda_1 + \lambda_2} f_2 \tag{3}$$

Where f was the composite score of BRI or LCI, f1 and f2 were the first principal component PC1 and the second principal component PC2 of BRI or LCI. x_1 , x_2 , x_3 , and x_4 represented body weight, sucrose preference, ambulation number, and rearing number for BRI or the levels of ALT, AST, ALP, and TBIL for LCI, zx was the standardized raw variable of x_i , λ was the rate of variance contribution, and k was the score of each group for every principal component.

The determination of the effective dose range for CUMS rats and the TD50 (median toxicity dose) for CUMS and control rats was as follows. Firstly, the effective and safe range was determined respectively based on the behavior and liver function of control rats (Mean \pm 1.96SD, Xie et al., 2010). Secondly, after administration with PBR, the CUMS rats adjusted to the effective range were defined as positive samples for effect, and the CUMS and control rats deviated from the safe range were defined as positive samples for toxicity. Finally, the numbers of positive samples were counted in different groups, and probit regression was used to determine the dose range of effect and toxicity.

Data Processing and Statistical Analysis

Raw data were processed using Compound Discoverer 2.0 (Thermo Fisher, United States) to obtain the matched and aligned peak data. The processing parameters were as follows: m/z 100–1,500 Da; mass tolerance 5 ppm, RT tolerance 0.05 min, and S/N threshold 3.

The data matrix was established by aligning peaks with the exact retention time and normalizing the peak value. The (Rt)m/z pair from each file was subjected to multivariate analysis using SIMCA-P software (version 13.0, Umetrics, Sweden), including PCA, partial least-squares discriminant analysis (PLS-DA), and orthogonal partial least squares (OPLS) discriminant analysis of the data from both positive and negative modes. PCA was performed to discern the natural separation between different stages of the samples by visual inspection of the score plots. The PLS-DA model was acquired by projecting the predicted variables and observable variables into a new space. In the OPLS-DA model, samples from different groups were classified, and the results were visualized as score plots to show the group clusters, and S-plots to show the variables contributing to classification. The variable importance in the projection (VIP) value reflects the influence of every variable on the classification, and the independent sample t-test was also included in the analysis of the discriminating variables. p < 0.05, and VIP>1 were considered statistically significant.

The Human Metabolome Database (HMDB), KEGG, and the LIPI\MAPS-Nature Lipidomics Gateway (http://www.lipidmaps.org/) and related literature were queried with the exact masses of the metabolites to identify the differential

metabolites and to understand better the metabolic pathways affected by CUMS stress or PBR. The metabolic correlation network and metabolic networks were constructed using Cytoscape software (v.3.5.0).

Dose-Effect and Dose-Toxicity Metabolic Screening

For further screening of the dose-effect and dose-toxicity metabolites, the related metabolites were analyzed by correlation analysis (SPSS 21, Pearson correlation analysis) between the different metabolites and the different dosages with p>0.05. The dose-effect and dose-toxicity metabolites were obtained based on regression analysis (Prism 8.0, linear regression analysis) between the related metabolites and dosages with R>0.6.

Construction and Evaluation of Dose-effect and Dose-toxicity Models

In this study, four models were used to integrate dose-response and dose-toxicity metabolites, including PCA, effect index (EI), SUM, and (R) SUM (additivity related to metabolites' R-values), and then the ROC curve was used to evaluate the performance of the four models and metabolites.

Dose-Effect and Dose-toxicity Index Calculations and Evaluations

In this study, the dose-effect index (DEI) and dose toxicity index (DTI) of each sample was used as the composite indicator. The formula for calculating DEI and DTI was as follows (Zhang ZZ. et al., 2015).

$$DEI = \sum_{i=1}^{n} \left| \frac{Ci - C\bar{M}i}{C\bar{M}i - \bar{K}i} \right| \times 100\%$$
 (5)

$$DTI = \sum_{i=1}^{n} \left| \frac{Zi - \bar{K}i}{\bar{K}i} \right| \times 100\%$$
 (6)

Ci was the relative level of one of the metabolites in every rat in the C4, C6, and C7 groups, Zi was the relative level of one of the metabolites in each rat in the Z4, Z6, and Z7 groups, Ki was the average relative level of one of the metabolites in the K group, and $C\overline{M}i$ was the average relative level of one metabolite in the CM group.

The dose-effect and dose-toxicity relationships were evaluated using regression analysis (Prism 8.0, linear regression analysis).

Statistical Analysis

Quantitative data were presented as the mean \pm SD. The significance of differences between groups in terms of behavioral changes was determined using one-way ANOVA with SPSS software (version 21.0). Student's t-test was used to compare two groups, and statistical significance was set at p < 0.05.

TABLE 2 Behavior on CUMS and healthy rats administration with PBR (Mean \pm SD, n = 8).

Group	Weight (∆%)	Rearings (∆%)	Crossings (∆%)	Sucrose preference value (Δ %)	
C1	0.351 ± 0.011**	-0.394 ± 0.181##	-0.261 ± 0.037**	-0.37 ± 0.053**##	
C2	0.311 ± 0.006*	$-0.486 \pm 0.259^{\#}$	$-0.303 \pm 0.075^*$	$-0.18 \pm 0.045^{\#}$	
C3	$0.339 \pm 0.007^{**}$	$-0.532 \pm 0.106^{##}$	$-0.342 \pm 0.187^{\#}$	$-0.22 \pm 0.064^{##}$	
C4	0.342 ± 0.008**	0.294 ± 0.112*##	$-0.253 \pm 0.102^{**}$	$-0.293 \pm 0.076^{*##}$	
C5	0.308 ± 0.001*	0.283 ± 0.201**#	$-0.186 \pm 0.070^{**}$	$-0.24 \pm 0.034^{##}$	
C6	0.312 ± 0.004*	0.126 ± 0.042**	$0.134 \pm 0.044^{**#}$	0.188 ± 0.051*	
C7	$0.181 \pm 0.009^{*#}$	0.052 ± 0.022**	$-0.032 \pm 0.008^{**}$	$-0.29 \pm 0.083^{\#}$	
Z1	0.312 ± 0.007**	0.094 ± 0.081**	$-0.277 \pm 0.048^*$	0.136 ± 0.025*	
Z2	0.316 ± 0.005**	0.104 ± 0.059**	$-0.268 \pm 0.059^*$	$0.166 \pm 0.048^*$	
Z3	0.318 ± 0.017**	0.148 ± 0.086**	$-0.312 \pm 0.086^*$	$0.103 \pm 0.053^*$	
Z4	$0.314 \pm 0.002^{**}$	0.078 ± 0.051**	$-0.329 \pm 0.102^*$	$0.149 \pm 0.063^*$	
Z5	$0.308 \pm 0.007^{**}$	$0.114 \pm 0.014^{**}$	$-0.316 \pm 0.081^*$	$0.114 \pm 0.074^*$	
Z6	$0.315 \pm 0.004**$	0.126 ± 0.053**	$-0.283 \pm 0.039^*$	$0.124 \pm 0.048^*$	
Z7	$0.309 \pm 0.011**$	0.058 ± 0.036**	$-0.296 \pm 0.019^*$	$0.096 \pm 0.043^*$	
CM	$0.243 \pm 0.008^{\#}$	-0.381 ± 0.235 ^{##}	$-0.3932 \pm 0.193^{##}$	$-0.2 \pm 0.028^{\#}$	
CY	$0.294 \pm 0.014^*$	$-0.398 \pm 0.179^{\#}$	$-0.292 \pm 0.075^*$	$0.118 \pm 0.022^*$	
K	$0.313 \pm 0.009^{**}$	0.121 ± 0.083**	$-0.307 \pm 0.096^*$	$0.037 \pm 0.009^*$	

Note: [CM] CUMS rats, [K] control rats, [C1] \sim [C7] CUMS rats given PBR (7 different dosages), [Z1] \sim [Z7] control rats administered PBR, and [CY] CUMS rats administered venlafaxine hydrochloride. #, compared with the K group (#p < 0.05, ##p < 0.01); *, compared with the CM group (*p < 0.05, **p < 0.01).

RESULTS

The Dose Range of the Effects and Toxicity in CUMS and Control Rats Administered PBR

Behavioral and Liver Function Indexes on CUMS and Control Rats Administration With PBR

The results of the behavioral tests, including body weight, sucrose preference test, and open-field test during the stress period of 21 days in CUMS and control rats are shown in Table 2 and Supplementary Table S2. PCA was applied to the behavior indexes, and the PCA scores were expressed in twodimensional scatter plots (PC1 and PC2 plotted on the x and y axes, respectively). The PCA score plot revealed the separation of CUMS rats from normal rats, suggesting that depressive-like behaviors developed in CUMS rats (Supplementary Figure S3A). The PCA score plot of C1-C7 groups was observed in the K and CM groups, indicating that the depressive-like behavior of CUMS rats was altered by PBR administration but existed in an effective dose range. As shown in **Table 2**, the growth rate (Δ %) of bady weight, rearings, crossings and sucrose preference values slower significantly (p < 0.05) in CUMS rats compared with the control group, and the concentration range of 12.5-100 g/kg (C4-C7) of the PBR significantly reversed the decrease of the growth rate, especially in the C6 group (50 g/kg), suggesting that PBR played an anti-depression role in improving the slow body weight gain, anhedonia, and locomotor activities in CUMS rats. However, there was no distinct impact of PBR on control rats (Table 2 and Supplementary Table S2).

Similarly, PCA was applied for liver function indices, and no obvious distinction was observed in the PCA score plot of each group (**Supplementary Figure S3B**), suggesting that there were no significant differences in liver function between the groups.

TABLE 3 Liver function indexes in CUMS and healthy rats administration with PBR (Mean \pm SD, n = 8).

Group	ALP	ALT	AST	TBIL
C1	226.5 ± 36.7 ^{##**}	51.8 ± 6.3**	129.3 ± 8.6**	11.1 ± 2.6
C2	196.6 ± 39.7	59.1 ± 21.6*	121.5 ± 21.1#***	$7.3 \pm 1.0^{\#}$
C3	193.9 ± 28.4	64.1 ± 37.9	120.6 ± 10.2 ^{#**}	$5.5 \pm 2.7^{\#}$
C4	176.8 ± 38.6	62.0 ± 9.3	118.3 ± 26.8#***	$6.7 \pm 2.9^{\#}$
C5	229.5 ± 45.1	59.5 ± 13.4	137.2 ± 30.5*	$7.7 \pm 1.5^{\#}$
C6	267.8 ± 46.36##**	67.1 ± 11.4	154.3 ± 18.6	9.2 ± 3.3
C7	251.6 ± 50.3###***	72.8 ± 14.9	141.1 ± 32.7*	$7.7 \pm 1.5^{\#}$
Z1	189.9 ± 28.6	64.2 ± 8.5	141.7 ± 17.6	9.6 ± 1.9
Z2	196.2 ± 28.6	66.9 ± 11.7	149.6 ± 15.5	10.7 ± 2.1*
Z3	235.3 ± 65.2 ^{##}	69.5 ± 11.4	161.7 ± 29.3	13.3 ± 5.2*
Z4	186.9 ± 22.7	84.7 ± 20.6	152.6 ± 22.0	10.3 ± 4.3*
Z5	200.7 ± 37.0##	87.6 ± 14.1	179.6 ± 25.2	10.0 ± 3.3*
Z6	240.2 ± 55.1##	69.3 ± 12.1	123.5 ± 28.3##	$9.0 \pm 4.0^{*}$
Z7	251.6 ± 50.3###	68.6 ± 19.4	148.9 ± 35.6	6.8 ± 1.2 [#]
CM	169.9 ± 24.4	78.8 ± 26.2	172.8 ± 44.6	$8.7 \pm 3.5^{\#}$
K	173.4 ± 19.4	64.0 ± 17.0	156.8 ± 44.5	10.8 ± 2.3*

Note: [CM] CUMS rats, [K] control rats, [C1] \sim [C7] CUMS rats given PBR (7 different dosages), [Z1] \sim [Z7] control rats administered PBR, and [CY] CUMS rats administered venlafaxine hydrochloride. #, compared with the K group (#p < 0.05, ##p < 0.01, ###p < 0.001); *, compared with the CM group (*p < 0.05, **p < 0.01, ***p < 0.001).

However, deviations were observed in the C1-C7, Z1-Z7, and CM groups compared with the normal group, occurring at various levels, suggesting that the modeling and administration caused changes in body liver function. As shown in **Table 3**, the levels of ALT and AST were markedly reduced in CUMS rats administered with low-dose and medium-dose treatment with PBR (C1-C5, 1–25 g/kg), suggesting that the lower doses of PBR showed obvious protective effects on liver function. While in control rats (**Table 3**), high-dose and medium-dose-treatment of PBR (Z4-Z7, 12.5–100 g/kg) deviated ALT and AST from the normal range, suggested that PBR in the concentration of D4 ~

125

100

Dose (g/kg) Total samples Effect [BRI, efficiency rate (%)] Toxicity [LCI, toxicity rate (%)] **CUMS** rats Control rats **CUMS** rats Control rats Λ 8 Λ 100 25 0 8 50 Λ 1 100 Λ 3 8 25 100 12.5 12.5 6 8 75 100 12.5 0 12.5 8 62.5 100 125 125 25 8 62.5 100 25 Λ 50 8 75 100 0 25

100

75

TABLE 4 | The rates of effect and toxicity on CUMS and normal rats administration with PBR.

D7 could cause liver injury in control rats. Thus, further research could be carried out to explore whether the administration of PBR caused liver damage and the toxicity dose range of PBR in CUMS and normal rats.

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PCA Analysis of BRI and LCI

For BRI, the variance contribution rate of the first principal component PC1 was 53%, and PC2 was 28%, accounting for 81% of the information of the original data set cumulatively (>80%). For LCI, the variance contribution rates of PC1 and PC2 were 52.9 and 35.5%, respectively, and the total variance contribution rate was 89% (>80%). The BRI and LCI can be expressed as **Eqs** 6–8 and **Eqs** 9–11.

For BRI,

$$f_1 = 0.517zx_1 - 0.131zx_2 + 0.52zx_3 + 0.165zx_4 \tag{6}$$

$$f_2 = 0.196zx_1 + 0.66zx_2 + 0.169zx_3 - 0.623zx_4 \tag{7}$$

$$f_{(BRI)} = 0.65f_1 + 0.35f_2 \tag{8}$$

For LCI,

$$f_1 = 0.115zx_1 + 0.758zx_2 + 0.803zx_3 + 0.721zx_4 \tag{9}$$

$$f_2 = 0.977zx_1 + 0.134zx_2 - 0.212zx_3 - 0.061zx_4 \tag{10}$$

$$f_{(LCI)} = 0.6f_1 + 0.4f_2 \tag{11}$$

The Dose Range of Effect and Toxicity Based on Behavior and Liver Indexes

From these two standard accuracy indices of the K group, the threshold values of efficacy and toxicity were determined (mean ± 1.96 SD) and used to screen for the effects and toxicity responses (Table 4). Ultimately, the probit function was used to calculate the dose range. The obtained effective dose range for the CUMS rats was from 12.6 g/kg to 163 g/kg (EC₅₀–EC₉₅) with the regression function PROBIT(P) = -0.139 + 0.11x, and the TC₅₀ for CUMS and normal rats was 388 g/kg and 207 g/kg with the regression function PROBIT(P) = -1.156 + 0.03xand PROBIT(P) = -1.669 + 0.081x. The results suggested that a broad effective dose range of PBR was observed in CUMS rats, and the lowest dose (12.6 g/kg) was consistent with these results in the behavioral test. The subthreshold toxicity doses of the CM group were higher than those of normal rats administered PBR, which revealed that the liver function of normal rats was more susceptible to PBR.

However, the specific mechanism of effect and toxicity of PBR in CUMS and normal rats remained to be determined.

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Comprehensive indicators, including BRI and LCI, showed a dose-dependent effect, and the regression models were used for dose-effect/toxicity relationship assessment (**Supplementary Figure S4**). The results showed that BRI and LCI exhibited a strong dose-effect/toxicity relationship evaluation (R > 0.8).

CK-18F Levels in Serum and Liver Samples of CUMS and Control Rats Administered PBR

As shown in **Figure 2**, there was no significant difference in the CK-18F level in serum and liver between the CM and K groups. In CUMS rats, the content of CK-18F did not significantly change in the serum of C1-C7 groups (**Figure 2A**) but increased significantly in the liver of the C7 group compared with the K group (p < 0.001, **Figure 2B**), suggesting that rats administrated with 100 g/kg PBR exhibited severe liver damage. After a comprehensive analysis, the effective dose range of PBR was 12.6–50 g/kg. In normal rats, CK-18F levels in the serum of the Z6-Z7 group were significantly increased (p < 0.05) (**Figure 2C**). In the liver, the CK-18F level in the Z5-Z6 groups was increased (p < 0.05) and significantly increased in the Z7 group compared with the K group (p < 0.001, **Figure 2D**).

To determine the specific mechanism of effect and toxicity of PBR in CUMS and normal rats, the lowest effective dose [C4] group, the most effective dose [C6] group, and the toxic dose [C7] group, and three corresponding groups [Z4], [Z6], and [Z7] were chosen for metabolomics analysis.

PBR Adjusted Differentially on Metabolites of Rat Liver by UHPLC-MS

Assessment of Stability in UPLC-MS System

The metabolic profiles of the liver samples were characterized using UHPLC-Q Exactive Orbitrap-MS. Typical total ions chromatograph (TIC) of [CM], [C4], [C6], [C7], [K], [Z4], [Z6], and [Z7] showed approximately 8,671 ions, and 409 metabolites were identified in the sample (**Figure 3**). The metabolites were mainly high polarity compounds including amino acids, sphingolipids, bile acids, etc.

The stability of the LC-MS system was assessed using QC samples. The PCA score plot indicated that the QC samples were tightly clustered (**Supplementary Figure S5**). Moreover, the peak areas and retention times of the ten extracted ions in the QC samples

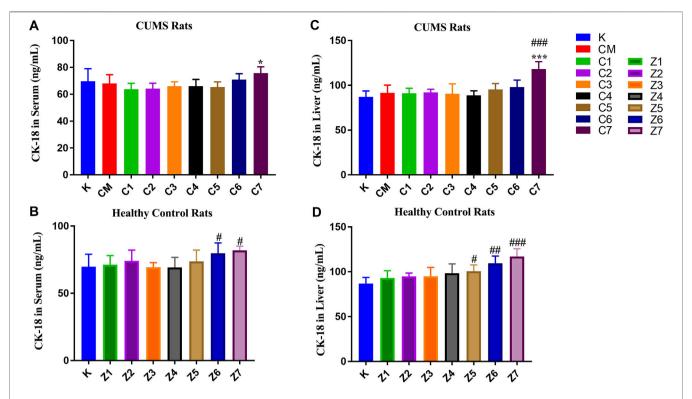


FIGURE 2 | CK-18F level in serum samples of CUMS rats **(A)** and control rats **(B)** administration with PBR. CK-18F level in liver samples of CUMS rats **(C)** and control rats **(D)** administration with PBR. [CM] CUMS rats, [K] control rats, [C1] \sim [C7] CUMS rats given PBR (7 different dosages), [Z1] \sim [Z7] control rats administered PBR, and [CY] CUMS rats administered venlafaxine hydrochloride. Data represent the mean \pm SD of each group. #, compared with the K group (#p < 0.05, ##p < 0.01, ###p < 0.001); *, compared with the CM group (*p < 0.05, ***p < 0.001).

also showed good stability (**Supplementary Table S3**). The RSDs of the ten peaks were 0.22-3.85% for retention times, $3.76-9.66\times10^{-5}\%$ for the m/z value, respectively. These results indicate that the UPLC-MS system is robust for metabolomic analysis.

Multivariate Statistical Analysis

A snapshot of the systematic metabolism in the [CM], [K], [C4], [C6], and [C7] groups was obtained using PLS-DA pattern recognition analysis. An obvious separation was observed between [CM] and [K], indicating that the alterations in metabolic profiles were related to CUMS stress. In addition, [C4], [C6], and [C7] moved away from [CM] in a dose-dependent manner in PLS-DA (**Figure 4A**), suggesting that the differences in metabolic profiles were related to the effects of PBR on CUMS-induced rats. The reliability of the multiple pattern recognition methods was evaluated by the R²Y and Q² values (R²Y represents goodness of fit, and Q² indicates goodness of prediction). The R²Y and Q² were 0.901 and 0.651, indicating that the PLS-DA model could accurately describe the data. These results of the permutation tests showed that the two models were credible without overfitting (**Figure 4A**).

CUMS Induced Deviation of Liver Metabolic Profile in Rats

To discover the liver metabolites between the [CM] and [K] groups, OPLS-DA analysis was applied to eliminate unrelated

variations in the spectra. The OPLS-DA score plot showed a statistically significant difference between the [CM] and [K] groups (Figure 4C), indicating a similar result that metabolic profiles were significantly altered in rat liver with CUMS stress. The corresponding OPLS S-plot (Figure 4E) in turn showed the contribution of different variables and ions far away from the origin were deemed as potential biomarkers. As a result, 21 candidates were screened from the corresponding S-plot between the [CM] and [K] groups with VIP > 1.0. The changes in these potential biomarkers are listed in Table 5 and Figures 5A,B,D. Compared with the [K] group, the levels of 15 metabolites, including leucine, betaine, isoleucine, valine, phenylpyruvic acid, L-tyrosine, nicotinamide, adenine, adenosine, xanthine, sphinganine, lysoPC (16:1 (9Z)), phytosphingosine, taurodeoxycholic acid, and taurochenodeoxycholic acid, decreased significantly in the [CM] group. In contrast, six metabolites, including 2-phenylacetamide, N6-acetyl-L-lysine, L-carnitine, L-acetylcarnitine, propionylcarnitine, and succinic acid, increased significantly in the [CM] group.

PBR Reversed Metabolic Profile in CUMS-induced Rats

After the administration of PBR, 17 differential metabolites were call-backed close to the [K] group after PBR treatment in the [C4], [C6], and [C7] groups, except L-carnitine, L-acetylcarnitine, and propionylcarnitine with an over-reversed regulation at the

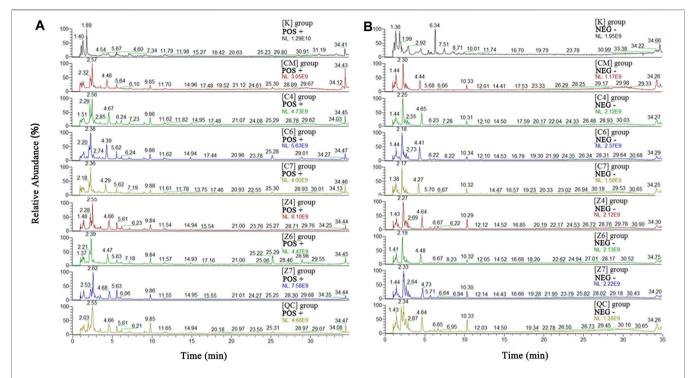


FIGURE 3 | Total ions chromatograph (TIC) in positive (A) and negative (B) ion of [K], [CM], [C1]–[C7], [Z1]–[Z7] and [QC] group. [CM] CUMS rats, [K] control rats, [C1] ~ [C7] CUMS rats given PBR (7 different dosages), [Z1] ~ [Z7] control rats administered PBR, and [CY] CUMS rats administered venlafaxine hydrochloride.

D7 dose. LysoPC (16:1 (9Z)), taurodeoxycholic acid, taurochenodesoxycholic acid, and succinic acid were not reversed at D6 and D7 of PBR.

The metabolic pathway was established based on related literature and the KEGG database to understand the correlation between these potential biomarkers. These metabolites were linked to amino acid metabolism, energy metabolism, β -oxidation of fatty acids, sphingolipid metabolism, glycerophospholipid metabolism, and bile acid metabolism (**Figure 6**). Next, differential metabolite pathway enrichment was performed using MetaboAnalyst software. Seven amino acid metabolism and sphingolipid metabolism pathways were obtained by impact value > 0.1 and -logP > 4 (**Figure 7A**), such as valine, leucine, and isoleucine biosynthesis, valine, leucine, and isoleucine degradation, aminoacyl-tRNA biosynthesis, phenylalanine metabolism, among others.

Differential Metabolic Profile in Control Rats

A significant separation was observed in the PCA score plots of the [K], [Z4], [Z6], and [Z7] groups (**Figure 4B**), suggesting that PBR could affect the metabolic profile of control rats. The goodness values of R^2 Y = 0.929 and Q^2 = 0.516 in the OPLS models in [Z7] versus [K] were computed, demonstrating that the models were reliable (**Figure 4D**). The contributions of different variables in [Z7] and [K] were extracted from the corresponding OPLS S-plots (**Figure 4F**).

As a result, 20 metabolites were significantly perturbed by PBR in normal rats (**Table 6**). Compared with the [K] group, leucine,

isoleucine, valine, hypoxanthine, adenine, adenosine, malic acid, sphinganine, phytosphingosine, lysoPE [0:0/20:4 (8Z, 11Z, 14Z, 17Z)], L-carnitine, L-acetylcarnitine, propionylcarnitine, taurodeoxycholic acid, taurochenodesoxycholic acid, and ascorbic acid-2-sulfate decreased significantly in the [Z4], [Z6], and [Z7] groups (Figures 5B,C,E). In contrast, the levels of other metabolites, including N6-acetyl-L-lysine, succinic acid, adenosine 2'-phosphate, and glycocholic acid, increased significantly in the [Z4], [Z6], and [Z7] groups. The changes in metabolites were associated with amino acid metabolism, metabolism, sphingolipid metabolism, glycerolphospholipid metabolism, fatty acid β-oxidation, and bile acid metabolism (Figure 6). Similarly, five pathways in amino acid metabolism, energy metabolism, sphingolipid metabolism, and bile acid metabolism were considered to be the most pertinent in control rats given PBR, such as valine, leucine, and isoleucine biosynthesis; valine, leucine, and isoleucine degradation; and sphingolipid metabolism (Figure 7B).

Metabolic Network Analysis of Metabolites in Both CUMS and Control Rats

Metabolites in both CUMS and control rats, six of them were returned to a healthy level after PBR treatment of CUMS-induced depression, including betaine, tyrosine, 2-phenylacetamide, phenylpyruvic acid, nicotinamide, and xanthine, while they were not significantly affected in control rats. This result

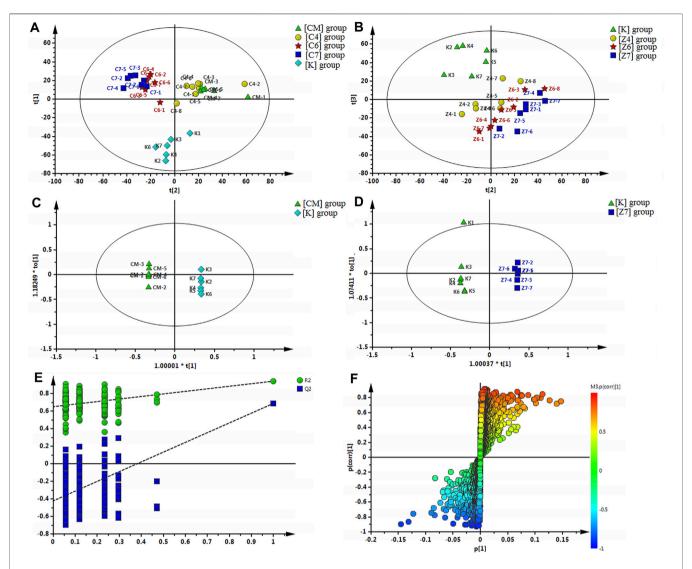


FIGURE 4 | (A) Multiple pattern recognition of liver metabolites in CUMS rats with or without exposure to PBR. PLS-DA score plot (n = 8, R2Y = 0.901, R2X = 0.51, Q2 = 0.651). (B) PCA of liver metabolites of normal rats with or without exposure to PBR. PCA score plot (n = 4, R2X = 0.531, Q2 = 0.149). (C) OPLS score plotof [K] group and [CM] group (n = 8, R2Y = 1, R2X = 0.455, Q2 = 0.868). (E) OPLS S-plot of [K] group and [CM] group. (D) OPLS score plot (n = 8, R2Y = 1, R2X = 0.337, Q2 = 0.59) of [Z7] group and [K] group and the corresponding OPLS S-plot (F). [CM] CUMS rats; [K] control rats; [C4], [C6], and [C7] CUMS rats given PBR (12.6, 50, 100 g/kg); [Z1], [Z6] and [Z7] control rats administered PBR (12.6, 50, 100 g/kg).

indicated that these six metabolites were highly correlated with the pharmacological effects of PBR and were associated with amino acid metabolism, sphingolipid metabolism, and energy metabolism (**Figure 7C**).

In addition, another 11 metabolites showed the same regulative differential metabolites in both CUMS and control rats administered with PBR (p < 0.05, Figure 7C), including leucine, valine, isoleucine, N6-acetyl-L-lysine, phytosphingosine, sphinganine, adenine, adenosine, L-carnitine, L-acetylcarnitine, and propionylcarnitine, which were associated with amino acid metabolism, fatty acid β oxidation, sphingolipid metabolism, and energy metabolism (Figure 7C). Among these, 3-acyl carnitines (L-carnitine, L-acetylcarnitine, and propionyl carnitine) were decreased

after PBR administration in both control and CUMS rats and could be significantly reversed to the level of the [K] group in the [C4] and [C6] groups. The other eight differential metabolites were reversed in both CUMS and control rats, indicating that the PBR might regulate the same sites under different body conditions, which caused it to present an opposite change tendency.

The rest of eight metabolites were significantly altered in control rats after PBR treatment, including glycocholic acid, taurodeoxycholic acid, taurochenodesoxycholic acid, hypoxanthine, adenosine 2'-phosphate, malic acid, succinic acid, and lysoPE (0:0/20:4 (8Z, 11Z, 14Z, 17Z)), which were associated with energy metabolism, glycerophospholipid metabolism, and bile acid metabolism (**Figure 7C**).

TABLE 5 | Identified differential metabolites in the liver of CUMS rats.

No	Metabolites	TR (min)	m/z	lon	CM/K	C7/CM	C6/CM	C4/CM	Metabolic pathway
1	Betaine	1.82	118.0864	M + H	↓ª	↑ª	↑	↑ª	Glycine, serine and threonine metabolism
2	Leucine ^b	3.16	132.1025	M + H	↓a	↑a	↑a	↑ª	Amino acid metabolism
3	Isoleucine ^b	3.42	132.1025	M + H	↓ª	↑ª	↑ª	↑ª	Amino acid metabolism
4	Valine ^b	1.40	118.0864	M + H	↓a	↑a	1	↑ª	Amino acid metabolism
5	2-Phenylacetamide	3.43	136.0756	M + H	↑a	↓ª			Phenylalanine metabolism
6	Phenylpyruvic acid	3.13	165.0533	M-H	↓a	↑a	↑	1	Phenylalanine metabolism
7	L-Tyrosine	2.78	182.0811	M + H	↓ª	↑ª	↑	1	Phenylalanine metabolism
8	N6-Acetyl-L-lysine	3.31	189.1232	M + H	↑a	\downarrow	↓a	↓ª	Lysine degradation
9	Nicotinamide	1.85	123.0554	M + H	↓a	↑a	↑	1	Nicotinate and nicotinamide metabolism
10	Adenine	3.79	136.062	M + H	↓a	↑a	↑a		Purine metabolism
11	Adenosine	3.46	268.1036	M + H	↓ª	↑ª	↑ª	1	Purine metabolism
12	Xanthine	2.80	153.0406	M + H	↓ª	↑ª	↑	1	Purine metabolism
13	L-Carnitine	1.39	162.1126	M + H	↑a	↓ª	↓a	↓ª	β-oxidation of fatty acid
14	L-Acetylcarnitine	2.36	204.1229	M + H	↑a	↓ª	↓a	\downarrow	β-oxidation of fatty acid
15	Propionylcarnitine	4.45	218.1386	M + H	↑a	↓ ^a	↓ ^a	↓ ^a	β-oxidation of fatty acid
16	Sphinganine	14.41	302.3058	M + H	↓ª	1	↑ ^a	1	sphingolipid metabolism
17	Phytosphingosine	11.73	318.3004	M + H	↓a	↑a	↑	1	sphingolipid metabolism
18	Succinic acid	2.99	117.0185	M-H	↑a		\downarrow	\downarrow	Citrate cycle
19	LysoPC [16:1 (9Z)]	15.94	494.3237	M + H	↓ª		↑		Glycerophospholipid metabolism
20	Taurodeoxycholic acid ^b	8.34	500.3014	M + H	↑a	1			Bile acid metabolism
21	Taurochenodesoxycholic acid	10.27	500.3014	M + H	Į ^a	1			Bile acid metabolism

Note: [CM] CUMS rats, [K] control rats, [C1] ~ [C7] CUMS rats given PBR (7 different dosages). ↑ shows up-regulated metabolite; ↓ shows down-regulated metabolite.

^aMeans a statistically significant difference at p < 0.05.

The metabolic networks involved in some enzymes and genes were constructed using Cytoscape to understand better the potential biomarkers' internal correlation in terms of enzyme or gene levels. The metabolic networks that were established based on the markedly differential metabolites are shown in **Figure 8.** Valine, leucine, isoleucine, and others involved in amino acid metabolism are shown in **Figure 8A.** Adenine, xanthine, malic acid, and others were also involved in energy metabolism (**Figure 8B**). As shown in **Figures 8C–E**, phytosphingosine, and sphinganine were involved in sphingolipid metabolism, L-carnitine and O-acetylcarnitine were involved in the β -oxidation of fatty acids, and glycocholate and taurodeoxycholate were involved in bile acid metabolism.

Dose-Effect/Toxicity Relationship AnalysisDose-Effect and Dose-Toxicity Metabolites Screening

The relationship of dose-effect/toxicity was mainly to show the dose-dependence of metabolites by calculating the correlation between metabolite concentrations and dose. The correlations of dose-effect and dose-toxicity are shown in Figure 9A. Nine of the metabolites were significantly related to the drug effect (p < 0.05), including adenine, isoleucine/leucine, betaine, L-valine, 2-phenylacetamide, nicotinamide. propionylcarnitine, L-acetylcarnitine, and L-carnitine. Sixteen metabolites were significantly related to drug toxicity (p < 0.05), including adenine, adenosine-2'-phosphate, L-valine, N6-Acetyl-L-lysine, adenosine, phytosphingosine, taurodeoxycholic acid, lysoPE [0:0/20:4 (8Z, 11Z, 14Z, 17Z)], hypoxanthine, L-acetylcarnitine, malic acid, and ascorbic acid-2-sulfate. In Figure 9B, the regression curve of doseeffect and dose-toxicity showed the capability of evaluating the

intensities of the relationship. Five pharmacodynamic metabolites, including isoleucine/leucine, L-valine, 2-phenylacetamide, L-acetylcarnitine, and L-carnitine, or five toxic metabolites including adenosine-2'-phosphate, L-valine, L-acetylcarnitine, malic acid, and ascorbic acid-2-sulfate were screened with R>0.6.

Model Comparison

To better evaluate the dose-effect/toxicity relationship of PBR, four computational methods including PCA analysis, EI analysis, the sum of metabolites (SUM), and (R)SUM were used to integrate the pharmacodynamic and toxic metabolites. The receiver operating characteristic curves (ROC) was applied to evaluate the computational methods. The evaluation results of the five pharmacodynamic metabolites and five toxic metabolites are shown in Figure 10 (ROC, 0.7222-0.7632 and 0.506-0.718), indicating that the metabolites have some ability to evaluate effect and toxicity. Furthermore, the four computational methods' ROC was 0.7398-0.9123 and 0.658-0.878, suggesting that all computational methods could improve the evaluation ability of metabolites to different degrees. The improvement in EI analysis was the most significant, indicating that the EI analysis was suitable for integrating metabolites. Therefore, EI analysis was used to calculate the dose-effect/toxicity indices (DEI/DTI) and estimate the dose-effect/toxicity relationship.

Dose-Effect/Toxicity Indices

The values of DEI and DTI in both CUMS and control rats following PBR treatment with C4, C6, and C7 dosage are shown in **Figure 11**. The DEI and DTI significantly increased with dosage augment. Regression models were used for the dose-effect/toxicity

^bValidated with standard. [CM] group compared with [K] group, CM/K; [C4] group compared with [CM] group, C4/CM; [C6] group compared with [CM] group, C7/CM.

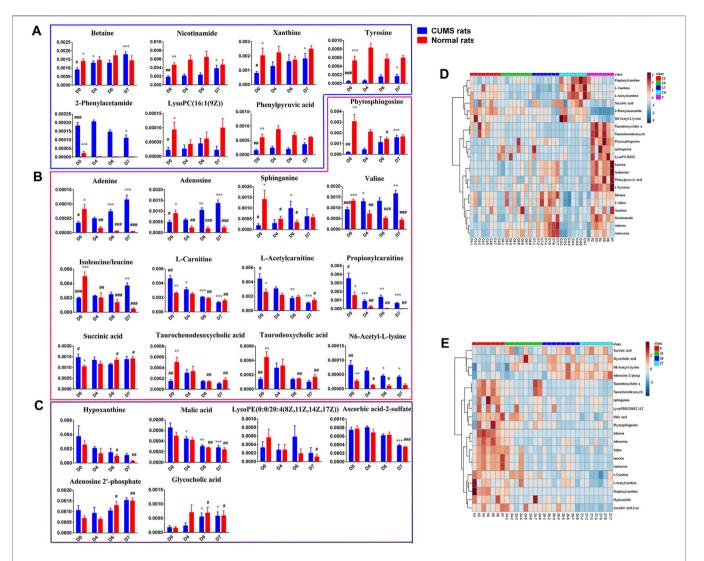


FIGURE 5 | (A): Differential metabolites only in liver samples of CUMS rats with PBR treatment. (B): Common differential metabolites in liver samples of both CUMS and normal rats with PBR administration. (C) Differential metabolites only in liver samples of normal rats with PBR administration. (D): Relative content of the heatmap of differential metabolites in liver samples of CUMS rats with PBR administration. (Normalized intensity levels of differential metabolites in liver samples of CUMS rats (\blacksquare blue), and the relative content of the corresponding metabolites in normal rats (\blacksquare red)). D0: administration of an equal volume of vehicle. D4-D7: the concentration of PBR was 12.5, 5, and 10 g/kg, respectively. (Expressed as the volume of raw materials). Data are presented as mean \pm SEM. n = 8 each group. *p < 0.05, **p < 0.01, ***p < 0.01, ***p < 0.01, **p < 0.01, **p < 0.01, ***p < 0.01, ***p < 0.01, **p < 0.01, **p < 0.01, ***p < 0.01, ***p < 0.01, **p < 0.01, **p < 0.01, ***p <

relationship assessment (**Figure 11**). The results showed that DEI and DTI exhibited a strong dose-effect/toxicity relationship evaluation (R > 0.85). The regression curve of the dose-effect/toxicity relationship in CUMS rats was y = 1.90 + 0.047x and y = 0.687 + 0.019 x. In normal rats, the regression curve of dose-toxicity was y = 1.23 + 0.22x. The results of probit regression analysis are shown in **Supplementary Table S4**, and the effective dose range for the CUMS rats was from 13.8 to 95.58 g/kg, the TC50 for CUMS and normal rats was 480 and 153 g/kg. Combined with the results of BRI and LCI, the dose range of effect and toxicity became larger in CUMS, and smaller in normal rats. This

difference might be resulting from the inconformity of dosage groups in the metabonomics analysis.

DISCUSSION

Bupleuri Radix, a top grade herbal drug in Shennong's Materia Medica, soothes the liver and relieves stagnation. This study focused on the effective and safe dose of PBR and its dose-effect/toxicity relationship. First, the BRI and LCI were obtained by integrated behavioral and liver indices and used

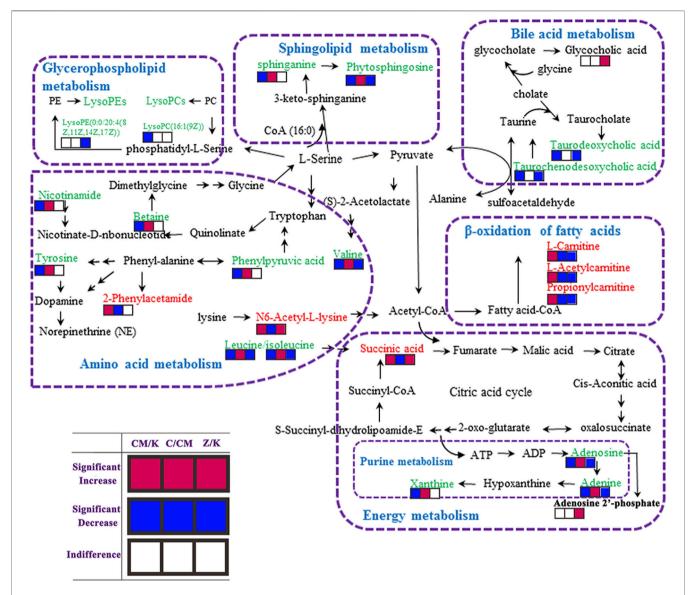


FIGURE 6 | Metabolic pathways involved in the [CM] group versus the [K] group, the [CM] group versus the [C4], [C6] or [C7] group and the [Z4], [Z6] or [Z7] group versus the [K] group. Red squares represent up-regulated metabolites in the [CM] vs. [K], [C] vs. [CM] and [Z] vs [K] group; Blue squares represent down-regulated metabolites in the [CM] vs. [K], [C] vs. [CM] and [Z] vs. [K] group; And blank squares represent indistinctive metabolites in the [CM] vs. [K], [C] vs. [CM] and [Z] vs. [K] group. [CM] CUMS rats; [K] control rats; [C4], [C6], and [C7] CUMS rats given PBR (12.6, 50, 100 g/kg); [Z1], [Z6] and [Z7] control rats administered PBR (12.6, 50, 100 g/kg).

to determine the dose range of effect and toxicity. The results showed that the effective dose range for CUMS rats was 12.6–163g (herb)/kg, the TD50 (median toxicity dose) for CUMS and normal rats were 388 and 207 g (herb)/kg, and the toxicological results showed that rats administrated with 100 g/kg PBR exhibited severe liver damage. After a comprehensive analysis, the use of PBR dose was determined to be 12.6–50 g (herb)/kg. Second, liver metabonomics was applied to gain insight into the related mechanisms, and the results showed that PBR could reverse amino acid metabolism, energy metabolism, sphingolipid metabolism, and β -oxidation of fatty acids based on liver metabolic profiles to produce an

anti-depressant effect in a dose-dependent manner in CUMS Extra two metabolic pathways, including glycerophospholipid metabolism and bile acid metabolism, were significantly perturbed in normal rats administered PBR. Finally, the dose-effect index (DEI) and dose toxicity index (DTI) were obtained by integrating the effects and toxic metabolites and were applied to precisely evaluate the doseeffect/toxicity relationship of PBR. The results showed that DEI and DTI had a remarkable ability to estimate the effect and toxicity. In addition, the DEI and DTI was used to determine the dose range of effect and toxicity, and it demonstrated high concordance with pre-experiment results. The CUMS

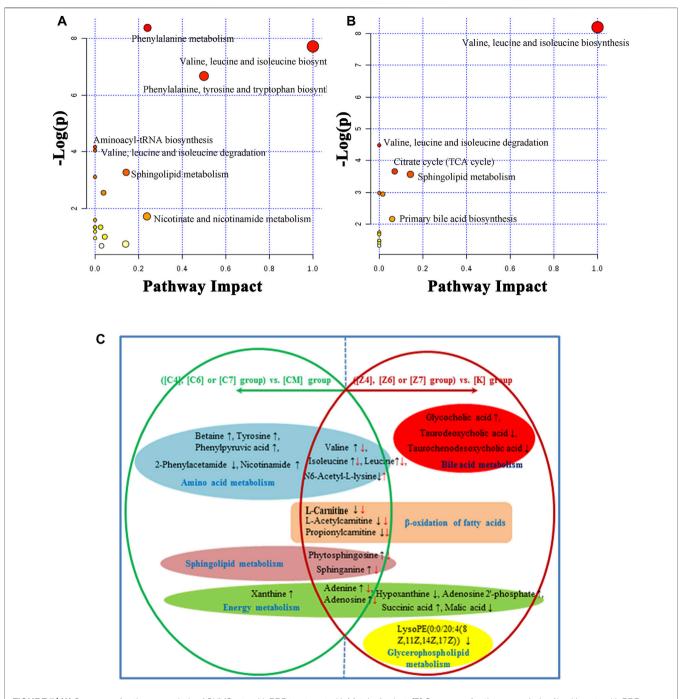


FIGURE 7 | (A) Summary of pathways analysis of CUMS rats with PBR treatment with MetaboAnalyst. (B) Summary of pathways analysis of healthy rats with PBR administration with MetaboAnalyst. Each point represents one metabolic pathway; the size of dot and shades of color are positively correlated with the impact of the metabolic pathway. (C) Different metabolites and corresponding pathways in CUMS rats or healthy rats following PBR administration. "↑" and "↓" represent that the metabolite is up- or down-regulated in CUMS rats or healthy rats following PBR administration. [CM] CUMS rats; [K] control rats; [C4], [C6], and [C7] CUMS rats given PBR (12.6, 50, 100 g/kg); [Z1], [Z6] and [Z7] control rats administered PBR (12.6, 50, 100 g/kg).

possessed a higher toxicity tolerance dose of PBR, which was consistent with the theory of "You Gu Wu Yun" in TCM. "You Gu Wu Yun" theory suggested that the toxic herb would not produce toxicity in a corresponding pathological state; on the contrary, it would have a therapeutic effect (Tan et al., 2013).

In this study, behavioral research suggested that PBR had a positive anti-depressant effect on CUMS rats but no distinct impact on control rats. However, there were larger intra-group errors in behavioral tests, and liver function, especially in the sucrose preference test. This may be due to the individual

TABLE 6 | Identified differential metabolites in the liver of healthy rats.

No	Metabolites	T _R (min)	m/z	lon	Z 4/K	Z 6/K	Z 7/K	Metabolic pathway
1	Leucine ^b	3.16	132.1025	M + H	↓ª	↓ª	↓ª	Amino acid metabolism
2	Isoleucine ^b	3.42	132.1025	M + H	↓ª	↓ª	↓ª	Amino acid metabolism
3	Valine ^b	1.40	118.0864	M + H	↓ª	↓ª	↓ª	Amino acid metabolism
4	N6-Acetyl-L-lysine	3.31	189.1232	M + H	1	↑a	↑a	Lysine degradation
5	Hypoxanthine	4.39	137.0458	M + H	\downarrow	↓ª	↓ª	Purine metabolism
6	Adenine	3.79	136.062	M + H	↓ª	↓ª	↓ª	Purine metabolism
7	Adenosine	3.46	268.1036	M + H	↓ ^a	↓ ^a	↓ ^a	Purine metabolism
8	Adenosine 2'-phosphate	1.78	348.0701	M + H		↑ª	↑ª	Purine metabolism
9	Succinic acid	2.99	117.0185	M-H		↑ª	↑ª	Citrate cycle
10	Malic acid	1.69	133.0135	M-H		↓ ^a	↓ª	Citrate cycle
11	Sphinganine	14.41	302.3058	M + H	↓ª	↓ª	↓ ^a	sphingolipid metabolism
12	Phytosphingosine	11.73	318.3004	M + H	↓ª	↓ª	↓ ^a	sphingolipid metabolism
13	LysoPE [0:0/20:4 (8Z,11Z,14Z,17Z)]	16.59	502.2918	M + H	\downarrow	\downarrow	↓ª	Glycerophospholipid metabolism
14	L-Carnitine	1.39	162.1126	M + H		↓ª	↓ª	β-oxidation of fatty acid
15	L-Acetylcarnitine	2.36	204.1229	M + H			↓ ^a	β-oxidation of fatty acid
16	Propionylcarnitine	4.45	218.1386	M + H	↓ª	↓ª	↓ ^a	β-oxidation of fatty acid
17	Glycocholic acid	9.98	464.3021	M-H	1	↑a	↑a	Bile acid metabolism
18	Taurodeoxycholic acid ^b	8.34	498.2897	M-H	\downarrow	↓ª	↓ª	Bile acid metabolism
19	Taurochenodesoxycholic acid	10.27	498.2897	M-H	\downarrow	↓ ^a	↓ ^a	Bile acid metabolism
20	Ascorbic acid-2-sulfate	1.82	254.9817	M + H			↓ ^a	oxidative stress

Note: [K] control rats, [Z1] ~ [Z7] control rats administered PBR (7 different dosages). ↑ shows up-regulated metabolite; ↓ shows down-regulated metabolite.

differences in animals. Consequently, larger sample size is needed to obtain a meaningful statistical difference in the future. In addition, to comprehensively evaluate the efficacy and toxicity, the overall pharmacological potency was applied to evaluate the activity and toxicity of PBR, and the BRI and LCI, which were obtained by integrated behavioral tests and liver indices, were used to determine the dose range of effect and toxicity. The results showed that BRI and LCI could better evaluate the efficacy and toxicity and showed a dose-dependent effect.

CK-18F is considered a biomarker of cell death and has been used as a predictive indicator of drug-induced liver injury (DILI, Kakisaka et al., 2017). In this study, the content of CK-18F changed more in the liver than in the serum of CUMS and normal rats administered PBR. In control rats, the CK-18F level was increased in the Z5-Z7 group (25-100 g/kg) compared with the K group, indicating that the control rats showed a risk of DILI at 25-100 g/kg. However, in the CUMS rats, there was no significant change in CK-18F level at the dose of C5-C6 (25-50 g/kg), but a significant increase at the dose of C7 (100 g/kg), indicating that CUMS stress attenuated the risk of DILI at the medium dose of PBR (25-50 g/kg), which was consistent with the theory of "You Gu Wu Yun" in TCM. However, this study does not verify the toxic dose of PBR. The in vivo and in vitro experiments will be used to verify the findings of the study in the next step.

The metabolomic changes were performed using the metabolomics method in this study. In the protein precipitation method, the effects of precipitators (methanol, acetonitrile, acetonitrile-0.1% formic acid, methanol-0.1% formic acid) were compared. In the liquid chromatography conditions, the effects of different acids including formic acid, trifluoroacetic acid, and phosphoric acid, as well as the amount of

acid (0.1, 0.2, and 0.3%) added into the mobile phase was compared and the chromatographic conditions of the mobile phase and gradient elution system were optimized to gain more information of metabolites. In addition, The QC samples were added in the process and observed tightly clustered in the result of PCA, suggesting that UHPLC- MS was a stable and reliable instrument in this population. The standards of metabolites were used to perform and ensure the accuracy of identification.

The perturbation of the amino acid neurotransmitter system plays an important role in the pathogenesis of depression (Ni et al., 2008). Amino acid metabolism is shown in Figure 8A. PBR mainly regulated branched-chain amino acids and affects synthetic norepinephrine (NE) in the treatment of depression. The delivery of branched-chain amino acids through the bloodbrain-carrier system is closely related to the rate of 5-HT synthesis. In addition, branched-chain amino acids, especially leucine, play a major role in the differentiation of glutamate and glutamine in astrocytes, thereby maintaining the steady-state balance of brain nitrogen. It also affects the function of the central nervous system (Shimomura and Harris, 2006). More importantly, leucine and isoleucine can increase the expression of BDNF in hippocampal neurons, and BDNF dominates the signal transduction pathways associated with depression (Furukawa-Hibi et al., 2011). In this study, the changes in leucine, isoleucine, and valine were consistent with the results of serum metabonomics (Gao et al., 2017), suggesting that branched-chain amino acids, including leucine, isoleucine, and valine, were potential markers for PBR in the treatment of depression. Both L-tyrosine and phenylalanine are synthetic precursors of NE (Meyers, 2000), while phenylalanine metabolism produces phenylpyruvic acid and 2-phenylacetamide. A study (Wang, 2001) reported that elevated phenylalanine/tyrosine ratios could cause damage to

^aMeans a statistically significant difference at p < 0.05.

bValidated with standard. [Z4] group compared with [K] group, Z4/K; [Z6] group compared with [K] group, Z6/K; [Z7] group compared with [K] group, Z7/K.

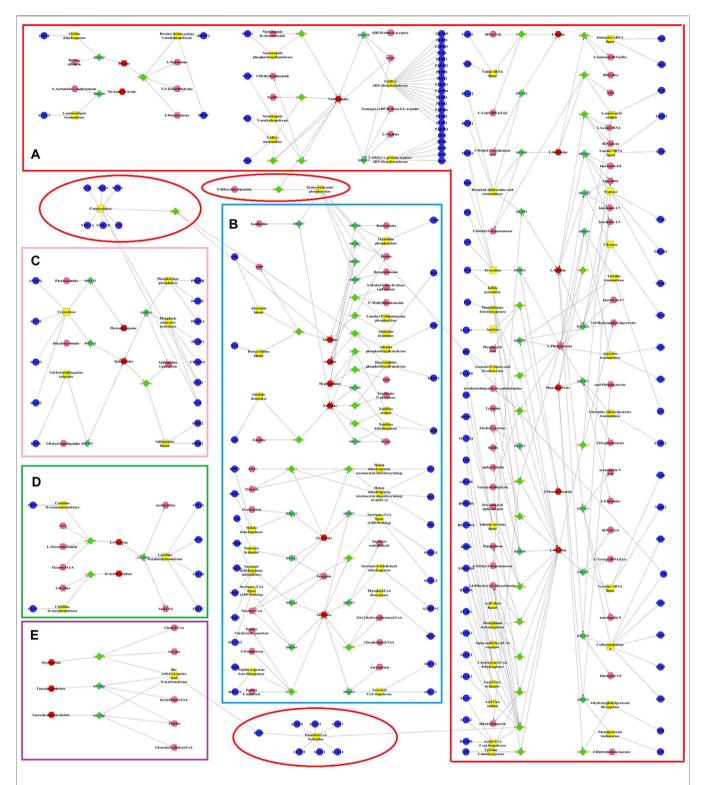


FIGURE 8 | Metabolic networks involved in enzymes and genes were established based on the differential metabolites in both CUMS and healthy rats following PBR treatment. The metabolic networks of amino acid metabolism (A), energy metabolism (B), sphingolipid metabolism (C), β-oxidation of fatty acid (D) and bile acid metabolism (E).

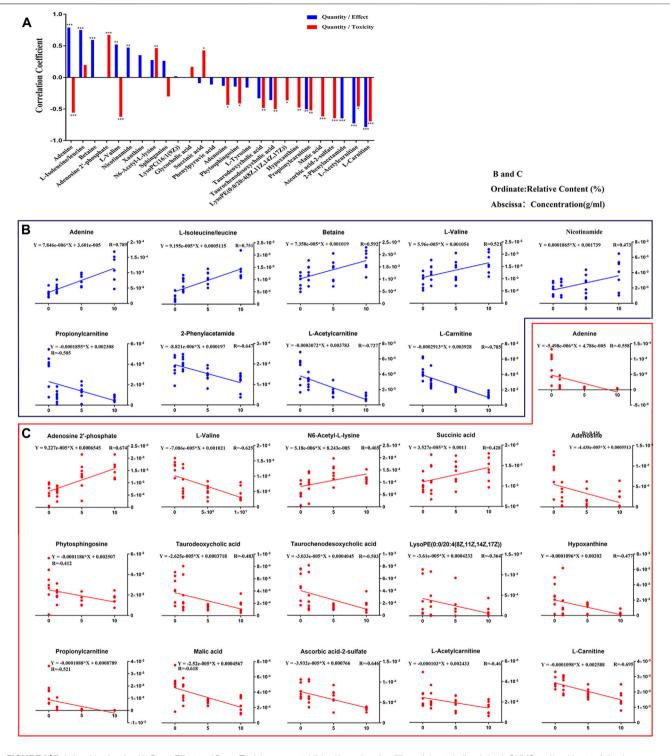
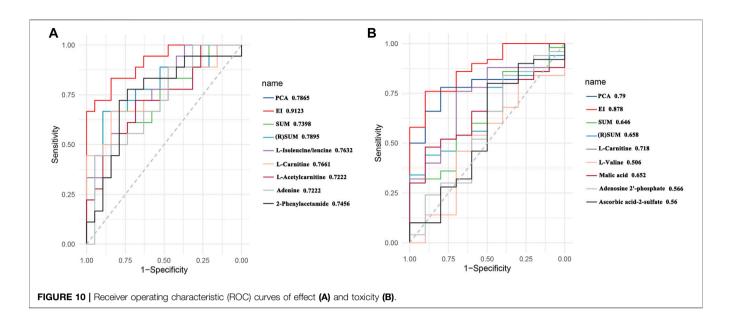
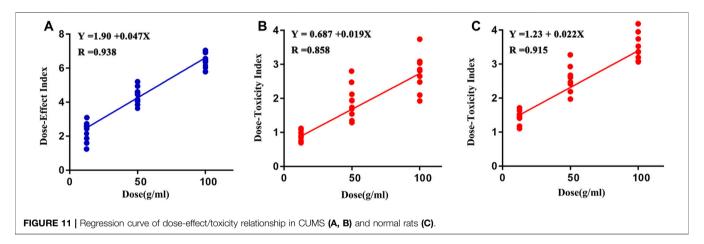


FIGURE 9 | Relationships involved in Dose-Effect and Dose-Toxicity were established based on the differential metabolites in both CUMS and healthy rats following PBR treatment. Correlation of Quantity/Effect and Quantity/Toxicity (A). Regression curve of Dose-Effect (B) and Dose-Toxicity (C).

the nervous system, leading to depression, mental development defects, and mental disorders. In this study, tyrosine and phenylpyruvic acid were significantly decreased, and 2-phenylacetamide was significantly

increased in the liver of CUMS rats, suggesting that the perturbation of phenylalanine metabolism might cause NE synthesis deficiency, leading to the occurrence of depression.





N6-acetyl-L-lysine is an acetylated lysine. Acetylation of lysine is a reversible modification of the protein residue after translation, which has been considered as a novel regulatory factor of mitochondrial bioenergy in recent years, and the regulatory factor controls massive cellular life processes (Anderson and Hirschey, 2012; Thapa et al., 2017). The increase of N6-acetyl-L-lysine in the liver of CUMS rats indicated that stress might disturb healthy mitochondrial biological function. Betaine is an osmotic pressure molecule that accumulates in tissues, regulating cell volume (Schliess and Haussinger, 2002; Lang, 2007). It is also an important methyl donor so that homocysteine can methylate to methionine and plays a vital role in biological functions (Lever and Slow, 2010). Nicotinamide is involved in the tryptophan/ kynurenine metabolic pathway. Additionally, both betaine and nicotinamide have a synergistic effect on synthetic anti-depressant drugs. The combination of betaine and s-adenosylmethionine in treating patients with mild to moderate depression is superior to s-adenosylmethionine alone. The combination of nicotinamide

and tryptophan can significantly enhance the therapeutic effects by reducing the peripheral catabolism of tryptophan (Chouinard et al., 1977). In this study, the levels of amino acids and their metabolites were significantly decreased in CUMS rats. After the administration of PBR, these metabolites were significantly reversed to healthy, indicating that PBR produced antidepressant effects by regulating amino acid neurotransmitter system metabolism. However, the branched-chain amino acids (leucine, isoleucine, and valine) were significantly reduced in the liver of control rats with PBR treatment, indicating that the amino acid transport was obstructed so that hepatic cells could not effectively absorb amino acids and ultimately cause liver injury. In this study, the levels of N6-acetyl-L-lysine were significantly increased in the liver of control rats with PBR treatment, indicating that the enhancement of lysine acetylation may disturb mitochondrial and cell functions and lead to liver cell damage.

The metabolic networks of energy metabolism involved in potential enzymes and genes are shown in **Figure 8B**. Energy is

Dose-Effect/Toxicity of Bupleuri Radix

an indispensable factor in the survival of an organism. It has been reported that insufficient energy is closely related to depression. The conversion of adenine produces xanthine. Both xanthine and adenine are intermediate metabolites of adenosine, which play an important role in converting ATP and ADP (Su et al., 2014). In this study, the levels of xanthine, adenine, and adenosine were significantly decreased in the liver of CUMS rats, indicating that depression could weaken adenosine metabolism and reduce the function of energy conversion pathways in depressed patients. Similarly, malic acid and succinic acid are intermediates of the tricarboxylic acid (TCA) cycle. Their presence in the [CM] group indicated that the TCA cycle and energy metabolism in patients with depression was disturbed. After the administration of PBR, the reduced concentrations of xanthine, adenine, and adenosine in the liver were significantly reversed to healthy, indicating that PBR produced anti-depressant effects by regulating energy metabolism. However, the levels of hypoxanthine, adenine, and adenosine were significantly reduced, and adenosine 2'phosphate was increased in the liver of control rats with PBR treatment, indicating that high doses of PBR may cause the adenosine metabolism to weaken and abnormal, and then cause the function of energy conversion pathways to attenuate, ultimately leading to hepatic cell damage due to insufficient energy supply for the survival of hepatic cells. Similarly, malic acid and succinic acid are intermediates in the TCA cycle, and their levels are abnormal in the liver of control rats with PBR treatment, indicating that high doses of PBR may lead to TCA weakening and abnormalities, leading to hepatic cell damage due to insufficient supply for normal survival processes of the hepatic cell.

Sphingolipid metabolism is shown in Figure 8C. Sphingolipids are an important component of meningeal lipids. An increased concentration of sphingolipids is closely related to depression (Dinoff et al., 2017). A study reported that sphingolipid levels in serum samples were significantly higher in depressed patients than in healthy individuals (Gracia-Garcia et al., 2011). In this study, the levels of phytosphingosine and sphinganine were significantly decreased in the livers of CUMS rats. After the administration of PBR, their levels in the liver of CUMS rats were significantly reversed to healthy, indicating that PBR produced anti-depressant effects by regulating sphingolipid metabolism. It has been reported that sphingomyelinase activation is a response to tumor necrosis factor-alpha (TNF-α) and other cytokines. Sphingomyelinase activation and C16-ceramide production are involved in TNFα-induced hepatocyte apoptosis (Kolesnick et al., 1998). In addition, the dynamic balance of intracellular ceramide and sphingosine 1-phosphate (ceramide/S1P) may determine cell survival (Osawa et al., 2005), suggesting that sphingolipids are closely linked to the activity and survival of cells. In this study, the PBR produced disturbances to endogenous metabolites of hepatic sphingolipids in control rats administered with PBR, including sphinganine and phytosphingosine, suggesting that high-dose PBR might cause liver damage by altering hepatocyte survival and membrane structure.

The metabolic networks of β -oxidation of fatty acids are shown in **Figure 8D** β -oxidation of fatty acids is an important pathway for fatty acid decomposition and energy production, and

its abnormality can lead to dysfunction of the nervous system. Acyl carnitines are long-chain acyl fatty acid esters of carnitine. They can carry long-chain fatty acids from the cytoplasm into the mitochondria, allowing long-chain fatty acids to oxidize in the mitochondria to produce energy. However, this transportation is dependent on carnitine (Malaguarnera et al., 2011; Ren et al., 2013). In this study, the levels of L-carnitine, L-acetylcarnitine, and propionylcarnitine were significantly increased in the liver of CUMS rats, indicating that the transportation of long-chain fatty acids into the mitochondria was disturbed, thereby interfering with the energy production of the long-chain fatty acid oxidation process. After the administration of PBR, the concentrations of L-carnitine, L-acetylcarnitine, and propionylcarnitine in D4 and D6 were significantly reversed to healthy, indicating that PBR produced an anti-depressant effect by regulating β-oxidation of fatty acids. Another study (Devaux, 1991) reported that acetyl-L-carnitine treatment improved liver function and quality of life in patients with mild hepatic encephalopathy. Therefore, in normal rats, the levels of acyl-carnitine were significantly decreased in the liver of control rats administered with PBR, indicating that PBR may alter acyl-carnitine to cause mitochondrial β-oxidation of fatty acid dysfunction, resulting in energy deficiency and eventually leading to liver damage.

The glycerophospholipid metabolism was only significantly changed in the livers of control rats administered with PBR. Lysophosphatidylethanolamine (LysoPEs) is produced by the metabolism of phosphatidylethanolamine (PE). Both PE and sphingolipids are the main components of cell membrane phospholipids and are distributed asymmetrically in the plasma membrane. Most PEs are embedded in the inner membrane of the cell membrane and constitute the membrane phospholipid bilayer (Jaeschke et al., 2002). The abnormality of LysoPEs in control rats administered with PBR suggested that PEs were perturbed, further affecting the plasma membrane structure and permeability. In this study, LysoPE [0:0/20:4 (8Z, 11Z, 14Z, 17Z)] was significantly decreased in the livers of control rats administered with PBR, indicating that PBR might cause liver damage by changing the structural integrity and permeability of the plasma membrane in normal rats. Bile acid metabolism is shown in Figure 8E. Bile acid metabolism was also significantly changed in control rats administered with PBR. Bile acids are sensitive indicators of liver and liver damage. Abnormally elevated bile acids, such as cholestasis, can cause the accumulation of toxic bile acids in the leading to pathophysiological effects, including mitochondrial dysfunction and overproduction of reactive oxygen and nitrogen (Palmeira and Rolo, 2004; Tan et al., 2007). More importantly, slight liver damage can cause bile acid perturbation in the serum and liver (Yamazaki et al., 2013). Various liver diseases, such as non-alcoholic fatty liver disease and drug-induced liver injury, can increase intrahepatic bile acid levels (Lake et al., 2013). In this study, glycocholic acid was significantly elevated in the liver, which was consistent with the results of serum metabonomics of control rats administered with PBR, indicating that high-dose PBR might accumulate intrahepatic bile acid and cause liver injury.

In this study, 8,671 metabolites were measured, and 409 metabolites were identified in the sample. The metabolites were

mainly high polarity compounds including amino acids, sphingolipids, bile acids, etc. While the less polarity compounds such as fatty acids and lipid metabolites were difficult to be detected. The GC-MS serum metabolomics was performed and the fatty acids were detected in our previous study (Gao, et al., 2014). The results showed that depression was associated with amino acid metabolism and energy metabolism, which were consistent with the results of this study. Therefore, the targeted metabolomics was applied to quantify the metabolites of amino acid metabolism and energy metabolism in follow-up studies.

The dose-effect/toxicity relationship is the essence of the clinical use of TCM. Because of the multi-component and multi-target characteristics of TCM (Wang et al., 2010), a comprehensive evaluation of the dose-effect/toxicity relationship is important to allow its application in modern medical practice. Although some convenient and effective evaluation indices have been used in previous dose-effect/toxicity studies, including body weight, blood pressure, blood glucose, transaminase, platelets, and cell number, there are still many disease effect indices that lack quantification, and depression is a major disease. With the development of studies regarding the essence of TCM syndrome based on metabonomics, the importance of metabonomics for evaluating overall effects was gradually being recognized (Wang et al., 2010). After administration, the endogenous small molecules shifted in the same direction as the dose increased. Metabolites representing the organic state were screened and integrated into a dose-effect/toxicity relationship analysis. A significant doseeffect/toxicity relationship was observed with a high dosedependence. The results showed that the comprehensive index was better for evaluating the dose-effect/toxicity relationship, which is consistent with the fact that it may be caused by the multi-component and multi-target characteristics of the TCM. In this study, four-function models were compared for metabolite integration, and the results showed that the different models might influence the evaluation characteristics of the metabolites. Therefore, exploring a more suitable functional model would help construct a metabolic evaluation system for depression. However, it is necessary to verify effect/toxicity biomarkers of PBR. The vitro cell experiments would be used to verify the specificity and accuracy of toxicity biomarkers in follow-up studies.

CONCLUSIONS

The current study demonstrates that the effective dose range and median toxicity dose of PBR for CUMS rats are 12.6–50 g (herb)/kg and 388 g (herb)/kg, and PBR produces anti-depressant effects by reversing amino acid metabolism, energy metabolism, sphingolipid metabolism, and β -oxidation of fatty acids in CUMS rats. In control rats, the median toxicity dose of PBR is 207 g (herb)/kg, and extra two metabolic pathways including glycerophospholipid metabolism and bile acid metabolism are significantly perturbed after administration with PBR. Moreover, the comprehensive metabolic indexes including DEI and DTI have a remarkable ability to predict effect and toxicity which needs further follow-up validation. Furthermore, the CUMS rats possessed a higher

toxicity tolerance dose of PBR, which was consistent with the theory of "You Gu Wu Yun". These results indicate that the metabonomics techniques combined with correlation analysis could be used to discover indicators for comprehensive evaluations of efficacy and toxicity.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding authors.

ETHICS STATEMENT

This animal study were performed under the NIH Guidelines for Care and Use of Laboratory Animals (United States) and the Prevention of Cruelty to Animals Act (1986) of China, and approved by the Animal Ethics Committee of Shanxi University (ethical batch number: SXULL2019004).

AUTHOR CONTRIBUTIONS

PW and XG conceived and designed the experiments; PW and XG wrote the paper; ML and YF performed the experiments; PW and YF analyzed the data; JJ detected samples with UHPLC-MS; JT, ZL, and XQ design of the study and writing the protocol. All authors have approved the final version of the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.627451/full#supplementary-material

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GLOSSARY

ALP alkaline phosphatase

ALT alanine aminotransferase

AST aspartate aminotransferase

BRI Behavioral Regulation Index

ceramide/S1P ceramide and sphingosine 1-phosphate

CK-18F cytokeratin-18 fragment

CUMS chronic unpredictable mild stress

DEI dose-effect index

DILI drug-induced liver injury

DTI dose toxicity index

EI effect index

LCI Liver Composite Index

LC-MS the liquid chromatography with mass spectrometry

LysoPEs Lysophosphatidylethanolamine

NE norepinephrine

OPLS orthogonal partial least squares

PBR lower polar fraction of Bupleuri Radix

PCA principal component analysis

PDA Photodiode Array

 ${\bf PE}$ phosphatidylethanolamine

PLS-DA partial least-squares discriminant analysis

QAMS quantitative analysis of multiple components by a single marker

QC Quality control

ROC receiver operating characteristic

TBIL total bilirubin

TCA tricarboxylic acid

TCM traditional Chinese medicine

TD50 median toxicity dose

TNF- α tumor necrosis factor-alpha

TIC total ions chromatograph

UHPLC ultra-performance liquid chromatography system





The Novel Chinese Medicine JY5 Formula Alleviates Hepatic Fibrosis by Inhibiting the Notch Signaling Pathway

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Fu Y, Xiao Z, Tian X, Liu W, Xu Z, Yang T, Hu Y, Zhou X, Fang J, Gao S, Zhang D, Mu Y, Zhang H, Hu Y, Huang C, Chen J and Liu P (2021) The Novel Chinese Medicine JY5 Formula Alleviates Hepatic Fibrosis by Inhibiting the Notch Signaling Pathway. Front. Pharmacol. 12:671152. doi: 10.3389/fphar.2021.671152 Advanced liver fibrosis can lead to cirrhosis, resulting in an accelerated risk of hepatocellular carcinoma and liver failure. Fuzheng Huayu formula (FZHY) is a traditional Chinese medicine formula treated liver fibrosis in China approved by a Chinese State Food and Drug Administration (NO: Z20050546), composed of Salvia Miltiorrhiza bge., Prunus davidiana (Carr.) Franch., cultured Cordyceps sinensis (BerK.) Sacc. Mycelia, Schisandra chinensis (Turcz.) Baill., Pinus massoniana Lamb., and Gynostemma pentaphyllum (Thunb.) Makino. However, the main active substances and mechanism of FZHY are unclear. The aim of this study is to identify a novel antifibrotic compound, which consists of the main active ingredients of FZHY, and investigate its mechanism of pharmacological action. The main active ingredients of FZHY were investigated by quantitative analysis of FZHY extracts and FZHY-treated plasma and liver in rats. The anti-fibrotic composition of the main active ingredients was studied through uniform design in vivo, and its mechanism was evaluated in carbon tetrachloride (CCl₄)and bile duct ligation (BDL)-induced liver fibrosis models in rats and mice, and transforming growth factor beta 1-induced LX-2 cell activation model in vitro. A novel Chinese medicine, namely JY5 formula, consisting of salvianolic acid B, schisantherin A, and amygdalin, the main active ingredients of FZHY, significantly alleviated hepatic hydroxyproline content and collagen deposition in CCl₄-and BDL-induced fibrotic liver in rats and mice. In addition, JY5 inhibited the activation of hepatic stellate cells (HSCs) by inactivating Notch signaling in vitro and in vivo. In this study, we found a novel JY5 formula, which exerted anti-hepatic fibrotic effects by inhibiting the Notch signaling pathway, consequently suppressing HSCs activation. These results provide an adequate scientific basis for clinical research and

Abbreviations: FZHY, fuzheng huayu formula; SORA, sorafenib; HSCs, hepatic stellate cells; ECM, extracellular matrix; TCM, traditional Chinese medicine; KCs, kupffer cells; LSECs, liver sinusoidal endothelial cells; CCl4, carbon tetrachloride; BDL, bile duct of ligation; ALT, alanine aminotransferase; AST, aspartate aminotransferase; ALP, alkaline phosphatase; TBil, total bilirubin; DBil, direct bilirubin; TBA, total bile acids; Hyp, hydroxyproline; IHC, immunohistochemical; H&E, hematoxylin & eosin; SR, sirius red; α -SMA, α -smooth muscle actin; RBP- κ B, recombination signal binding protein- κ B; HCC, hepatocellular carcinoma; NICD, notch intracellular domain.

application of the JY5 formula, which may be a potential novel therapeutic candidate for liver fibrosis.

Keywords: traditional Chinese medicine, JY5 formula, fuzheng huayu, hepatic fibrosis, notch signaling pathway

INTRODUCTION

Liver fibrosis is a common pathological feature of chronic liver diseases including chronic viral hepatitis, metabolic-associated fatty liver disease, and cholestatic liver diseases. It is a consequence of an abnormal wound healing response, characterized by excessive deposition of extracellular matrix (ECM). If the injury persists, liver fibrosis can progress to cirrhosis and hepatocellular carcinoma, ultimately leading to liver failure (Friedman, 2015). The effective treatment for liver fibrosis is to address the root cause and prevent progression. Some clinical studies (Lee et al., 2015) have shown that liver fibrosis, even early cirrhosis, is reversible, providing reliable evidence for conducting clinical studies on anti-hepatic fibrosis drugs. With several types of animal models of liver fibrosis becoming increasingly mature, there has been a greater understanding of the pathogenesis of liver fibrosis in the last few decades (Cordero-Espinoza and Huch, 2018). A number of anti-hepatic fibrosis drug studies have been conducted in recent years, some of which have been researched in clinical trials (Lemoinne and Friedman, 2019). However, to date, there are no clinically approved by FDA or effective medical therapies aimed specifically towards hepatic fibrosis.

Traditional Chinese medicine (TCM) has marked clinical effects on the treatment of liver fibrosis. Among these, Fuzheng Huayu (FZHY) formula which composed of Salvia miltiorrhiza Bunge (Dansen), Prunus davidiana (CarriŠre) Franch (Taoren), cultured Cordyceps sinensis (BerK.) Sacc. Mycelia (Chongcao), Schisandra chinensis (Turcz.) (Wuweizi), Pinus massoniana Lamb. (Songhuafen), and Gynostemma pentaphyllum (Thunb.) Makino (Jiaogulan), is a complex preparation to treat liver fibrosis in China approved by a Chinese State Food and Drug Administration (NO: Z20050546). The anti-fibrotic effect has been confirmed in a phase II clinical trial of hepatic fibrosis post-hepatitis C in the United States (Zhang and Schuppan, 2014). However, there are some challenges with TCM, such as its multi-component, multitarget, ill-defined active ingredients and mechanisms, which limit their clinical application. In recent years, our team has conducted a large amount of research to elucidate the mechanisms underlying the role of FZHY in the prevention and treatment of chronic liver diseases, including inhibiting the inflammatory response, protecting hepatocytes (to relieve hepatocyte damage and inhibit hepatocyte apoptosis), inhibiting hepatic stellate cell (HSC) activation, reducing collagen deposition, inhibiting Kupffer cell (KC) activation, inhibiting liver sinusoidal endothelial cell (LSEC) capillarization and angiogenesis, and promoting liver regeneration (Liu et al., 2009; Chen et al., 2019). We further studied the anti-fibrosis effects of different compounds of FZHY. Phenolic acids in Salvia miltiorrhiza play a prominent role in inhibiting the inflammatory response, protecting hepatocytes, and inhibiting HSC activation (Wang et al., 2012; Tao et al., 2013; Kan et al., 2014; Yan et al., 2017; Wang et al., 2019). Amygdalin, as one of the major active compounds of *Peach kernel*, has the main role in inhibiting the inflammatory response, reducing collagen deposition, and inhibiting HSC activation (Luo et al., 2016; Luo et al., 2018). The lignan compounds from *Schisandrae* play an important role in protecting hepatocytes and inhibiting HSC activation (Kang et al., 2019; He et al., 2020). These findings suggest that the related bioactive ingredients in FZHY may have anti-fibrotic effects.

Notch signaling is a highly conservative pathway during evolution. Notch receptors interact with ligands on the surface of adjacent cells, then cleave inside the cell membrane, translocate into the nucleus, and regulate the transcription of multiple target genes. Previous studies (Adams and Jafar-Nejad, 2019) have shown that as an important intercellular or intracellular signaling pathway, Notch plays an important role in liver development and pathophysiology. Notch has a great impact on the occurrence and development of hepatic fibrosis and can interact with transforming growth factor beta (TGF-β), Hedgehog, and Hippo signaling pathways to mediate cell-cell interactions. Activation of HSCs is a critical cellular event in liver fibrosis. **HSCs** transdifferentiate into mvofibroblasts, accompanied by activation of Notch signaling pathway (Zhang et al., 2015). After Notch activity levels are suppressed, this process can be reversed. In addition, with the progression of liver fibrosis induced by carbon tetrachloride (CCl₄) and bile duct ligation (BDL), the Notch signaling pathway is significantly activated. Efficient inhibition of the Notch pathway can significantly mitigate liver fibrosis and reduce hepatocyte apoptosis (Chen et al., 2012). Thus, targeting the Notch signaling pathway can regulate the activation of HSCs, thereby suppressing the occurrence and progression of hepatic fibrosis.

In this study, we found that salvianolic acid B, schisantherin A, and amygdalin were the main active ingredients of FZHY formula by quantitative analysis of FZHY extracts and FZHY-treated plasma and liver in rats. A novel TCM formula, namely JY5, was obtained through uniform design. The anti-hepatic fibrosis efficacy of JY5 was comparable to that of FZHY in CCl_4 -induced hepatic fibrosis in rats (**Supplementary Figures S3 and S4**). Further studies demonstrated that JY5 alleviated liver fibrosis by inhibiting the activation of HSCs via inhibition of the Notch signaling pathway.

MATERIALS AND METHODS

Animals

Adult Wistar or Sprague-Dawley male rats (160–180 g, specific pathogen-free [SPF] grade) were purchased from Shanghai Xipuer-Bikai Experimental Animal Co., Ltd (Shanghai, China)

and fed in the Laboratory Animal Center at School of Pharmacy, Fudan University (Shanghai, China). Adult male C57/BL6 mice (aged 6–8 weeks, 18–20 g, SPF grade) were purchased from Shanghai Southern Model Biotechnology Co., Ltd (Shanghai, China) and maintained in the Shanghai Research Center of the Southern Model Organisms (Shanghai, China). Rats and mice were housed under constant conditions (ambient temperature 25 ± 2°C, relative humidity 40–60%, and 12/12 h light-dark cycle) with free access to standard diet and water. All rat experiments were reviewed and approved by the Experimental Animal Ethics Committee of School of Pharmacy, Fudan University (Approval No. 2018–07-SZYD-LP-01). All mice experiments were approved by the Institutional Animal Care and Use Committee (IACUC) at Shanghai Research Center of the Southern Model Organisms (Approval No. 2019–0031).

Drugs

Reference standards: salvianolic acid B, salvianic acid, salvianic acid A, rosmarinic acid, gypenoside XLIX, ginsenoside Rb3, amygdalin, schisantherin A, schisandrol A, schisandrol B, deoxyschizandrin, schisandrin В, tanshinone. cryptotanshinone, adenosine, and cordycepin were purchased from Shanghai Standard Technology Co., Ltd (Shanghai, China). The purity of all standards was more than 98%. FZHY decoction: mixture of Salvia miltiorrhiza Bunge at 533 g, Prunus davidiana (CarriŠre) Franch. at 133 g, and Gynostemma pentaphyllum (Thunb.) Makino at 400 g, was heated to boiling with water for 2 h for the first time and for 1.5 h for the second time. The combined decoction was filtered, and concentrated to a relative density at 1.20 g/ml (50-55°C). After cooling down, the decoction was precipitated by adding 70% alcohol, and then filtrate 1 was generated after filtration and concentration. A combination of cultured Cordyceps sinensis (BerK.) Sacc. Mycelia at 267 g and Schisandra chinensis (Turcz.) Baill. at 133 g was heated with 70% alcohol for 2 h for the first time and 1.5 h for the second time, and the combined decoction was filtered and concentrated as filtrate 2. Pinus massoniana Lamb. at 133 g was infiltrated with 50% alcohol for 4 h for the first time and 2 h for the second time, and the combined decoction was filtered and concentrated as filtrate 3. Filtrates 1-3 were combined and concentrated to 800 ml at 2 g raw drug/mL. The voucher specimens, Salvia miltiorrhiza Bunge (No. 1600001), Prunus davidiana (CarriŠre) Franch (No. 1600002), Gynostemma pentaphyllum (Thunb.) Makino (No. 1600003), cultured Cordyceps sinensis (BerK.) Sacc. Mycelia (No. 1600004), Schisandra chinensis (Turcz.) Baill (No. 1600005), and Pinus massoniana Lamb. (No. 1600006) were deposited in the Shanghai Institute of Materia Medica.

Pharmacokinetic Study of Fuzheng Huayu Decoction in Rats

This study was conducted according to the guidelines of the IACUC of the Shanghai Institute of Materia Medica, Chinese Academy of Sciences (Shanghai, China). The experimental protocol is shown in **Supplementary Material: Materials and Methods 1.1**.

Instrumentation

There were 16 compounds determined in various biosamples by the UltiMate 3000 ultra-high-performance liquid chromatograph linked to the active quadrupole electrostatic field orbital trap high-resolution mass spectrometer, connected to an electrospray ionization source (Thermo Fisher Scientific, Waltham, MA, United States). The operating parameters were set as shown in **Supplementary Material: Materials and Methods 1.2**.

Experimental Liver Fibrosis Models

 ${\rm CCl_4}$ -induced liver fibrosis rat model, BDL-induced liver fibrosis rat model, and ${\rm CCl_4}$ -induced liver fibrosis mouse model were used in this study. The experimental protocols are shown in Supplementary Material: Materials and Methods 1.3.

Cell Culture

The immortalized human hepatic stellate cell line (LX-2) was provided by the Institute of Liver diseases, Shanghai University of Traditional Chinese Medicine (Shanghai, China). LX-2 cells (1.25 \times 10⁵) were seeded in 6 cm dishes or 6-well plates and maintained in Dulbecco's Modified Eagle Medium containing 1% penicillin/ streptomycin and 10% fetal bovine serum at 37°C and 5% CO₂. After post-inoculation for 24 h, all LX-2 cells except the control group were treated with TGF-\(\beta\)1 (5 ng/ml), and simultaneously treated with different concentrations of JY5 as follows: low-dose group (6.587 µg/ml) (salvianolic acid B 8 µM, amygdalin 0.25 µM, schisantherin A 1 µM), medium-dose group (13.174 µg/ml) (salvianolic acid B $16\,\mu\text{M}$, amygdalin $0.5\,\mu\text{M}$, schisantherin A 2 μM), and high-dose group (26.348 μg/ml) (salvianolic acid B $32 \,\mu\text{M}$, amygdalin $1 \,\mu\text{M}$, schisantherin A $4 \,\mu\text{M}$). SB431542 (10 μM), a TGF-β receptor inhibitor, was used as a positive control. After incubation for 24 h, LX-2 cells were lysed and collected for Western blotting and quantitative PCR (qPCR) analysis.

Serum Biochemistry Analysis

Serum alanine aminotransferase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP), total bilirubin (TBil), direct bilirubin (DBil), and total bile acid (TBA) levels were measured using the TBA-40FR automatic biochemistry analyzer (Toshiba Medical, Tokyo, Japan) at the Science and Technology Experiment Center, Shanghai University of TCM.

Histopathological and Immunohistochemical Analysis

Liver injury and fibrosis were assessed with hematoxylin and eosin (H&E) and Sirius Red (SR) staining using 4 μ m thick paraffin-embedded liver sections. Immunohistochemistry (IHC) staining of collagen type I (Col-I), Col-IV, *a*-smooth muscle actin (α -SMA), and desmin was performed. The detailed protocols are shown in **Supplementary Material:** Materials and Methods 1.4.

Hepatic Hydroxyproline Content Assay

According to the kit instructions, hydroxyproline (Hyp) content in liver tissue was detected using the Hydroxyproline Testing Kit-

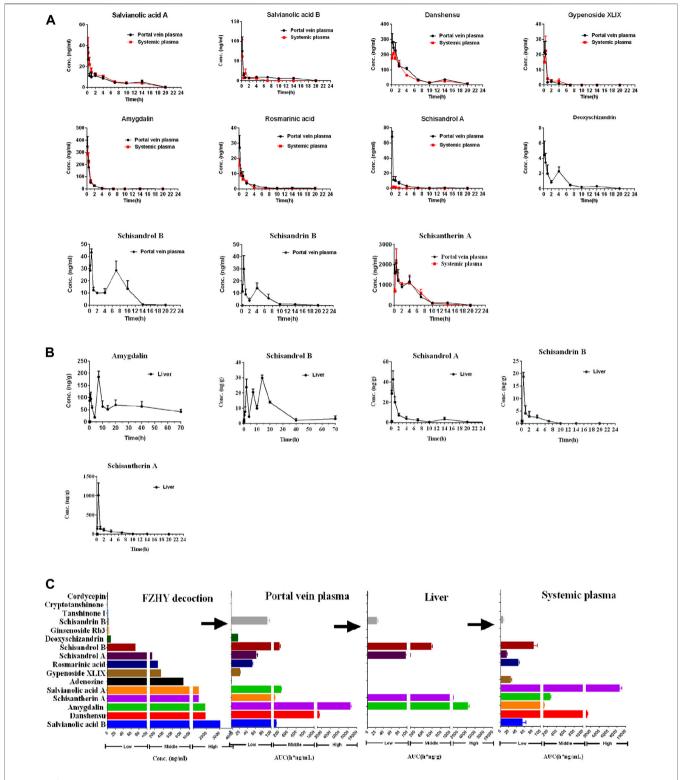


FIGURE 1 | Quantitative analysis of FZHY decoction and FZHY biological samples. Concentration—time curves of compounds in the plasma (A) and liver (B) after oral administration of FZHY decoction (20 g/kg) in rats (n = 5). (C) Summary of the contents and AUC of compounds in the FZHY decoction or FZHY biological samples.

TABLE 1 | The PK parameters of 11 compounds in the portal vein plasma, systemic plasma and liver, following oral administration of FZHY decoction in rats.

Compounds	Portal vein plasma			Systemic plasma			
	T _{max} (h)	C _{max} (ng/ml)	AUC(h*ng/ml)	T _{max} (h)	C _{max} (ng/ml)	AUC(h*ng/ml)	
Salvianolic acid A	0.167	26.7 ± 11.2	108.7 ± 9.1	0.167	33.1 ± 14.9	122.3 ± 5.7	
Salvianolic acid B	0.167	74.8 ± 36.4	144.4 ± 7.3	0.167	61.5 ± 42.1	55.9 ± 18.6	
Danshensu	0.167	279.8 ± 58.8	1515.9 ± 64.6	0.5	206.6 ± 41.6	1362 ± 95	
Gypenoside XLIX	0.5	21.5 ± 7.3	21.3 ± 3.5	0.5	22.4 ± 9.8	26.4 ± 3.8	
Amygdain	0.167	347.7 ± 82.5	254.7 ± 23.2	0.167	286.2 ± 44.2	262.8 ± 23.9	
Rosmarinic acid	0.167	27.1 ± 8.1	51.9 ± 4	0.167	15.4 ± 4.9	45.5 ± 4.7	
Schisandrol A	0.167	68.2 ± 7.2	62 ± 8.6				
Schisandrol B	0.5	43.4 ± 3	215.1 ± 49.3	0.5	35.9 ± 0.6	84.3 ± 19.8	
Deoxyschizandrin	0.167	4.4 ± 1.8	15.6 ± 1.1				
Schisandrin B	0.5	29.9 ± 11	89.4 ± 15.7				
Schisantherin A	0.5	1657.7 ± 584.3	8542.1 ± 566.2	0.5	2094.4 ± 681	8672.6 ± 1093.6	

Compouds	Liver		
	T _{max} (h)	C _{max} (ng/g)	AUC(h*ng/g)
Amygdain	7	185 ± 24.1	4423.2 ± 599.8
Schisandrol A	0.5	42.5 ± 8.4	96.4 ± 13.7
Schisandrol B	14	29.9 ± 1.8	578.7 ± 50.3
Schisandrin B	0.5	18.7 ± 1.7	24.1 ± 4.6
Schisantherin A	0.5	1011.1 ± 322.6	1070.3 ± 103.4

Alkaline Hydrolysis Method (Cat No. A030-2; Nanjing Jiancheng Bioengineering Institute, Nanjing, China).

Western Blot Analysis

Total protein in liver tissues or cells was extracted using RIPA lysis buffer containing proteinase and phosphatase inhibitor (Cat No. P0013B; Biyuntian Biotechnology Co., Ltd., Shanghai, China). Total protein concentration was determined using a BCA protein assay kit (Lot TD265229; Thermo Fisher Scientific). Proteins (30-50 μg) were denatured at 100°C for 5 min, and then separated by 8% or 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis. The proteins were electrotransferred onto polyvinylidene fluoride (PVDF) membranes. The membranes were blocked in 5% BSA at room temperature for 60 min, and then incubated with primary antibody (Supplementary Table S1) overnight at 4°C. The following day, the membranes were incubated in the dark for 1 h at room temperature with fluorescence-labeled secondary antibody (Supplementary Table S1). The PVDF membranes were scanned using the Odyssey 2.1 software of Odyssey infrared scanner (LI-COR Biosciences, Lincoln, NE, United States). After scanning, target protein bands were cut out according to the molecular weight of target protein without any edit. The greyscale values relative to GAPDH of the target proteins were analyzed using ImageJ software.

Quantitative PCR Analysis

Total RNA in liver tissues or cells was extracted and reverse transcribed using a nucleic acid purification kit (Code: NPK-201F, Lot. 742,100; Toyobo Co., Ltd., Osaka, Japan) and the ReverTra Ace qPCR RT Kit (Code: FSQ-301, Lot. 616,800; Toyobo Co., Ltd., Osaka, Japan). The qPCR primer sequence information is listed in **Supplementary Table S2**. The PCR cycling program was 95°C for 60 s, 40 cycles of 95°C for 15 s, and 60°C for 60 s, followed by melting curve analysis. The GAPDH gene was used as the internal reference

for normalization of the target genes. The relative mRNA expression of each group was calculated using the $2^{-\Delta\Delta Ct}$ method.

Dual-Luciferase Reporter Assay

The transcriptional activity of Notch was measured using RBP-κβ luciferase reporter plasmid constructed by Shanghai Jikai Gene Chemical Technology Co. Ltd. following the supplier's instructions. The RBP-kB-Luc vector were engineered in GV238 backbone vector. The target gene sequence of RBP-κB (NM_005,349-promoter-1) was amplified by PCR using the primers as follows: forward: 5'-CTAGCCTAGGCGACAGAG CAAG-3'; reverse: 5'-CTTTATGTTTTTGGCGTCTTCCA-3'. The amplicons were inserted into the cloning sites of KpnI and XhoI located upstream of the firefly luciferase gene. and then a dual-luciferase reporter assay was performed using Dual-Lumi[™] luciferase reporter gene assay kit (RG088S, Beyotime Biotechnology, China). The transiently co-transfected LX-2 cells with the corresponding transfection mix containing 200 ng RBPκB-Luc plasmid (firefly) and 20 ng pRL-TK control vector (renilla) using Lip8000TM (C0533, Beyotime Biotechnology, China) were treated with TGF-β1 (5 ng/ml),simultaneously treated with salvianolic acid B (32 µM), amygdalin (1 μ M), schisantherin A (4 μ M) or JY5 (26.348 μ g/ ml) for 24 h, respectively. RBP-KB luciferase activity was detectedby Dual-Lumi[™] luciferase reporter gene assay kit following the manufacturer's instructions. With renilla luciferase as the internal control in each transfection, the relative luciferase activity was calculated as the ratio of fireflyto-renilla luciferaseactivity.

Statistical Analysis

All data were analyzed using the SPSS 21.0 software package. All data are expressed as the mean \pm standard deviation (SD).

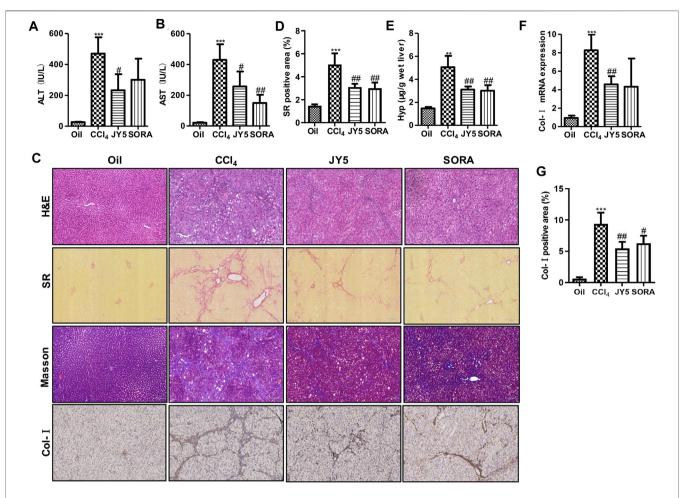


FIGURE 2 JY5 significantly alleviates hepatic inflammatory injury and collagen deposition in CCl_4 -induced rat liver fibrosis. Serum levels of ALT **(A)** and AST **(B)** were measured in each group. **(C)** H&E staining (100x), SR staining (100x), Masson staining (100x) and IHC staining of Col-I (100x), and semi-quantitative analysis **(D)** of collagen disposition (%) in SR-stained liver sections **(E)** Hyp content in wet liver tissue was detected by alkaline hydrolysis. **(F)** The mRNA levels of *Col-I* in liver tissue were analyzed by qPCR. **(G)** quantitative analysis of immunohistochemical staining for Col-I. **p < 0.01, ***p < 0.001 vs the control group, *p < 0.05, **p < 0.01 vs the CCl₄ group. Oil: control group.

Comparisons between multiple groups were analyzed by the one-way analysis of variance, followed by the least significant difference test. p < 0.05 was considered statistically significant. In addition, the pharmacokinetic (PK) parameters were calculated by noncompartmental analysis in WinNonlin software with a sparse sampling algorithm (Pharsight 6.2, Cary, NC, United States).

RESULT

Quantitative Analysis of Fuzheng Huayu Decoction and Fuzheng Huayu Biological Samples

The chemical structure and concentration of 16 compounds in the FZHY decoction (2 g/ml) are shown in **Supplementary** Figures S1, S2 and Supplementary Table S3 respectively. The concentration-time curves of compounds in the plasma and liver after oral administration of FZHY decoction (20 g/kg) in rats are shown in Figures 1A,B, and the corresponding PK parameters are shown in Table 1. The summary of the contents and area under the curve (AUC) of compounds in the FZHY decoction or FZHY biological samples are shown in Figure 1C. There were 16 compounds determined in the FZHY decoction, including six derived from Salvia miltiorrhiza, five derived from Schisandra chinensis, two derived from Gynostemma pentaphylla, two from Cordyceps mycelium, and one compound from Gynostemma pentaphylla. Among the compounds, salvianolic acid B had the highest content in the FZHY decoction, followed by danshensu, amygdalin, schisantherin Α, and salvianolic acid (concentration≥1000 µg/ml). Adenosine, gypenoside XLIX, rosmarinic acid, and schisandrol A were in the middle

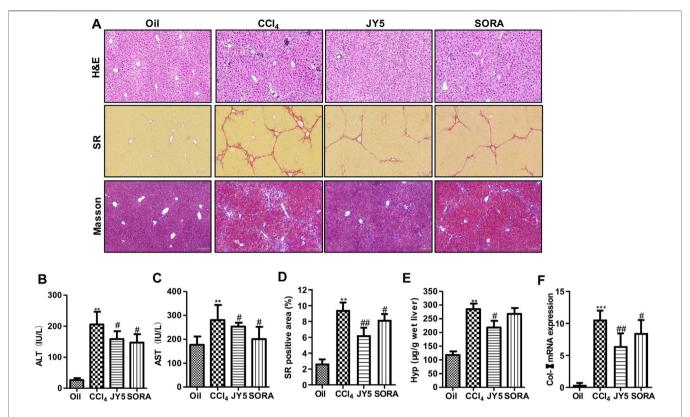


FIGURE 3 JY5 significantly alleviates hepatic inflammatory injury and collagen deposition in CCl₄-induced mouse liver fibrosis. **(A)** H&E staining (100x), SR staining (100x) and Masson staining (100x) in liver tissue. Serum levels of ALT **(B)** and AST **(C)** were measured in each group. **(D)** Semi-quantitative analysis of collagen disposition (%) in SR-stained liver sections. **(E)** Hyp content in wet liver tissue was detected by alkaline hydrolysis. **(F)** The mRNA expression of *Col-I* in mice liver tissue was analyzed by qPCR. **p < 0.01, ***p < 0.001 vs the control group, **p < 0.05, **p < 0.01 vs the CCl₄ group. Oil: control group.

content group (100 μg/ml < concentration<1000 μg/ml), and the concentrations of the remaining compounds, including schisandrol В, deoxyschizandrin, ginsenoside schisandrin tanshinone I, cryptotanshinone, В, and cordycepin, were very low (concentration≤100 μg/ml). The portal vein blood is the first site after gut absorption but before hepatic disposition, which is responsible for transferring the substances to the liver post-dose. Following oral administration of FZHY in rats, there were 11 compounds accurately detected in the portal vein plasma, of which tanshinone I, cryptotanshinone, cordycepin, ginsenoside Rb3, and adenosine were undetected, probably due to the low content in the formula or poor physicochemical property. T_{max}s of all compounds were within 0.5 h in portal vein plasma, indicating fast absorption. Schisantherin A exhibited maximum exposure in the portal vein plasma, followed by danshensu (AUC≥1000 h*ng/mL). Four compounds, including amygdalin, schisandrol B, salvianolic acid B, and salvianolic acid A, belonged to the middle exposure group (100 h*ng/mL < concentration <1000 h*ng/mL). The remaining five compounds were in the low exposure group (AUC≤100 h*ng/mL). After hepatic disposition, the compounds were transported to the systemic plasma, which is responsible for delivering substances to the other organs, except the liver. Compared to those in the portal vein plasma, there were eight compounds determined in the systemic plasma, of which schisandrol A, schisandrin B, and deoxyschizandrin were undetected. Similar to those in the portal vein plasma, the absorption of those compounds was quick; schisantherin A and danshensu were in the high exposure group (AUC≥1000 h*ng/mL), and schisantherin A had the highest exposure in the systemic plasma. The middle exposure group (100 h*ng/mL < AUC <1000 h*ng/mL) included amygdalin and salvianolic acid A; the remaining compounds belonged to the low exposure group (AUC≤100 h*ng/mL). Following oral administration of FZHY decoction, only five compounds were detected in the liver. Tmaxs of schisandrol A, schisandrin B, and schisantherin A was 0.5 h, similar to that in the plasma. By contrast, T_{max}s of schisandrol B and amygdalin was 14 and 7 h, respectively, consistent with their multi-peak phenomenon in the concentration-time curves. By contrast to levels in the plasma, amygdalin had the highest hepatic exposure, followed by schisantherin A, whose exposure was >1000 h*ng/g. Schisantherin A was in the middle exposure group (100 h*ng/g < AUC <1000 h*ng/g), and the hepatic exposure of schisandrol A and schisandrin B was very low (AUC≤100 h*ng/g). Finally, salvianolic acid B, schisantherin

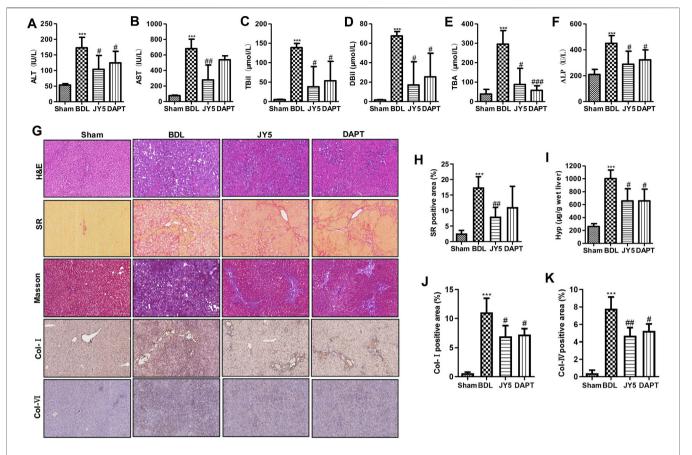


FIGURE 4 | JY5 significantly alleviates hepatic inflammatory injury and collagen deposition in BDL-induced rat liver fibrosis. The levels of serum ALT **(A)**, AST **(B)**, TBil **(C)**, DBil **(D)**, TBA **(E)**, and ALP **(F)** were measured in each group. **(G)** H&E staining (100x), SR staining (100x), Masson staining (100x) and IHC for Col-I and Col-IV (100x) staining, and semi-quantitative analysis **(H)** of collagen disposition (%) in SR-stained liver sections. **(I)** Hyp content in wet liver tissue was detected by alkaline hydrolysis. Quantitative analysis of immunohistochemical staining for Col-I **(J)** and Col-IV **(K)**. ***p < 0.001 vs the sham group, p < 0.05, p < 0.01 vs the BDL group.

A, and amygdalin, which had the highest content in the FZHY decoction, plasma, and liver, respectively, were selected to evaluate the anti-hepatic fibrosis effects *in vivo*.

JY5 Significantly Alleviates Hepatic Injury and Collagen Deposition in CCl₄-Induced Rat and Mouse Liver Fibrosis

Compared with the control group (Oil), the levels of serum ALT and AST were significantly increased in the CCl₄ group. After treatment with JY5 (salvianolic acid: B 16 mg/kg, amygdalin: 0.5 mg/kg, schisantherin A: 2 mg/kg) or FZHY (2 g/kg), the levels of ALT and AST were significantly decreased (**Figures 2A,B** and **Supplementary Figures S3D,E**). The serum AST level was decreased in the sorafenib group (SORA, 5 mg/kg) compared with the CCl₄ group (**Figure 2B**). H&E staining showed that the hepatic lobular structure was severely collapsed with formation of more complete pseudo-lobules in the CCl₄ group. As the fibrous tissue became denser, the hepatocytes were disordered and ballooning degeneration

occurred. There was a large number of inflammatory cells infiltration surrounding the hepatic sinusoid, central vein, and portal tract. The above lesions were obviously attenuated with less pseudo-lobules and inflammatory cells infiltration, after treatment with JY5 or FZHY or SORA (Supplementary Figure S3A and Figure 2C, upper panel). SR and Masson staining showed that compared to the control group, collagen deposition was obviously increased in the CCl4 group. The fibrotic septum became significantly widened and distributed from the portal tract to the periphery in a reticular manner, forming pseudo-lobules with varying sizes. By contrast, collagen deposition was obviously decreased, the fibrotic septum became narrower, and pseudo-lobules structures were observed less in the JY5-, FZHY-, or SORA-treated groups (Supplementary Figure S3A, lower panel and Figure 2C, middle panel). Both the hepatic Hyp content and collagen deposition were significantly increased in the CCl₄ group compared to the control group. The above indicators were significantly reduced after intervention with JY5, FZHY, or SORA (Supplementary Figures S3B,C and Figures 2D,E). These

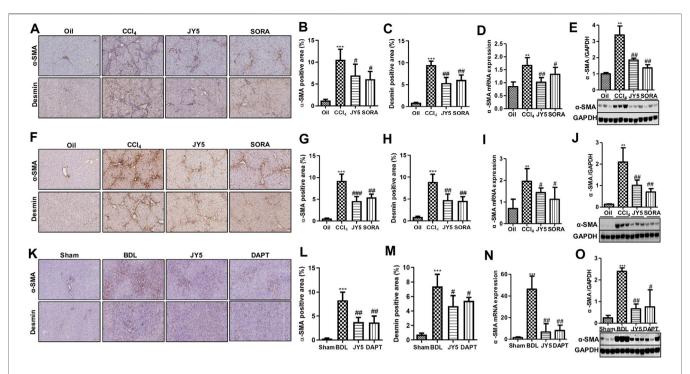


FIGURE 5 | JY5 inhibits the activation of HSCs *in vivo*. (A) In the CCI₄-induced rat liver fibrosis experiment, representative images of IHC (100x) staining for a-SMA and desmin. Quantitative analysis of immunohistochemical staining for a-SMA (B) and desmin. (C) The protein and mRNA levels of a-SMA were, respectively, analyzed by qPCR (D) and Western blotting (E). (F) In the CCI₄-induced liver fibrosis mice experiment, representative images of IHC (100x) staining for a-SMA and desmin in liver tissue from mice treated with the various treatments. Quantitative analysis of immunohistochemical staining for a-SMA (G) and desmin. (H) The protein and mRNA levels of a-SMA in mice liver tissue were, respectively, analyzed by qPCR (I) and Western blotting (J). (K) In the BDL-induced rat liver fibrosis experiment, representative images of IHC (100x) staining for a-SMA and desmin in liver tissue. Quantitative analysis of immunohistochemical staining for a-SMA (L)and desmin (M). The protein and mRNA expression of a-SMA was, respectively, analyzed by qPCR (N) and Western blotting (O). **p < 0.001, ***p < 0.001 vs the control group or sham group, **p < 0.05, **p < 0.01 vs the CCI₄ group or BDL group. Oil: control group.

results demonstrated that JY5 formula had significant antihepatic fibrosis effects. IHC staining showed that compared with the control group, Col-I expression was visible in the fibrotic septum in the CCl₄ group. By contrast, JY5 and SORA significantly reduced Col-I expression in the liver tissue (**Figure 2C**, lower panel and **Figure 2G**). In addition, qPCR results showed that *Col-I* mRNA expression was significantly more elevated in the CCl₄ group than in the control group. However, compared to the CCl₄ group, *Col-I* mRNA expression was significantly reduced in the JY5-treated group (**Figure 2F**). Consistent with the CCl₄-induced rat liver fibrosis model, JY5 (salvianolic acid B, 22.4 mg/kg amygdalin, 0.7 mg/kg schisantherin A, 2.8 mg/kg) significantly alleviated hepatic injury and collagen deposition in CCl₄-induced liver fibrosis in mice (**Figure 3**).

JY5 Significantly Alleviates Hepatic Injury and Collagen Deposition in Bile Duct Ligation-Induced Rat Liver Fibrosis

Compared with the sham group, the levels of ALT, AST, TBil, DBil, TBA, and ALP were significantly increased in the BDL group. After JY5 (salvianolic acid B, 16 mg/kg amygdalin,

0.5 mg/kg schisantherin A, 2 mg/kg) or DAPT (30 mg/kg) treatment, the levels of ALT, AST, TBil, DBil, TBA, and ALP were significantly decreased (**Figures 4A–F**). Consistent with CCl₄-induced liver fibrosis, JY5 reduced hepatic Hyp content and collagen deposition, and downregulated the expression of Col-I and Col-IV in BDL-induced rat liver fibrosis (**Figures 4G–K**). These results suggest that JY5 significantly alleviates hepatic injury and collagen deposition in BDL-induced liver fibrosis.

JY5 Significantly Represses the Activation of Hepatic Stellate Cells *In Vivo*

In both the CCl₄-induced rat and mouse liver fibrosis experiments, IHC staining showed that high *a*-SMA and desmin was expressed in the fibrotic septum in the CCl₄ group. By contrast, both *a*-SMA⁽⁺⁾ cells and desmin⁽⁺⁾ cells were decreased in the JY5- and SORA-treated group (**Figures 5A-C,F-H**). Western blot analysis and qPCR showed that *a*-SMA expression was significantly elevated compared to the control group. However, compared to the CCl₄ group, both *a*-SMA mRNA and protein expression was significantly reduced in the JY5- and SORA-treated groups (**Figures**

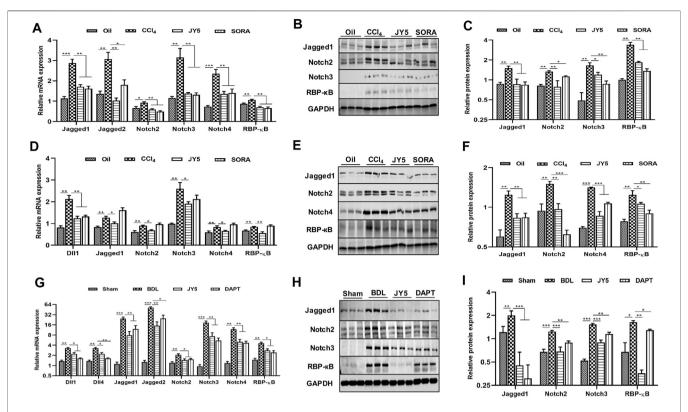


FIGURE 6 J Y5 may ameliorate liver fibrosis by inhibiting the Notch signaling pathway *in vivo*. (A) In the CCl₄-induced rat liver fibrosis experiment, the mRNA levels of Jagged1, Jagged2, Notch2, Notch3, Notch4 and RBP- κB were measured by qPCR. Western blotting (B) and quantitative analysis (C) of Jagged1,

5D,E,I,J). Similarly, in the BDL-induced liver fibrosis experiment, the treatment effect of JY5 was consistent with the results in the CCl_4 -induced liver fibrosis experiments (**Figures 5K–O**). These results demonstrate that JY5 significantly represses the activation of HSCs in CCl_4 -and BDL-induced liver fibrosis.

JY5 Significantly Inhibits Activation of the Notch Signaling Pathway *In Vivo*

In the CCl_4 -induced liver fibrosis rat experiment, qPCR showed that the mRNA expressions of *Jagged1*, *Jagged2*, *Notch2*, *Notch3*, *Notch4* and *recombination signal binding protein-\kappa B* (*RBP-\kappa B*) were significantly more upregulated in the CCl_4 group than those in the control group. However, compared to the CCl_4 group, the mRNA expressions of *Jagged1*, *Jagged2*, *Notch2*, *Notch3*, *Notch4*, and *RBP-\kappa B* were significantly reduced in the JY5- and SORA-treated groups (**Figure 6A**). Western blotting showed that the protein expression of Jagged1, Notch2, Notch3 and RBP- κB was significantly increased in the CCl_4 group, compared to the control group. Above these proteins expression was significantly more reduced in the JY5- and SORA-treated groups than in the CCl_4

group (**Figures 6B,C**). While in CCl₄-induced liver fibrosis mice experiment, JY5 not only decreased the mRNA expressions of *Jagged1*, *Notch2*, *Notch3*, *Notch4* and *RBP-κB*, but also downregulated the expression of *Dll1* (**Figure 6D**). Western blotting showed that the proteins expression of Jagged1, Notch2, Notch4 and RBP-κB was significantly more reduced in the JY5- and SORA-treated groups than in the CCl₄ group (**Figures 6E,F**). Consistent with the CCl₄-induced rat liver fibrosis model, JY5 decreased the expressions of *Jagged1*, *Notch2*, *Notch3*, *Notch4* and *RBP-κB* in the BDL-induced liver fibrosis model. In addition, the mRNA expressions of *Dll1*, *Dll4* and *Jagged two* were significantly decreased after treatment with JY5 (**Figures 6G-I**). These results suggest that JY5 can significantly inhibit the activation of Notch signaling pathway in CCl₄-and BDL-induced liver fibrosis.

JY5 may Inhibit the Activation of LX-2 Cells Induced by TGF-β1 by Regulating the Notch Signaling Pathway

LX-2 cells were activated by TGF-β1 to observe the effect of JY5 at various concentrations *in vitro*. Immunofluorescence showed

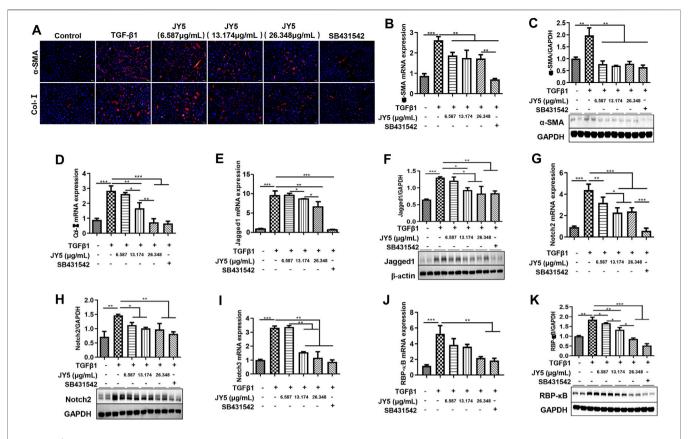


FIGURE 7 | JY5 inhibits the activation of LX-2 cells induced by TGF-β1 by repressing the Notch signaling pathway. (A) Representative images of Immunofluorescence staining (100x) for *a*-SMA and CoI-I. The mRNA expressions of *α*-SMA (B), CoI-I (D), Jagged1 (E), Notch2 (G), Notch3 (I) and RBP- κ B (J) were measured by qPCR. Western blotting and quantitative analysis of *a*-SMA (C), Jagged1 (F), Notch2 (H) and RBP- κ B (K) protein in cell lysate. *p < 0.05, **p < 0.01, and ***p < 0.001.

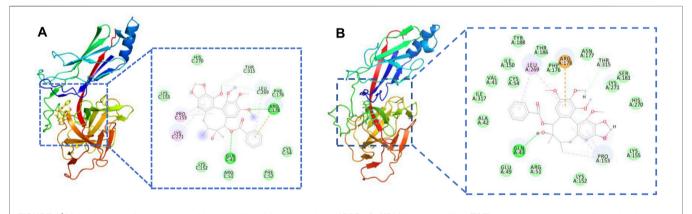


FIGURE 8 | Molecular interactions between schisantherin A and the key residues of RBP-κB. (A) Molecular docking. (B) The molecular interactions after molecular dynamics simulations.

that both a-SMA⁽⁺⁾ cells and Col-I⁽⁺⁾ cells were significantly elevated in TGF- β 1-treated cells compared to the control cells. However, these positive cells were significantly reduced after treatment with various concentrations of JY5 and SB431542 (**Figure 7A**). qPCR showed that the mRNA levels of α -SMA, Col-I, Jagged1, Notch2, Notch3 and RBP- κ B were significantly

elevated in TGF-β1-treated cells compared to the control cells. However, above these genes mRNA expression were significantly reduced after treatment with various concentrations of JY5. *Col-I, Jagged1, Notch2* and *Notch3* mRNA expressions were significantly decreased in the high-dose JY5 group, compared to the low-dose JY5 group (**Figures 7B,D,E,G,I,J**). Western blot

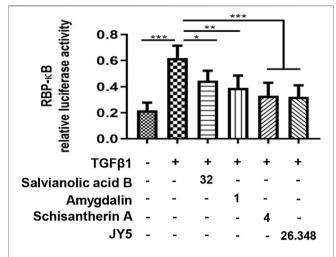


FIGURE 9 | RBP-κB luciferase reporter activity. RBP-κB luciferase reporter activity in LX-2 cells after 24 h treatment with salvianolic acid B (32 μM), amygdalin (1 μM), schisantherin A (4 μM) or JY5 (26.348 μg/ml). *p < 0.05, *p < 0.01, **p < 0.001.

analysis showed that the protein expressions of a-SMA, Jaggeed1, Nothc2 and RBP- κ B were significantly increased after treatment with TGF- β 1. Compared with the TGF- β 1 group, above these proteins expression were significantly reduced in the JY5-treated groups. Of these, the protein expression of Jagged1 and RBP- κ B was significantly reduced in the high-dose JY5 group, compared to the low-dose JY5 groups (**Figures 7C,F,H,K**). These results suggest that JY5 may inhibit the activation of LX-2 cells induced by TGF- β 1 by regulating the Notch signaling pathway.

Molecular Docking and molecular Dynamics Simulations

To investigate the binding mechanism of JY5 towards Jagged1, Notch2 and RBP-κB, molecular docking and molecular dynamics simulations was conducted. The lowest binding energy docking module was schisantherin A interacted with RBP-KB (Supplementary Table S4), and intermolecular interactions have shown schisantherin A has formed hydrogen bond with residues Gln43 and Arg178 of RBP-kB respectively (Figure 8A), and the results of molecular dynamics simulations also shown that schisantherin A has formed hydrogen bond with residues Gln43 (Supplementary Figure S5, Figure 8B), which suggested that RBP-kB may be the specific target by which JY5 regulated the Notch pathway.

We proceeded to test whether JY5-mediated RBP- κ B was accompanied by transcriptional activation of RBP- κ B using luciferase reporter assay. Exposure of LX-2 cells to TGF- β 1 for 24 h resulted in a statistically significant increase in RBP- κ B luciferase reporter activity (**Figure 9**), however, after simultaneously treated with salvianolic acid B, amygdalin, schisantherin A or JY5 for 24 h (**Figure 9**), the RBP- κ B luciferase reporter activity was reduced, which further suggested that RBP- κ B may be the target by which JY5 regulated the Notch pathway.

DISCUSSION

Liver fibrosis is an abnormal repair response to tissue damage, characterized by excessive deposition of ECM, leading to the persistence and development of pathological scar. Hepatic fibrosis is common in most chronic liver diseases process, which is a clinically important problem. To develop effective anti-hepatic fibrotic drugs, researchers have conducted a large number of basic and clinical studies. Despite achieving certain results in recent years, most of these drugs are in the preclinical or clinical trials stage, and some have failed clinical trials due to severe toxic side effects (Yoon et al., 2016). TCM has marked clinical effects on the treatment of liver fibrosis, which are closely correlated with its characteristics of multi-ingredients compatibility and multi-targets. However, the components of TCM are complex, and their mechanisms are not very clear, which somewhat increases the complexity of TCM studies. Regarding the intensive development of multidisciplinary crossover study, active ingredients screening, extraction, and purification from Chinese herbs provide a new approach for TCM formula research.

Salvianolic acid B is the main water-soluble phenolic acid compound. Numerous studies (Yan et al., 2010; Wang et al., 2012; Tao et al., 2013; Yan et al., 2017) have indicated that salvianolic acid B exerts significant anti-hepatic fibrosis effects through the following mechanisms: inhibiting the activation of HSCs by downregulating the TGF-β1/SMAD signaling pathway, protecting hepatocytes from apoptosis via inhibiting death receptor pathway, and stabilizing the mitochondrial membrane and regulating NF-κΒ/ΙκΒα signaling pathway. Amygdalin is the major ingredient of peach kernel. Amygdalin can inhibit the activation of HSCs by downregulating the TGF-β/CTGF signaling pathway and induce activated HSC apoptosis by upregulating Bax gene expression, subsequently exerting antihepatic fibrotic effects (Luo et al., 2016; Luo et al., 2018). Lignans are the main bioactive components of Schisandrae. Studies have shown that these lignans can suppress inflammation, protect hepatocytes, and inhibit the activation of HSCs by downregulating the TGFB/SMAD and MAPK signaling pathways (He et al., 2020).

In this study, we measured the content of various compounds in FZHY extract, plasma, and liver in rats after intragastric administration of FZHY. We obtained the three main bioactive ingredients of FZHY: salvianolic acid B, which had the highest content in FZHY extract; schisantherin A, which had maximum exposure in plasma; and amygdalin, which had highest hepatic exposure in the liver. Then we conducted uniform design and validation experiments to explore their composition and determine the best ratio for treating the rat hepatic fibrosis model. We obtained a new formula, namely JY5, which had anti-fibrotic effects comparable to that of FZHY. Further studies have shown that JY5 can significantly decrease serum ALT and AST levels and inhibit inflammation reaction while reducing collagen deposition in CCl₄-or BDL-induced liver fibrosis models.

The activation of HSCs is a pivotal event in liver fibrosis. Under persistent stimulation from CCl₄ and BDL, HSCs are

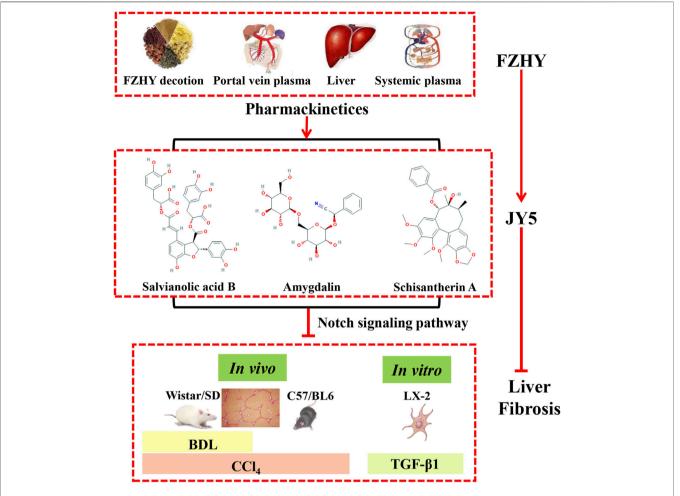


FIGURE 10 | A brief diagram of this study was shown. JY5 formula, which consists of the main active ingredients of FZHY, could exert anti-hepatic fibrotic effect through regulating Notch signaling pathway and inhibiting the activation of HSCs.

largely activated and transformed into myofibroblasts, which cause excessive ECM accumulated in the liver, eventually leading to hepatic fibrosis formation. Activated HSCs, as one of the main sources of hepatic ECM, can secrete Col-I and Col-III proteins. a-SMA is a specific marker of activated HSCs. This study found that JY5 significantly reduced the mRNA and protein expression of a-SMA, and decreased Col-I mRNA expression in CCl_4 -and BDL-induced liver fibrosis in rats and mice. The results were further confirmed in TGF- β 1-induced LX-2 cell activation. JY5 significantly downregulated the expressions of a-SMA and Col-I in activated LX-2 cells induced by TGF- β 1. These results suggest that JY5 significantly inhibits the activation of HSCs.

Notch signaling is a highly conserved pathway evolutionarily, which influences intercellular signal transduction and cell fate decisions, and regulates the growth and development homeostasis of multiple tissues and organs, and in particular, the progression and development of diseases (Siebel and Lendahl, 2017). The Notch signaling pathway mainly consists of four Notch receptors (Notch1, Notch2,

Notch3, Notch4), five Notch ligands (Jagged1, Jagged2, Dll1, Dll3, Dll4), and the transcriptional regulatory elements of downstream signals (D'Souza et al., 2010). Previous studies (Ni et al., 2018) have shown that Notch plays an important role in the progress and development of hepatic fibrosis, which can interact with other signaling pathways such as TGF-β, Hedgehog, and Hippo. TGF-β1 can promote the proliferation and activation of HSC-T25 cells by regulating the Notch signaling pathway (Aimaiti et al., 2019). The Jagged1 gene was successfully knocked down by using rAAV1-Jagged1shRNA in CCl₄-induced liver fibrosis, resulting in alleviation of liver fibrosis (Tang et al., 2017). In addition, knockout of the RBP-κB gene, which is considered a key transcription factor in the Notch pathway, can inhibit the proliferation and activation of HSCs to alleviate CCl4-induced liver fibrosis in mice (He et al., 2015). Blockade of the Notch pathway can effectively inhibit the activation of HSCs, which in turn attenuates liver fibrosis. In this study, the expressions of Jagged1, Jagged2, Notch2, Notch3, Notch4, and RBP-κB were significantly increased in CCl₄-and BDL-induced liver fibrosis in rats and

mice. While after intervention with JY5, the expressions of these Notch-related genes and proteins were significantly decreased. This was further confirmed by LX-2 cell activation induced by TGF- β 1 experiments *in vitro*. These results suggest that JY5 might exert anti-fibrotic effects by regulating the Notch signaling pathway to inhibit the activation of HSCs.

In this study, we used SORA and DAPT as positive controls. SORA, as a multi-receptor tyrosine kinase inhibitor that can inhibit the proliferation of multiple tumor cells and promote cell apoptosis, is commonly used for the treatment of hepatocellular carcinoma clinically (Keating, 2017). DAPT, as a y-secretase inhibitor, can block the release of the Notch intracellular domain, thereby inhibiting activation of the Notch signaling pathway (Ni et al., 2018). In accordance with previous studies (Deng et al., 2013; Zhang et al., 2016), our results show that both SORA and DAPT have significant anti-hepatic fibrosis effects. Interestingly, SORA also can significantly downregulate the mRNA expressions of Jagged1, Jagged2, Notch2, Notch3, Notch4 and RBP-κB, and the protein expression of RBP-κB. We speculate that SORA exerts anti-hepatic fibrosis effects, which might be related to the regulation of the Notch pathway; however, the precise mechanism needs to be further investigated. In addition, DAPT inhibits liver fibrosis by blocking the Notch pathway (Chen et al., 2012). This conclusion was further confirmed in our study. However, it is important to note that γ -secretase inhibitors, as a nonspecific Notch blocker, have shown severe side effects in clinical trials (Ni et al., 2018). So the clinical application of DAPT may be limited. Compared with SORA and DAPT, JY5 may have synergistic anti-fibrosis effects via multiple pathways, not specifically blocking a particular target or pathway, which confers relatively higher safety and more effectiveness.

The results of molecular docking, molecular dynamics simulations and RBP-κB luciferase reporter assay suggested that RBP-κB may be the specific target by which JY5 regulated the Notch pathway. In addition, given that JY5, as a component of TCM compounds, has shown good efficacy in two different liver fibrosis models, we speculate that JY5 might alleviate hepatic fibrosis through other mechanisms. In response to these issues, a series of related studies to elaborate upon the compatibility mechanisms of anti-liver fibrosis effect of JY5 will be conducted. These studies will provide an adequate scientific basis for clinical research and application of JY5 formula.

CONCLUSION

In summary, we obtained a novel anti-hepatic fibrosis component of TCM compounds, namely, JY5, through uniform design and validation experiments *in vivo*, and explored its part of

mechanisms for the first time. Our study showed that JY5 may exert anti-hepatic fibrotic effects by regulating the Notch signaling pathway to inhibit the activation of HSCs (**Figure 10**). Thus, the JY5 formula may be a potential novel therapeutic candidate for liver fibrosis.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusion of this article will be made available by the authors, without undue reservation.

ETHICS STATEMENT

The animal study was reviewed and approved by The Experimental Animal Ethics Committee of School of Pharmacy, Fudan University, and the Institutional Animal Care and Use Committee (IACUC) at Shanghai Research Center of the Southern Model Organisms.

AUTHOR CONTRIBUTIONS

YF, ZX, XT, CH, JC and PL wrote the manuscript and were involved with project concept and submission; YF, ZX and XT completed the main part of the experiment; WL, XZ, YH, TY and JF participated in the pharmacokinetic experiment; XZ, SG and YM participated in the *in vivo* experiment; DZ, HZ and YH participated in the *in vitro* experiment; CH, JC and PL revised the manuscript and were responsible for final approval. All authors read and approved the final manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.671152/full#supplementary-material

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Standardization of *Berberis aristata*DC and *Nigella sativa* L. Using HPTLC and GCMS and Their Antineoplasia Activity in 7,12-Dimethylbenz[a] anthracene-Induced Mouse Models

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Mazhar M and Agrawal SS (2021) Standardization of Berberis aristata DC and Nigella sativa L. Using HPTLC and GCMS and Their Antineoplasia Activity in 7,12-Dimethylbenz[a]anthracene-Induced Mouse Models. Front. Pharmacol. 12:642067. doi: 10.3389/fphar.2021.642067 Berberis aristata DC and Nigella sativa L. are officially listed in various Indian Pharmacopoeia and AYUSH official documents. Prescribed for different ailments for proven medicinal activities, they thus became part of polyherbal medications. With reverse pharmacology and scientific validation, more than 30 patents are filed on different formulations of B. aristata and granted. Nigella sativa L. has been broadly studied for its therapeutic potential and wide range of activities against cardiovascular, diabetic, cancer, and life style disorders. Thus, this study is aimed at standardizing B. aristata and N. sativa and their antineoplasia activity in 7, 12-dimethylbenz[a]anthracene (DMBA)-induced mouse models. Molecular docking was done using the Schrodinger program Maestro 9.0. Herbal extracts and essential oil (B. aristata and N. sativa) were standardized and quantified using high-performance thin-layer chromatography (HPTLC) (CAMAG) and gas chromatography-mass spectrometry (GCMS) (Agilent 2010GC System) with validated methods. DMBA was administered orally once a week (1mg/ 200 µL) to each animal except the normal control. Hematology, histopathology, and immunoassays were performed, and data were analyzed and depicted with GraphPad and SPSS. In molecular docking, thymoquinone showed the highest docking score (9.519, 9.211, and 9.042, respectively) in the active site pockets of IL6 (PDB ID: 4CNI and 5FCU), TNF (PDB ID: 2AZ5), and VEGF (PDB ID: 4KZN). Out of all four target sites, thymoguinone and berberine showed good binding affinity with IL6 (PDB ID: 4CNI) compared to α- and β-pinenes. HPTLC analysis of the hydroalcoholic extract showed the presence of berberine both qualitatively and quantitatively (5.4% berberine), and thymoquinone detected 0.17% in the N. sativa extract. GCMS for essential oil showed 26 compounds including ±pinene. Leukocytes and erythrocytes of N. sativa and B. aristata were analyzed, and significant improvements were recorded (P < 0.05) and graphically presented. Mean survival time was calculated by the Kaplan Meier method (119 days). Immunoassay analyses were conducted, namely, TNF-α and VEGF, and interpreted and marked.

Keywords: antineoplasia, GCMS, HPTLC, molecular docking, phytopharmaceuticals

INTRODUCTION

Certain chemotherapeutic agents have been aborted for use in the treatment of malignancy because of their toxicity. Over these years, there has been an increase in medical research in a broad range of therapeutics, many of which use plant-derived lead compounds (Vincristine and Paclitaxel) and are under extensive research for cancer cure. When the world is moving toward organic products, certain plants are thought to have enormous potential of cure against incurable diseases like cancer and COVID 19, and thereby, these create a pool of natural chemicals that may provide a therapeutic effect against cancer and other malignancies. Herbal medicines are in practice and considered the second method to treat cancer in developing nations (Kennedy, 2005; Ezeome and Anarado, 2007). B. aristata DC (family: Berberidaceae) is the main constituent of rasaut, darvyadi (kvatha, leha, taila), rasanjana, and Dashanga lepa. Aromoline, oxyberberine, oxyacanthine, berbamine, berberine chloride, 1-O-methylpakistanine, and pseudopalmatine chloride are the main chemical constituents of B. aristata (Pasrija et al., 2010). Antidiarrheal activity, cardiotonic hepatoprotective activity, antidiabetic activity, and anticancer activity are reported. Being potential therapeutic agents, more than 30 patents are filed on the different formulations granted and marketed (4, 5). Nigella sativa L. (Ranunculaceae) has been researched for its pharmacological potential and shown to possess a wide spectrum of activities, namely, diuretic, cardioprotective, antihyperglycemic, antineoplastic, analgesic, antimicrobial, antiinflammatory, spasmolytic, hepatoprotective, nephroprotective, and antioxidant properties (6). Most of the therapeutic properties of this plant are due to the presence of thymoquinone (TQ), which is a major active chemical component of the essential oil. α-Pinene and β-pinene are other biomarkers that possess biological activity (6). In silico methods have been designed, developed, and applied to pharmacology hypothesis development and testing using software, for example, FoldX. In silico methods are primarily used alongside the generation of in vitro data and their correlation, with both to create the model and to test it. Such models have seen frequent use in the drug discovery and optimization of novel molecules with affinity to a target, the clarification of pharmacokinetics and pharmacodynamics, and physicochemical characterization. With this background, we aimed at standardizing B. aristata (bark) and N. sativa L. high-performance (black seed) using chromatography (HPTLC) and gas chromatography-mass spectrometry (GCMS) and their antineoplasia activity in 7,12dimethylbenz[a]anthracene (DMBA)-induced mouse models.

MATERIALS AND METHODOLOGY

Molecular Docking

Docking studies were performed to study the molecular binding energy and patterns of some natural derivatives with the active site pockets of crystal structures of IL6 (PDB ID: 4CNI and 5FCU), IL10 (PDB ID: 1WQ8), TNF (PDB ID: 2AZ5), and VEGF (PDB ID: 4KZN) using the Schrodinger program Maestro 9.0.

TABLE 1 | Docking and gliding with their respective PDB codes.

PDB	Compound	Docking score	Glide score	
TNF-2AZ5	Thymoquinone	4.468	4.468	
	Berberine	4.426	4.426	
	α-Pinene	4.150	4.150	
	β-Pinene	4.173	4.173	
VEGF-4KZN	Thymoquinone	4.525	4.525	
	Berberine	2.948	2.948	
	α-Pinene	2.963	2.963	
	β-Pinene	3.978	3.978	

The binding energies and their respective docking scores of all synthesized molecules are summarized in a tabular form and represented in **Table 1**.

Collection and Authentication

B. aristata (bark) and *N. sativa* (seeds) were collected from Delhi, and both were authenticated by NISCAIR (Reference No. NISCAIR/RHMD/Consult/2018/3136-85-1/2).

Chemicals and Materials

Berberine chloride was procured from Prolab Marketing Pvt. Ltd. (India), and thymoquinone and α - and β -pinene were procured from TCI Chemicals (India).

All the described chemicals and reagents used in the present study were HPLC-grade-certified.

Extraction

1) B. aristata Bark: The bark (2 kg) was air-dried, crushed to smaller pieces, re-dried, and coarsely powdered and was then exhaustively extracted with water:alcohol (95%, methanol) (1:1) in Soxhlet's apparatus for 72 h. The extract was dried using an Allied lyophilizer with a co-solvent system (the temperature at -80°C and the pressure at 760 Pa), and a dark-brown mass (2.5%) was obtained. 2) Nigella sativa L.: Continuous hot solvent extraction was performed with Soxhlet's apparatus for 6 h at 40°C using a coarse powdered crude drug to hydroalcoholic methanol ratio of 1:10 gmL⁻¹ (Alhaj et al., 2008), and the percentage yield obtained was 5.16%. 3) Essential oil extraction: In a Clevenger apparatus, each plant material was separately soaked in distilled water (1 L) at 90°C for 6 h (Nair et al., 2018). Using hydrodistillation, the volatile components were collected by the addition of equal volumes of n-hexane, dried over anhydrous sodium sulfate, stored in an amber-colored bottle (-20°C) with a label. The extract yield was calculated as 0.50 to 0.60% with repetitions.

Preparation of Standard Solutions

The berberine Cl working standard was accurately weighed and transferred to $10\ mg/10\ ml$ and dissolved in methanol to obtain a solution concentration of $1\ mcg/\mu L$ (for HPTLC), and in the same way, three sets of controls for berberine were prepared from a separate stock so as to lie in the lowest, middle, and highest regions of the calibration curves. Similarly, $1\ ppm$ thymoquinone standard solution was prepared for the calibration curve.

TABLE 2 Absorbance versus concentrations of α -tocopherol, *B. aristata*, and *N. sativa*.

Conc. (µg/ml)	% Inhibition of tocopherol	% Inhibition of <i>B. aristata</i>	% Inhibition of <i>N.</i> sativa
100	00	00	
100	38	29	34
80	32	21	30
60	28	17	25
40	21	13	21.9
20	18.8	4	17.7
Mean	22.6	11.33333	25.72
SD	±7.13	±8.84	±6.44
Pearson correlation	0.991*	0.988*	0.988*
Sig. (two-tailed)	0 0.001	0.002	0.000
N	5	5	5

*Correlation is significant at the 0.01 level (two-tailed).

DPPH Assay

The 2,2-diphenyl-1-picryl-hydrazyl-hydrate (DPPH) assay was performed as per Brand-Williams et al. (1995). The reagent is prepared by dissolving DPPH (11.82 mg) in 500 ml of ethanol to meet 6×10^{-5} mol/L solution. α -Tocopherol acetate is treated as a standard antioxidant (1000 µg/ml with ethanol). The stock solution is further diluted to make concentrations of 20, 40, 60, 80, and 100 µg/ml with methanol. Each herbal extract test solution is prepared by dissolving 1000 µg/ml with ethanol. Methanol was used as a blank solution and control. 0.2 ml of methanol is mixed with 7.8 ml of DPPH, as shown in **Table 2**.

In vitro Activity (MTT Assay)

1 mg/10 ml of anastrazole used as a positive control and different concentrations of anastrazole (1, 10,100, 200, and 500 µM) were used. DMSO at 0.04% was used as a solvent control, whereas a negative control (medium) and positive control (anastrazole) were used as treatments. The cell line was purchased from the National Center for Cell Sciences, Pune, with a seeding density of 2.0 × 104 cells/well stored in liquid nitrogen for further testing purposes. Before the 3-(4,5-dimethylthiazol-2-yl)-2,5diphenyltetrazolium bromide (MTT) assay, MCF-7 cells were thawed at $37 \pm 1^{\circ}$ C in a gaseous environment of $5 \pm 1\%$ carbon dioxide in a humid environment in tissue culture flasks containing the medium, Dulbecco's modified Eagle's medium (DMEM) (Genetix Biotech Asia) supplemented with 10% fetal bovine serum (Genetix Biotech Asia) and penicillin (100 units) and streptomycin (100 µg) antibiotics (Genetix Biotech Asia) to obtain the subconfluence of cells (70-90% confluent). Test solution concentrations are presented in **Table 3**.

Instrumentation: (I) High-Performance Thin-Layer Chromatography

CAMAG Automatic TLC Sampler 4 (New ATS4) is used for the identification using a D_2 lamp at a wavelength of 254 nm, with a PM high voltage (286 V). Methanol is used as the sample solvent type having a dosage speed of 150 nL/, an inert gas (N_2) is used as the spray gas, and Merck silica gel 60F 254 is used as the stationary phase. The bond length is kept at 8.0 mm with a syringe size of 25 μL in all tracks. n-Butanol:acetic acid:water

(3:1:1) (v/v/v/) and C_6H_{14} : CH3COOC2H5 (8:2) v/v are used as mobile phases in a twin trough chamber (20 \times 10 cm) for *B. aristata* and *N. sativa* L., respectively, and drying is done at room temperature. Scanning is performed at a speed of 20 mm/s with slit dimensions of 6.00 \times 0.45 mm.

2) GCMS analysis: Filtered through 0.25 μ M PTFE; then, a volume of 2 μ L was injected at a split ratio of 1:40 into an Agilent 2010 Gas Chromat System and a CTPAL autosampler with a silica column (30 m \times 0.25 mm, film thickness 0.25 μ m) and interfaced with an electron ion spray mass detector (m/z 40–650 at 1250 s/scan). The interface was set up at 290°C, and the ion source was adjusted to 220°C with the carrier gas (helium at 2 mLmin⁻¹). After a 2 min solvent setback time at 70°C, the oven temperature was increased to 5°C/min–280°C with a solvent cut time of 4.50 min. The pressure was kept at 69.0 kPa, and a total flow of 52.6 mLmin⁻¹, a column flow of 1.21 mLmin⁻¹, and a linear velocity of 39.9 cm s⁻¹ were maintained. The volatile constituents were identified by matching the retention index and fragmentation pattern data with those of the standards using WILEY and NIST(12).

Animal Study

Female Swiss albino mice from the institute animal house, 14-15 weeks old, weighing 24-28 g, were arranged into 10 groups (n= 6 animals per group), and DMBA was administered orally once a week (1 mg/200 µL olive oil) to each animal except the normal control up to 5 weeks and classified as Group I: normal control, Group II: disease control, vehicle-treated Group III: marketed standard Anastrazole, 1 mg/kg, Group IV: thymoquinone, 10 mg/kg, Group V: α-pinene, 0.50 ml/kg, Group VI: β-pinene, 200 mg/kg, Group VII: Nigella sativa L. extract, 200 mg, Group VIII: N. sativa oil, 50 μl, Group IX: berberine Cl, 30 mg, Group X B. aristata extract, 400 mg). The standard and validated conditions maintained were a temperature of 20 \pm 1 C and a relative humidity (RH) of $50 \pm 5\%$, and mice were fed a standard rodent diet and water ad libitum and sustained at a 12 h light/dark cycle. All experimental procedures were carried out in compliance with the Declaration of Helsinki and the protocol approved by the Ethical Committee of DIPSAR (IAEC/2016-I-Prot.No-17), India. The blood samples were collected using a Retro-orbital, stored in a preheparinized vacutainer, stored under standard conditions, and sent to the lab, and doses are calculated as per OECD guidelines, 2014.

TABLE 3 | Final stock concentration in the study for MTT Assay.

S. No.	Test name	Final stock in DMEM	Concentration in RPMI			
1	Thymoquinone	12.5 μg/ml	(2.5 ,5 ,7.5 ,10 ,12.5) µg/ml			
2	Berberine chloride	1 μM	1 μM(10 ,100 ,200 ,500) nm			
3	α-Pinene	100 μg/ml	(5, 10 ,20 ,30 ,40) μg/ml			
4	β-Pinene	25 μg/ml	Aruna and Sivaramakrishnan (1990); Banchrof et al. (1996); Bower et al. (2002); Organization (2007); Saied et al. (2007)			
5	Berberis aristata extract	500 μg/ml	(1, 10, 50, 300, 500) µg/ml			
3	Nigella sativa extract	250 µg/ml	(250, 200, 170, 110, 45) µg/ml			
4	Nigella sativa oil	1%	(0.60, 0.50, 0.40, 0.30, 0.20)%			

Tissue specimens from the mammary gland of female mice of each experimental groups were fixed in neutral buffered formalin 10% and processed by a conventional verified method, embedded in paraffin, sectioned at 4–5 μ m, and stained with dyes, namely, hematoxylin and eosin (10).

Immnuhistochemistry: The procedure immunohistochemical analysis was performed as described previously (Liu et al., 2009). Tumor tissues were sectioned at a thickness of 4 µm and incubated in methanol (0.3% H₂O₂) for 30 min and treated with 0.1% Triton X-100 for 10 min. The sections were washed with PBS three times and blocked with 1% bovine serum albumin and 0.01% Triton X-100 for 1 h at room temperature. The sections were incubated with the VEGF antibody (1:100) or TNF α (1:50) or the TGF β antibody overnight at 4°C. Negative controls were analyzed by staining with isotype-matched IgG or PBS. Following rinsing in PBS, the sections were incubated with anti-mouse biotinylated monoclonal secondary antibodies for 1 h at room temperature. The sections were washed three times with PBS and then incubated in avidin-biotin, and IHC slides were examined under a microscope (Olympus CX31; Olympus Corporation, Tokyo, Japan) and analyzed by Advance Histo lab.

RESULTS AND DISCUSSION

Molecular Docking

Docking studies were carried out to study the molecular binding pattern of natural derivatives with the active site pockets of crystal structures of IL6 (PDB ID: 4CNI and 5FCU), IL10 (PDB ID:

1WQ8), TNF (PDB ID: 2AZ5), and VEGF (PDB ID: 4KZN), and adaptable resolution (<2 A) and the docking score are the criteria. The binding energies and docking scores of all synthesized molecules are represented in Table 1. Docking of the compounds thymoquinone, berberine, α -pinene, and β -pinene into the active sites of enzymes revealed that several molecular interactions (hydrogen bonds, π-interactions, and hydrophobic interactions) were considered to be responsible for the observed affinity of the compound. Thymoquinone formed only one hydrogen bond between oxygen of the -C=O group of thymoquinone and amino acid PHE 33. Berberine formed one hydrogen bond between hydrogen of the dioxane ring of berberine and amino acid ASP 31, and another hydrogen bond is formed between hydrogen of the phenyl ring of berberine with SER 102 amino acid. α-Pinene and β-pinene showed no hydrogen bond; they only show bad contact with amino acids (Figures 1A,B,C,D) and showed the details of binding modes of the docked compounds thymoguinone, berberine, α-pinene, and β-pinene, thus exhibiting the antitumor properties in the targeted herbal drug extract.

Anti-oxidant Activity (DPPH Assay)

The antiradical activities of *B. aristata* and *N. sativa* and their radical forms are studied and results are presented in **Table 2**. DPPH has an absorption band at 515 nm which disappears upon reduction by an antiradical compound (Brand-Williams et al., 1995). Phytochemistry explained (Bors, 1996) that more phenolic groups were believed to produce more antioxidant activity. Many plant constituents scavenge free radicals. **Figure 2** explains the potential of the extract in determining the significant antioxidant activity from

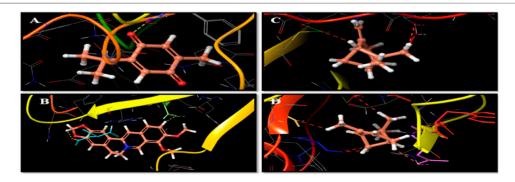
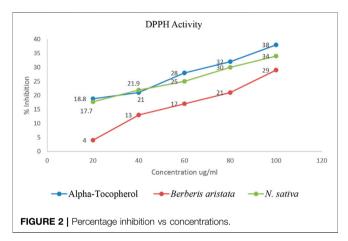


FIGURE 1 | (A) Thymoquinone and amino acid PHE 33 interactions. **(B)** Berberine, amino acid ASP 31, and hydrogen bond interactions. **(C)** β -Pinene interaction with amino acid cysteine. **(D)** α -Pinene interaction with amino aspartate.

TABLE 4 | Inhibitory concentration (IC $_{50}$) values of standards and test compounds.

S. No.	Name	IC ₅₀	
1	Anastrazole	412.28 nM (±47.74)	
2	Berberine Cl	686.49 nM (±161.46)	
3	Thymoquinone	7.5 µg/ml (±0.202)	
4	α-Pinene	6.72 µg/ml (±1.34)	
5	β-Pinene	11.08 µg/ml (±0.63)	
6	B. aristata extract	103.72 μg/ml (±54.17)	
7 Nigella sativa extract		107.89 mg/ml (±12.05	
8	Nigella sativa oil	0.33% (±0.026)	

Values are expressed in mean n = 3, SD (±).



natural sources. Demand for the natural antioxidants is shooting up nowadays as neutraceuticals, biopharmaceuticals, and food additives due to consumer preference. Dietary intake of antioxidant foods decreases the incidence of human diseases. Also, plant-based antioxidants are preferred against the synthetic ones because of their multiple mechanisms of actions and non-toxic nature. Our study used the bark of *B. aristata and N. sativa* that contains the berberine and thymoquinone active constituents, respectively, and other phytoconstituents including phenolic compounds.

MTT Assay

As per the objective of the study, MTT assay were performed to find out the inhibitory concentration of various standards and test samples (B. aristata and N. sativa Extracts). The results are presented into graphical data **Figure 3** and respective IC₅₀ values expressed in **Table 4** (sample n = 3 and standard deviation).

CHROMATOGRAPHY

B. aristata Characterization

Optimization of the HPTLC solvent system for quantitative analysis was done using a combination of solvent systems of varying polarity, and the most suitable solvent system was found to be n butanol:acetic acid:water (3:1:1) v/v/v. Quantitative analysis for berberine was performed through HPTLC techniques, and the result showed that the content of berberine in *B. aristata* was found to be 53.5 μ g in 1 mg through HPTLC techniques compared to standard

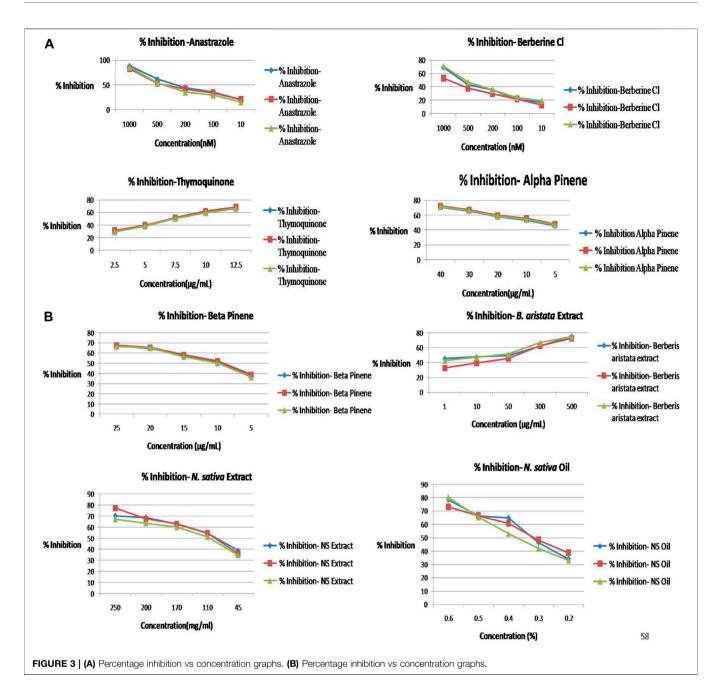
berberine Cl. The respective HPTLC chromatograms of bark extracts are presented in **Figures 4A,B**. In the present analysis, the calibration curve of standard berberine was found to be linear (y= $-4.097 \times 10^{-13} \text{ s}^2 + 7.5666 \times 10^{-7} \text{x} + 5.943 \times 10^{-2}$, R = 99.99), which is presented in **Figure 4C**. The interpretation of results suggests that the sample contained a considerable amount of berberine of 53.5 µg in 1 mg of the solution, which is approximately 5.4%.

Nigella sativa L. Characterization

 C_6H_{14} : $CH_3COOC_2H_5$ (8:2)v/v used as a mobile phase for quantitative and qualitative analysis of thymoquinone in the *Nigella sativa* L. extract done using HPTLC methods, and the result showed that the presence of thymoquinone in *Nigella sativa* was found to be 17.3 mg per 10 g compared to the pure compound thymoquinone. The respective HPTLC chromatograms of thymoquinone and the herbal extract are shown in **Figures 4E-F**. During the present study, the calibration curve of standard thymoquinone was found to be linear (y = $-3.761 \times 10^{-16} \text{ s}^2 + 6.272 \times 10^{-9} \text{x} + 8.375 \times 10^{-3}$, R= 99.98%), which is presented in **Figure 4G**. Graphical data of standard thymoquinone and the *N. sativa* extract are presented in **Figure 4H**. The percentage of thymoquinone detected was 0.17% w/w.

Results revealed the presence of several constituents in the extracts as evidenced with the chromatogram of the methanolic extract of *B. aristata* and *Nigella sativa*, which showed 10 peaks at different Rf values and the peak area at 366 nm in n butanol:acetic acid:water (3:1:1) v/v/v and n hexane: ethyl acetate (Ezeome and Anarado, 2007; Alhaj et al., 2008) v/v solvent systems, whereas peaks were present in the HPTLC fingerprinting chromatogram at 254 nm of both extracts. The number of constituents (No. of peaks-11) in the extract and their retention factors (Rf) and chromatographic profiles are shown in **Figures 4A–D**. The chromatogram of 26 compounds was obtained by GCMS analysis of NS (**Table 5**).

The major compounds that could be identified were linoleic acid (66.2%), β-pinene (13.66%), hexadecanoic acid (5.69%), thymoguinone (0.76%), and α -pinene (0.25%). Until 2018, 39 clinical trials are recorded to berberine, and some of them are in phases II and III. The thymoquinone molecule has registered with 17 clinical trials, and nine have been completed with promising results; however, two new clinical trials were recruited until 2019. Toxicological and reference standards both together may evolve the new paradigm in treating the illness with herbal drugs. With the advancement of technology, it is evident that the herbal industry needs to follow strict guidelines, and such regulations are necessary for quality control and assurance to bring potential evidenced research on phytopharmaceuticals. Herbal drug regulations and their harmonization in Asia, Europe, and the United States may stimulate and strengthen phytopharmaceuticals by using the modern analytical techniques for standardization of marker compounds (Choudhary and Sekhon, 2011). As per WHO guidelines, 2007, quality of the herbal product needs to be standardized with respect to safety before releasing it into the market (15).



Mean Survival Time

A reliable criterion for judging the value of any anticancer drug is prolongation of the life span. Anastrazole showed the highest increase in life span of tumor-bearing animals and significantly increased the mean survival time (MST) to 112 days. Neither the BA extract nor the NS extract was not as effective as anastrazole and increased the MST to only 107 and 108 days; however, their marker compounds thymoquinone and berberine showed potential increment in MST. The higher rate of reduction in tumor volume indicated that *B. aristata* and *N. sativa* played a direct role in killing tumor cells and enhanced the curative effect of tumor chemotherapy. A decrease in tumor volume mentioned

above reduced the tumor burden and might have enhanced the life span of the tumor-bearing mice (Figure 5) and increased the MST (16).

Hematology

The elevated white blood cell (WBC) count in tumor-bearing mice was significantly reduced by anastrazole, thymoquinone, and berberine and relatively less reduced by the *B. aristata* and *N. sativa* extract treatments, which were significant (p < 0.05) and potentially reversed the tumor-induced rise in total counts of WBC (**Figure 6B**). However, the extracts were not as efficacious as anastrazole in reversing the tumor-induced total counts.

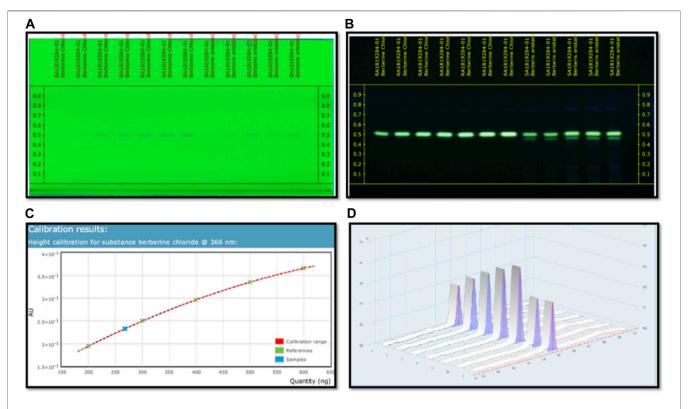


FIGURE 4 | (A) HPTLC fingerprinting chromatogram of *Berberis aristata* at 254 nm. (B) HPTLC fingerprinting chromatogram of *Berberis aristata* at 366 nm. (C) Standard curve of thymoquinone using the polynomial regression mode. (D) Area under the curve in 3D of thymoquinone. (E) HPTLC fingerprinting chromatogram of *Nigella sativa* at 254 nm. (F) HPTLC fingerprinting chromatogram of *Nigella sativa* at 366 nm. (G) Standard curve of thymoquinone using the polynomial regression mode. (H) Area under the curve in 3D of thymoquinone.

The anastrazole, thymoquinone, and berberine treatments inhibit tumor cell growth, enhance the survival of treated mice, and restore the hematological parameters. Thus, the present study suggested that B. aristata and N. sativa possess potent antitumor activity and increase the life span of the treated animal. However B. aristata (400 mg/kg) shows more significant antitumor activity among all test extract groups in the animal study. Usually, in cancer chemotherapy, the major problems that are being encountered are myelosuppression and anemia, but the results have clearly shown that BS and NS treatments have brought back not only the hemoglobin content to normal but also the red blood cell (RBC) count to normal (Figure 6C). Anastrazole as well as the extracts reversed these changes significantly (p < 0.05). However, the extracts were less efficacious than anastrazole in their effects, but their respective marker compounds showed relatively good effects on the RBC count (p < 0.05). Tumor development in the animals caused significant anemia (a decrease in hemoglobin content), while anastrazole treatment reversed this significantly (p < 0.05). The treatments with α -pinene, β -pinene, and the N. sativa extract failed to correct the anemia (Figures 6A,C), but thymoquinone, berberine, and the B. aristata extract were found to be significant (p < 0.05). Analysis of the hematological parameters showed a minimum toxic effect

in the mice, which were treated with both extracts (Figures 6A-C).

HISTOLOGY AND IMMUNOHISTOCHEMISTRY

A variety of herbal extracts were practiced for treating a number of diseases affecting the human body. Therefore, the objective of the current study was to evaluate the efficacy of N. sativa and B. aristata extracts on suppressing the several underlying tumor pathologies. For in vivo experiments, the DMBA mouse model was used to evaluate the protective effects of the lead herbal extracts (Russo et al., 2000). Active proliferation of the terminal ducts in the breast tissue for the mouse becomes very susceptible to carcinogens and tumor development (Ariazi et al., 2005). The histopathological examination of the current study revealed that DMBA-treated mice supplemented with TQ, the berberine NS extract, NS oil, and BA extracts showed suppression in the progress of the tumor cell proliferation (Figures 7D,G,H,J). In agreement with our findings (19), there was a limitation in the neoplastic changes during the sequential steps of carcinogenesis in DMBA-treated male Syrian hamsters supplemented with N. sativa. Another study found that the anticarcinogenic efficiency of N. sativa

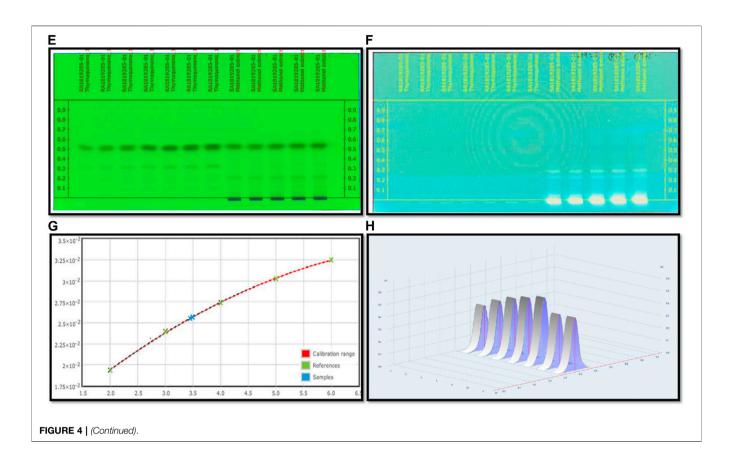
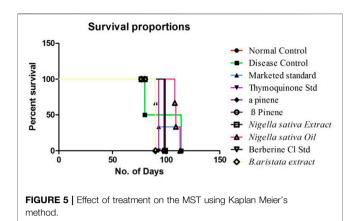


TABLE 5 | Composition of *N. sativa* oil: integration peak, R time, area, and % area.

Peak	R. Time	Area	Area%	Name	CAS No. (FFNSC 2 Lib)
1	6.532	3,008,277	0.36	Thujene α	2867-05-2 (FFNSC 2 Lib)
2	6.813	75,532,375	8.93	Bicyclo[3.1.1]hept-2-ene, 2,6,6-trimethyl-80-56-8 (FFNSC 2 Lib)	
3	7.308	1,063,045	0.13	Camphene α	79-92-5 (FFNSC 2 Lib)
4	8.414	115,567,825	13.66	Pinene oxide β	6931-54-0 (FFNSC 2 Lib)
5	10.244	9,042,970	1.07	Cymene <para-></para->	99-87-6 (FFNSC 2 Lib)
6	10.408	342,467	0.04	Cyclohexene, 1-methyl-4-(1-methylethenyl)-,(S)-	5989-54-8 (FFNSC 2 Lib)
7	13.368	4,033,463	0.48	3-Oxatricyclo[4.1.1.0(2,4)]octane, 2,7,7-trimethyl-	1686-14-2 (FFNSC 2 Lib)
8	13.904	2,122,686	0.25	Pinene oxide α	1686-14-2 (FFNSC 2 Lib)
9	14.261	1,263,376	0.15	(1R,4R,5S)-1-lsopropyl-4-methoxy-4-methylbicyclo[3.1.0]hexane	11001111-06-5(FFNSC 2 Lib) 11
10	15.158	365,669	0.04	Nopinone	24,903-95-5 (FFNSC 2 Lib)
11	15.330	2,293,068	0.27	Pinocarveol	5947-36-4 (FFNSC 2 Lib)
12	16.227	1,444,460	0.17	Pinocarvone	30,460-92-5 (FFNSC 2 Lib)
13	17.736	2,646,046	0.31	Myrtenal	564-94-3 (FFNSC 2 Lib)
14	18.319	835,255	0.10	Verbenone	80-57-9 (FFNSC 2 Lib)
15	20.305	6,423,268	0.76	Thymoquinone	6617-34-1 (NIST14 Lib)
16	22.575	568,936	0.07	Thujyl acetate <neoiso-3-> DB5-1081 (Classical name = neo-3-)</neoiso-3->	0-00-0(SZTERP Lib)
17	22.869	876,235	0.10	Pinocarveol <trans-> DB5-724</trans->	0-00-0(SZTERP Lib)
18	26.892	1,176,740	0.14	(+)-Longifolene	475-20-70(NIST14s Lib)
19	34.853	462,953	0.05	Dodecane	112-40-3 (FFNSC 2 Lib)
20	41.091	397,933	0.05	Tetradecanoic acid	544-63-8 (FFNSC 2 Lib)
21	48.341	48,096,480	5.69	Hexadecanoic acid	57-10-3 (FFNSC 2 Lib)
22	51.439	2,139,770	0.25	9,12-Octadecadienoic acid (Z,Z)-, methyl ester	56,599-58-7 (NIST14 Lib)
23	51.653	5,090,837	0.60	9-Undecenal, 2,10-dimethyl-	0-00-0 (NIST14 Lib)
24	54.211	560,235,582	66.24	Linoleic acid	506-21-8 (NIST14 Lib)
25	61.160	478,053	0.06	3-Cyclopentylpropionic acid, 2-dimethylaminoethyl ester	0-00-0 (NIST14 Lib)
26	65.858	278,309	0.03	Squalene	1111-02-4 (NIST14 Lib)
	Total	845,786,078	100.00		



was found with the increase of glutathione-S-transferase activity (Aruna and Sivaramakrishnan, 1990). In line with these findings, the results of the current study found that NS oil and TQ were able to decrease the progress of tumors as well as decrease the values of TNF-α. Treatment with pure anastrazole caused partial necrosis of tumor tissues remaining in the form of "islands" (Figure 7C) and no effect observed with the vehicle-treated group, and a significant therapeutic effect was observed in tumor tissues after treatment with anastrazole, thymoquinone, and berberine (Figures 7C, D, I). We observed tumor cells with cytoplasm vacuolization and signs of karyolysis and inflammatory lymphocytic infiltration expressed weakly around the tumor (Figure 7B).

In our experiments, treatments with α - and β -pinene administered to mice did not induce changes in histology compared to the normal control group treated with the vehicle (**Figures 7E-F**). Protective effects could be explained by the ability of phytoconstituents (berberine) to inhibit the tumor cell target, which could account for the observed cancer protective potential of *B. aristata* that is pro-apoptotic and endowed with cell cycle arrest properties. However, anastrazole (1 mg/kg), berberine (30 mg/kg), and the *B. aristata* extract (400 mg/kg) against DMBA induced significantly improved tumor pathology. The ductal epithelial cells were bigger than normal cells and had an increased cytoplasm nucleus, which was observed in the group treated with the *B. aristata* extract.

Immunohistochemistry

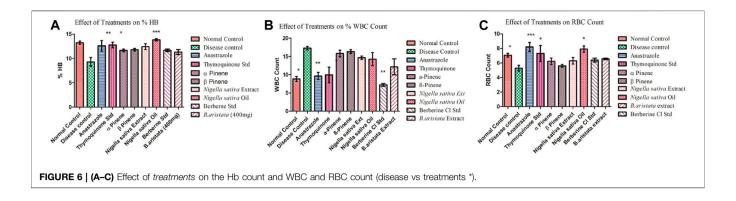
Tumor necrosis factor alpha (TNF- α) is a master proinflammatory cytokine and multifunctional cytokine involved in apoptosis, inflammation, and immunity (21). TNF- α has been reported to be elevated in the serum of patients diagnosed with advanced stages and correlate with an increased number and size of metastatic sites (Berberoglu et al., 2004). Therefore, the TNF-TNFR2 axis was implicated in the suppression of immune response and affects tumor progression and metastasis (Mantovani et al., 2008). In the following sections, we will interpret a possible role of targeting TNF- α interactions with the herbal extract

platform in the tumor. Positive staining for TNF- α was observed in all the groups (**Figures 8B–J**), except that the normal control group showed the negative expressions (**Figure 8A**). In the disease control group treated with the vehicle, the strong positive expressions of TNF- α were shown (**Figure 8B**); however, the group treated with anastrazole showed the least expression for TNF- α (**Figure 8C**) and thus an increase in MST. On comparing the group treated with the thymoquinone standard, α - and β -pinene with the *N. sativa* extract and NS oil were more promising and showed potency in reducing TNF- α , but NS oil has relatively less expression than the *N. sativa* extract. α - and β -pinene showed moderate TNF- α on comparing with the anastrazole-treated group.

Results depict that NS oil showed less TNF-α expression. that is, its phytoconstituent contained thymoquinone, and thus enabled an increase in the MST. The pure compound has better efficacy and potency among all the other standard compounds, and NS oil showed more efficacy due to the presence of thymoquinone. Now, comparing the standard treated group (Figure 8C) with pure berberine (30 mg/kg) and B. aristata (400 mg/kg) among test compounds, pure berberine showed (Figure 8I) moderately strong cytoplasmic positivity for TNF-α in the ductal epithelial cells; however, treatment with the *B. aristata* extract showed (**Figure 8J**) less strong cytoplasmic positivity for TNF-α. On the basis of TNF α expression, pure compounds have more antitumor potency against the extracts. The increased levels of TNF- α in the DMBA group, as compared to the control group, agree with the findings of other studies (Ardizzoia et al., 1992; Bower et al., 2002). This high level may be due to increased production by the tumor-infiltrating lymphocytes and/or by the tumor cells (Lind et al., 1993; Kopreski et al., 1996).

Vascular Endothelial Growth Factor

VEGF is a potent angiogenic factor and upregulated in many tumors, and its contribution to tumor angiogenesis is well defined. It is the key mediator of angiogenesis and binds two VEGF receptors (VEGF receptor-1 and VEGF receptor-2), which are expressed on vascular endothelial cells. Different agents including antibodies, aptamers, peptides, and small molecules have been extensively investigated to block VEGF and its pro-angiogenic functions. For multicellular tumor clones to grow beyond this size, they must recruit new blood vessels by angiogenesis and vasculogenesis. In the present study, all tumor disease controls (Figures 9B) to treatments (Figures 9C-J) were found to be VEGF-positive, which is in agreement with previous reports. Not only does VEGF have a direct influence on breast cancer invasion and migration but also it has been shown to act as a survival factor for metastatic breast carcinoma cells (Pidgeon et al., 2001). Studies in the laboratory have shown that VEGF protects both human and murine breast carcinoma cells from apoptosis (Chung et al., 2002). The standard group showed (Figure 9C) very weak cytoplasmic positivity for VEGF in the ductal epithelial cells on comparing with the disease control group (Figure 9B). This indistinct feature elaborates the



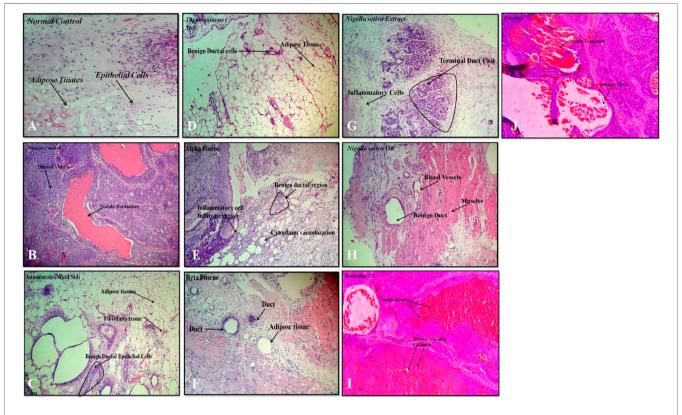


FIGURE 7 | Histopathology: (A) normal control, (B) disease control, (C) marketed standard, (D) thymoquinone Std, (E) α -pinene Std, (F) β -pinene Std, (G) N. sativa extract, (H) N. sativa oil, (I) berberine Cl std, and (J) Berberis aristata extract.

potential role of VEGF in tumor pathogenesis with the past studies (Torres et al., 2016). Thymoquinone showed (**Figure 9D**) poor positive expression of VEGF in the ductal epithelial cells, which is similar to other studies that proved that thymoquinone attenuated tumorigenic signaling, including those controlled by EGF, FGF, VEGF, TGF, and various metastatic, angiogenic, and pro-mitogenic factors (Rashid et al., 2019). α -pinene (**Figure 9E**) showed moderately strong cytoplasmic positivity for VEGF in the ductal epithelial cells and β -pinene (**Figure 9F**) depicted moderately strong cytoplasmic positivity for VEGF in the ductal epithelial cells, which mean that these isomers have

less affinity toward the VEGF receptors and thus are unable to cause the apoptotic action in tumor tissues. The *N. sativa* extract (**Figure 9G**) and NS oil (**Figure 9H**) show moderate cytoplasmic positivity for VEGF in the ductal epithelial cells; thus, the NS extract and NS oil have anti-VEGF potential in this regime (Zhang et al., 2014) and demonstrated that berberine inhibits the expression of hypoxia-inducible factor 1α and increases the expression level of VEGF in prostate cancer. Therefore, the anticancer effect of berberine hydrochloride on tumor cells may occur via the activation of the VEGF signaling pathway. The berberine Cl Std (**Figure 9I**) tissue shows moderately strong cytoplasmic positivity for VEGF in

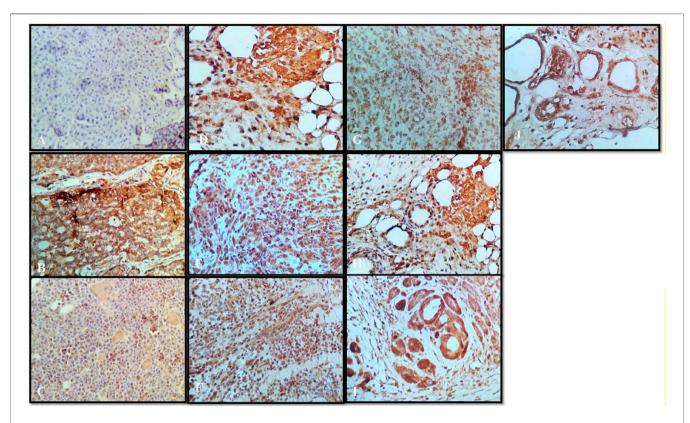


FIGURE 8 | Immunochemistry TNF- α : (A) normal control, (B) disease control, (C) marketed standard, (D) thymoquinone Std, (E) α -pinene Std, (F) β -pinene Std, (G) N. sativa extract, (H) N. sativa oil, (I) berberine Cl Std, and (J) Berberis aristata extract.

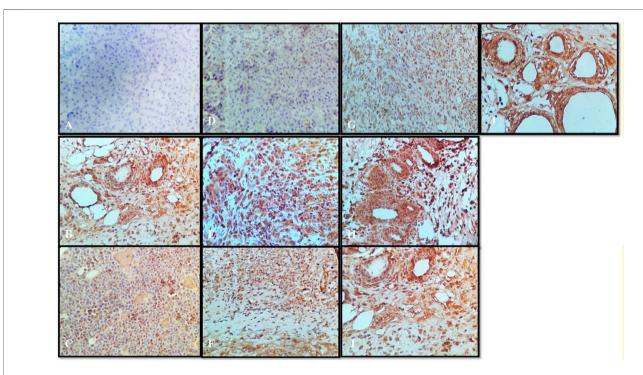


FIGURE 9 | Immunochemistry VEGF: (A) normal control, (B) disease control, (C) marketed standard, (D) Thymoquinone Std, (E) α -pinene Std, (F) β -pinene Std, (G) N. sativa extract, (H) N. sativa oil, (I) berberine Cl Std, (J) Berberis aristata extract.

the ductal epithelial cells; however, the *B. aristata* extract (**Figure 9J**) depicted weak cytoplasmic positivity for VEGF.

CONCLUSION

In conclusion, the results of the present study give clear evidence that the *N. sativa* extract and *B. aristata* extract and their marker compounds thymoquinone, ±pinene, and berberine Cl induce no harmful effects on female mice. Moreover, they exert a protective effect against the DMBA-induced tumor model. The antioxidant property is mediated by their actions and investigating other underlying mechanisms, merits, and further studies. The present study thus demonstrated the chemopreventive potential of thymoquinone, ± pinene and berberine Cl in the DMBA-induced tumor model. Despite the exact mechanism of action of chemopreventive potential of marker compounds, the antilipidperoxidative, antioxidant, and modulating effects on the detoxification cascade could play a possible role.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

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ETHICS STATEMENT

The animal study was reviewed and approved by the Delhi Institute of Pharmaceutical research.

AUTHOR CONTRIBUTIONS

MM, research planning and conduction, data collection, data analysis and interpretation, drafting the article, critical revision of the article, and final approval of the version to be published; SA, conception or design of the work.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.642067/full#supplementary-material

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Metabolomic Profiling and Immunomodulatory Activity of a Polyherbal Combination in Cyclophosphamide-Induced Immunosuppressed Mice

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The study was aimed to develop a characterized polyherbal combination as an immunomodulator containing *Phyllanthus emblica* L., *Piper nigrum* L., *Withania somnifera* (L.) Dunal, and *Tinospora cordifolia* (Willd.) Miers. Through response surface methodology (RSM), the ratio of aqueous extracts of four plant materials was optimized and comprised 49.76% of *P. emblica*, 1.35% of *P. nigrum*, 5.41% of *W. somnifera*, and 43.43% of *T. cordifolia* for optimum immunomodulatory activity. The optimized combination showed antioxidant potential and contains more than 180 metabolites, out of which gallic acid, quercetin, ellagic acid, caffeic acid, kaempferitrin, and *p*-coumaric acid are some common and significant metabolites found in plant extracts and in polyherbal combination. Treatment with the polyherbal combination of different doses in cyclophosphamide-induced immunosuppressed mice significantly (p < 0.01) enhanced the subsets of immune cells such as natural killer (NK) cells (60%), B cells (18%), CD4 cells (14%), and CD8 cells (7%). The characterized polyherbal combination exhibited potent immunomodulatory activity, which can be further explored clinically for its therapeutic applicability.

Keywords: metabolomics, immunomodulatory activity, splenocyte, *Phyllanthus emblica*, *Withania somnifera*, *Tinospora cordifolia*

INTRODUCTION

Herbs are in increasing demand in developed and developing countries for primary health care. Plant-based products have been extensively exploited as an essential source for drugs because of their biological activities and higher safety margins. Immunomodulation using medicinal plants can provide a substitute for conventional therapy for a variety of diseases, especially when the host's defense mechanism has to be generated under the conditions of an impaired immune response (Ganju et al., 2003). People, every year, turn to herbal medicine because they believe that plant remedies are free from undesirable side effects. It is also known that herbs have been used in

traditional systems of medicine as an immunomodulator for a decade (Kumar et al., 2012; Nagoba and Davane, 2018). Plant extracts have been proven for their activity in boosting the humoral (Rehman et al., 1999) as well as cell-mediated immunity against viruses, bacteria, fungi, and cancer (Sarvanandaa et al., 2018). In the Indian traditional system of medicine, several food-grade plants have been used as immunomodulators, and most of them were proven individually for their immune-enhancing effect. The bioactive constituents of these plants that are responsible for the activity were also determined. In recent years, many herbs from the Indian system of medicine that modulate the immune system of the body were scientifically validated. Some herbs such as Phyllanthus emblica L. (family: Phyllanthaceae) (Liu et al., 2012), Piper nigrum L. (family: Piperaceae) (Majdalawieh and Carr, 2010), Tinospora cordifolia (Willd.) Miers (family: Menispermaceae) (Mathew and Kuttan, 1999), Withania somnifera (L.) Dunal (family: Solanaceae) (Davis and Kuttan, 2000), Curcuma longa L. (family: Zingiberaceae) (Kim et al., 2014), Ocimum sanctum L. (family: Lamiaceae) (Mondal et al., 2011), Azadirachta indica A. Juss. (family: Meliaceae) (van der Nat et al., 1987), Achilla millefolium L. (family: Asteraceae) (Mohammed Al-Ezzy et al., 2018), and many more are the reported herbs exhibiting excellent immunomodulatory activity. Based on our preliminary study, we focused only on the first four plants, namely, P. emblica, P. nigrum, T. cordifolia, and W. somnifera.

P. emblica, Indian gooseberry, is an essential medicinal plant in the Indian traditional system of medicine and is used as a dietary combination. It has various properties that can combat age-related illnesses such as cancer, cardiac diseases, renal failure, immune deficiency, arthritis, cataracts, and wrinkling of the skin (Mathai et al., 2015). T. cordifolia is of great interest to scientists around the world due to its anti-inflammatory, antiarthritic, antioxidant, antiallergic, antistress, antileprotic, antimalarial, hepatoprotective, immunomodulatory activities (More and Pai, 2011; Alsuhaibani and Khan, 2017). The modern medical literature, as well as traditional medical literature, reports many potential health benefits of W. somnifera in stress, neurotoxicity, and immune disorders (Singh et al., 2011; Zahiruddin et al., 2020). P. nigrum is used extensively as a spice around the world and in traditional medicine as an antioxidant, antimicrobial, anticarcinogenic, anti-inflammatory, and gastroprotective drug (Parveen et al., 2015; Bui et al., 2019). These four selected plant extracts were further subjected to optimization of the ratio by response surface methodology (RSM) to develop a polyherbal combination.

Across the globe, several herbal formulations are being sold claiming to be immunomodulators. Vivartana, Chyawanprash, Brahma Rasayana, IM-133, and Septilin are the few formulations used in the Indian traditional system of medicine, which have been experimentally proven as immunomodulators (Gnanasekaran et al., 2015). But these formulations have not been fully explored scientifically, and the dose and frequency of these formulations are much higher than those of modern medicines. In the present study, we selected eight traditionally used plants according to the literature reported for

immunomodulatory activity, and out of eight, only four named *P. emblica*, *P. nigrum*, *T. cordifolia*, and *W. somnifera* were found to be the best immunomodulators in our preliminary studies. These four selected plants were used to develop a polyherbal combination. The proposed study aims to develop a polyherbal combination as an immunomodulator, which can be used for the management of immunity for the prevention of various bacterial and viral infections. This herbal combination has been chromatographically characterized and scientifically validated through *in vitro* and *in vivo* experiments.

METHODOLOGY

Collection of Plant Materials

The fruits of *P. emblica*, *P. nigrum*, stem of *T. cordifolia*, and roots of *W. somnifera* were purchased from Universal Biotech, Farash Khana, Delhi, India. The voucher specimens (*P. emblica*-BNPL/JH/Ph.D/12/17/01, *T. cordifolia*-BNPL/JH/Ph.D/12/17/02, *W. somnifera*-BNPL/JH/Ph.D/12/17/03, and *P. nigrum*-BNPL/JH/Ph.D/12/17/04) of each plant material have been deposited in the Bioactive Natural Product Laboratory (BNPL), Jamia Hamdard, New Delhi, India, for future reference.

Preparation of the Extract

Accurately weighed 150 g of powder of each plant material were divided into three equal parts. These were macerated overnight using water, ethanol, and 50% ethanol to form aqueous extract (AE), ethanolic extract (EE), and hydroethanolic extract (HEE), respectively. The EE and HEE were further refluxed for 3 h after maceration. All three extracts were filtered, and the filtrate was evaporated to dryness under reduced pressure. The extractive values and percentage yields of different extracts were calculated and stored at 4°C for further analysis.

Quantitative Analysis of Specific Marker Compounds From Raw Extracts

Gallic acid, piperine, berberine, and withaferin-A were selected as specific marker compounds for fruits of P. emblica, P. nigrum, stem of T. cordifolia, and roots of W. somnifera, respectively (Chatterjee et al., 2012; Gorgani et al., 2017; Neag et al., 2018; Tiwari et al., 2018). These markers were quantified using highperformance thin-layer chromatography (HPTLC). Ten milligrams of each extract were dissolved separately in highperformance liquid chromatography (HPLC)-grade methanol to get 10-mg/ml solutions. The stock solutions of standard gallic acid, berberine, piperine, and withaferin-A (Sigma Aldrich, India) were prepared in HPLC-grade methanol to get a concentration of 500 μ g/ml. The prepared samples were filtered using a 0.2- μ m polytetrafluoroethylene (PTFE) membrane filter before HPTLC analysis. The prepared extracts and standards were applied separately on Silica gel 60 F254 precoated TLC plates, 10 cm × 10 cm (Merck, Germany), with the help of a Camag Linomat (CAMAG, Switzerland) applicator with nitrogen flow providing a delivery speed of 120 nl/s from the syringe. Toluene:ethyl acetate: formic acid (5:4:1; v/v/v) were used as developing solvents for

TABLE 1 | Four-variable Box-Bhenken design with experimental and predicted values of pinocytic and splenocyte proliferation of different combinations of aqueous extracts

Run no.	Concentration of aqueous extract (mg)				Pinocytic activity		Splenocyte proliferation	
	Α	В	С	D	Predicted	Actual	Predicted	Actual
1	100	6	455	333	0.028	0.058	0.027	0.012
2	1,000	6	455	333	0.027	0.019	0.180	0.220
3	100	60	455	333	0.017	0.004	0.055	0.110
4	1,000	60	455	333	0.180	0.150	0.031	0.081
5	550	33	10	6	0.004	0.033	0.260	0.240
6	550	33	900	6	0.059	0.051	0.240	0.270
7	550	33	10	660	0.078	0.076	0.240	0.320
8	550	33	900	660	0.110	0.067	0.047	0.160
9	100	33	455	6	0.022	0.001	0.140	0.077
10	1,000	33	455	6	0.067	0.083	0.240	0.260
11	100	33	455	660	0.055	0.053	0.240	0.160
12	1,000	33	455	660	0.055	0.091	0.140	0.150
13	550	6	10	333	0.059	0.070	0.280	0.270
14	550	60	10	333	0.029	0.040	0.220	0.180
15	550	6	900	333	0.005	0.007	0.140	0.130
16	550	60	900	333	0.110	0.110	0.240	0.190
17	100	33	10	333	0.028	0.017	0.052	0.120
18	1,000	33	10	333	0.170	0.130	0.320	0.250
19	100	33	900	333	0.062	0.071	0.074	0.100
20	1,000	33	900	333	0.039	0.048	0.260	0.150
21	550	6	455	6	0.020	0.008	0.160	0.190
22	550	60	455	6	0.070	0.077	0.230	0.220
23	550	6	455	660	0.063	0.070	0.270	0.230
24	550	60	455	660	0.048	0.074	0.230	0.160
25	550	33	455	333	0.120	0.057	0.260	0.230
26	550	33	455	333	0.071	0.057	0.230	0.230
27	550	33	455	333	0.012	0.057	0.240	0.230
28	550	33	455	333	0.100	0.057	0.290	0.230
29	550	33	455	333	0.005	0.057	0.120	0.230

A: P. emblica; B: P. nigrum; C: W. somnifera; D: T. cordifolia. Levels for P. emblica concentration are 100 mg (-1), 550 mg (0), and 1,000 mg (+1); for P. nigrum are 6 mg (-1), 33 mg (0), and 60 mg (+1); for W. somnifera are 10 mg (-1), 455 mg (0), and 900 mg (+1); and for T. cordifolia are 6 mg (-1), 333 mg (0), and 660 mg (+1).

gallic acid, piperine, and withaferin-A. For berberine, n-butanol: water:acetic acid (4:5:1; v/v/v) was used as a developing solvent. Plates were developed horizontally in a CAMAG twin trough glass chamber (10 cm \times 10 cm), which was presaturated with the mobile phase for 30 min. The developed plates were air-dried and scanned by CAMAG TLC densitometric scanner III operated by WinCATs software. Gallic acid and piperine were scanned at 254 nm, while berberine was scanned at 366 nm. For quantitative analysis of withaferin-A, the air-dried plate was derivatized by dipping in 5% anisaldehyde sulfuric acid solution and scanned at 540 nm.

Response Surface Methodology for Optimization of Extract Ratio

RSM was used to optimize the ratio of four extracts, which is a collection of statistical techniques to design experiments, build models, evaluate the effect of factors, and find the optimum conditions. Four extracts at three different concentration levels were combined by Box–Behnken response surface design (BBD), where pinocytic activity in macrophages and splenocyte proliferation assay were taken as the response of different combinations. Different concentrations of the aqueous extract of *P. emblica, P. nigrum, W. somnifera*, and *T. cordifolia* were

selected to optimize the effective concentration. The dose of each selected plant extract was calculated from its extractive values, which is equivalent to the dose mentioned in Ayurveda Pharmacopoeia of the respective plant materials. The selected concentrations for P. emblica were 100 mg (-1), 550 mg (0), and 1,000 mg (+1); concentrations of *P. nigrum* were 6 mg (-1), 33 mg (0), and 60 mg (+1); concentrations of W. somnifera were 10 mg (-1), 455 mg (0), and 900 mg (+1); and the concentration levels for *T. cordifolia* were 6 mg (-1), 333 mg (0), and 660 mg (+1). A total of 29 experimental combinations with three central points were generated through BBD using Design Expert 8.0.1.7 software (Stat-Ease Inc., USA), and all these combinations were tested for their pinocytic activity in macrophages and splenocyte proliferation assay (Table 1). The point prediction tool of the software determined an optimum value of the factors for the maximum in vitro immunomodulatory activity.

Metabolomic Profiling of Extracts and the Developed Polyherbal Combination by Ultra-Performance Liquid Chromatography-Mass Spectrometry

The optimized polyherbal combination and four aqueous extracts used to make the polyherbal combination were dissolved

separately in LC-MS-grade methanol and filtered through a 0.2μm membrane filter. The filtered solutions were diluted in a ratio of 1:5 (v/v) using methanol. High-throughput profiling of metabolites was carried out by ultra-performance liquid chromatography-mass spectrometry (UPLC-MS) (Zahiruddin et al., 2017). The UPLC was performed on a Water's ACQUITY UPLC(TM) system (Serial No. F09 UPB 920M; Model code # UPB, Waters Corp., MA, USA) equipped with a binary solvent delivery system, an auto-sampler, column manager, and a tunable MS detector (Serial No. JAA 272; Synapt; Waters, Manchester, UK) installed and controlled by Mass Lynx V 4.1 (Waters, USA). Data acquisition has been carried out in positive modes. Chromatography was performed using acetonitrile (A) and water (B) as the mobile phase on a monolithic capillary silica-based C18 column [ACQUITY UPLC(R) BEH C18, 1.7 μ m, 2.1 \times 100 mm], with the precolumn split ratio of 1:5 min at ambient temperature. Chromatographic separation was achieved by gradient elution mode (initially, 10% A; 0-5 min 40% A; 5-10 min 60% A; 10-13 min, 90% A; 13-15 min, 100% A; 15-16 min 10% A), and the total run time was 16 min. The flow rate of the nebulizer gas was set at 10 µl/min; for the cone gas, set to 50 L/h, and the source temperature was set at 100°C. The cone and capillary voltages were set to 40.0 and 3.0 kV, respectively. For collision, argon was employed at a pressure of 5.3×10^{-5} Torr. The accurate mass and composition for the precursor ions and the fragment ions were calculated using the Mass Lynx V 4.1 software incorporated in the instrument.

Raw data obtained from UPLC-MS analysis were processed in Progenies Software (Waters, USA). By using this software, the maximum number of mass peaks was detected, which were further identified through the library based on their molecular weight. Chromatographically separated and identified metabolites were matched with the plant's native metabolites. All detected metabolites were processed in XLStat software for statistical differentiation between the plants used for the development of polyherbal combination. A metabolite-based comparison was performed in different extracts to identify the major metabolites present in the specific plant extract.

Characterization of Polyherbal Combination Determination of Total Phenol and Flavonoid Contents

The total phenol content (TPC) and the total flavonoid content (TFC) of the polyherbal combination were determined using the Folin–Ciocalteu (FC) and aluminum chloride methods, respectively (Khan et al., 2017). The optimized combination was dissolved in methanol to prepare 5 mg/ml. For the determination of the total phenolic content (TPC), 500 μl of methanolic solution (5 mg/ml) was thoroughly mixed with 2.5 ml FC and 2.5 ml of sodium carbonate (7.5% w/v). The mixture was incubated for 30 min at room temperature, and after incubation, absorbance was measured at 765 nm. For the determination of the TFC, 0.1 ml of aluminum chloride (10% w/v) and 0.1 ml of potassium acetate (0.1 mM) were added in 500 μl of sample solution (5 mg/ml). The resulting mixture solution was kept at room temperature for 30 min, and absorbance was measured at 415 nm. TPC and TFC were calculated from the calibration curve

of gallic acid and rutin (Sigma Aldrich, India), respectively, and the results were expressed as milligrams gallic acid and rutin, respectively, equivalent per gram weight of the polyherbal combination.

Antioxidant Activity of the Optimized Combination

The antioxidant potential of the developed polyherbal combination was determined by measuring the scavenging potential of 2,2-diphenyl-1-picrylhydrazyl (DPPH; SRL, India). One milliliter of freshly prepared DPPH solution (0.3 mM in methanol) was mixed with 1.0 ml of optimized combination dissolved in water. The resulting mixture was kept at room temperature in the dark for 25 min, and after incubation, absorbance was recorded at 515 nm. Different concentrations of optimized combinations were used to determine DPPH radical scavenging activity (Liu et al., 2009). The ability of the sample to scavenge the DPPH radicals was calculated using the following formula:

DPPH radical scavenging effect = $(A_{control} - A_{sample}) \times 100/A_{control}$

where $A_{control}$ is the absorbance of the DPPH solution without polyherbal combination; A_{sample} is the absorbance of the sample with DPPH solution.

To determine the reducing power, 500 μ l of an aqueous solution of the optimized combination was thoroughly mixed with 2.5 ml of potassium ferricyanide (1% w/w) and 2.5 ml of phosphate buffer (pH 6.6), and the mixture was incubated for 30 min in a water bath at 50°C. After incubation, the mixture was cooled, and 2.5 ml of trichloroacetic acid (10% w/v in water) was added. Furthermore, it was centrifuged and the supernatant was diluted with an equal amount of deionized water, and freshly prepared 0.5 ml of ferric chloride (0.1% w/w) was added. The mixture was thoroughly mixed, and its absorbance was measured at 700 nm (Bhalodia et al., 2013). For control, water was used in place of an optimized combination, and the reducing power was compared with the control. For both assays, ascorbic acid was used as a positive control.

In Vitro Immunomodulatory Activity of the Developed Polyherbal Combination Animals

BALB/c mice (6 weeks old, 25 ± 5 g) were provided by Central Animal House Facility, Jamia Hamdard (Registration No. 173/GO/RE/S/2000/CPCSEA). Before initiation of the experiment, all experimental protocols were approved by the Institutional Animal Ethics Committee, and the experiments were strictly carried out according to the guidelines of the committee (Animal Approval Number 1551). The animals were housed in a polypropylene cage and placed in the experimental room, where they were allowed to acclimatize for a week before the experiment. An air conditioning unit (with 10% air exchange per hour) was maintained along with a relative humidity of 50 ± 10 RH, 12/12 h light–dark cycle, and a temperature of 25° C $\pm 2^{\circ}$ C was kept in the animal house facility throughout the experimental period.

Splenocyte Proliferation Assay

BALB/c mice were euthanized, and the spleen was removed aseptically for isolation of splenocytes. The spleen was further homogenized using sterile phosphate-buffered saline (PBS) by passing it through a mesh (0.4 microns) and centrifuged at $300 \times$ g for 5 min. Red blood cells (RBCs) were lysed from the cell pellet by adding 500 μl of lysis buffer (Tris-HCl-NH₄Cl, pH 7.2). The reaction was stopped by adding Roswell Park Memorial Institute (RPMI) medium (RPMI-1640, Millipore Sigma Aldrich, India) and washed two times to remove any debris. The cell pellet was resuspended in RPMI medium to get 3.0×10^6 cells/ml, and 100μ l of cell suspension was seeded per well in a 96-well plate. Here, 25 μl of mitogen concanavalin A (Con A; 2.0 μg/ml) was added, and 25 µl of the polyherbal combination was added to the cells per well containing splenocytes and incubated at 37°C in a CO2 incubator for 72 h. After incubation, 20 µl of tetrazolium dye 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) were added and incubated at 37°C, 5% CO2 for another 6 h. Furthermore, the tetrazolium crystals formed in live cells were dissolved after 6 h of incubation, and cell proliferation was measured at 490 nm using a microplate reader (Shi and Fu, 2011). The media treated with polyherbal combination was used as a negative control, and spleen cell treated with levamisole was used as the positive control.

Pinocytic Activity Assay

One milliliter of thioglycolate (1.0 mg/ml in PBS) was injected intraperitoneally (i.p.) in 2 mice, and peritoneal macrophages were isolated after 48 h by injecting PBS into the peritoneal cavity. Isolated macrophages were washed twice with media and resuspended at 1.0 \times 10⁶ cells/ml in RPMI medium containing 10% fetal bovine serum (FBS). Here, 200 µl of cells were transferred to 96-well plates and incubated overnight at 37°C, 5% CO2 to allow macrophages to adhere to the plate. Non-adherent cells were gently washed with RPMI medium, and 100 µl of fresh RPMI medium was added to each well. Furthermore, 25 µl of the polyherbal combination was added to the cells in each well and incubated for 48 h at 5% CO2 and 37°C. After incubation, 100 µl of neutral red solution (0.1% in 10 mM PBS) was added, and after 2 h of incubation, a free neutral red solution was removed by gently washing the cells with PBS. The macrophages were further lysed by adding 100 µl of neutral red detainer (ethanol and 0.1% acetic acid in a ratio of 1:1, v/v) and incubated at room temperature overnight, and optical density was recorded the next day at 540 nm (Shi and Fu, 2011). For negative control, RPMI medium was used in place of the combination, and the results were expressed as compared to the negative control.

Immunoprotective Effect of the Polyherbal Combination

To determine the effect of the developed polyherbal combination on the immune system, BALB/c mice $(25\pm 5~g)$ were used for the study. Animals were randomly divided into seven groups consisting of six animals per group. Groups I–III received normal saline for 14 days, and group I served as normal control. In addition to normal saline, Groups II and III received polyherbal combination at an oral dose of

260 and 520 mg/kg, respectively, for 14 days. Groups II and III served as a sham control of the polyherbal combination. Groups IV–VII received cyclophosphamide (80 mg/kg, i.p.) for 4 days of the experimental period (from days 8 to 11), followed by a washout and normalization period of cyclophosphamide for 3 days. In addition to cyclophosphamide, Group IV received normal saline throughout the experimental period and served as a toxic control; Group V and Group VI received polyherbal combination orally at a dose of 260 and 520 mg/kg, respectively; Group VII received levamisole hydrochloride at a dose of 10 mg/kg orally for 14 days and served as a positive control. The oral dose of the polyherbal combination was decided on the basis of the RSM result and administered as a suspension in 0.1% carboxymethylcellulose. At the end of the experiment, blood samples were collected from each animal from the retro-orbital vein and used for further analysis.

Determination of Fluorocytometry-Based Immunological Parameters

Blood samples were collected at the end of the 14-day study period in anticoagulant-containing collection tubes. The RBCs were lysed using ammonium-chloride-potassium (ACK) lysis buffer for 10 min at room temperature, and the reaction was stopped by adding RPMI medium. For flow cytometry analysis, cells were washed twice with cold FACS buffer and pelleted by centrifugation at 400 g for 5 min. Cells were resuspended in FACS buffer containing antibodies at 1:100 dilution (CD3e-FITC, CD4-PE-Cy7, CD8-APC-Cy7, CD19-APC, and CD335-PE) and incubated for 25 min at 4°C in the dark. After the incubation period, cells were washed twice with FACS buffer and resuspended in 200 µl of FACS buffer before being acquired on a BD LSR II flow cytometer (BD Bioscience, USA). Data were analyzed using FCS Express 7 Research Edition, and results were expressed in terms of percentage of CD4 cells, CD8 cells, natural killer (NK) cells, and B cells. The gating strategy for selected populations of T cells, B cells, and NK cells is shown in Figure 1.

Determination of Hematological Parameters

Blood samples from mice were collected in a tube containing ethylenediaminetetraacetic acid (EDTA), and white blood cell (WBC), RBC, hemoglobin (HGB), and platelet (PLT) counts were determined using a fully automated hematology analyzer (XP 100, Sysmex, Japan) (Anjum et al., 2017).

Statistical Analysis

Data are shown as mean \pm SEM, and the difference between groups was analyzed by two-way ANOVA followed by Bonferroni posttest using GraphPad Prism 5.00. A p-value <0.05 was considered statistically significant.

The ANOVA provision of Design Expert was used to establish statistical validation of the equation supplied by the software. Using BBD and the Design Expert 8.0.1.7 program (Stat-Ease Inc., USA), a total of 29 experimental combinations with three central points were created, and all of these combinations were evaluated for pinocytic activity and splenocyte proliferation assay. The models were assessed using R^2 values and statistically significant coefficients. The validation of the RSM results was carried out to determine the optimal combination compositions across the entire experimental

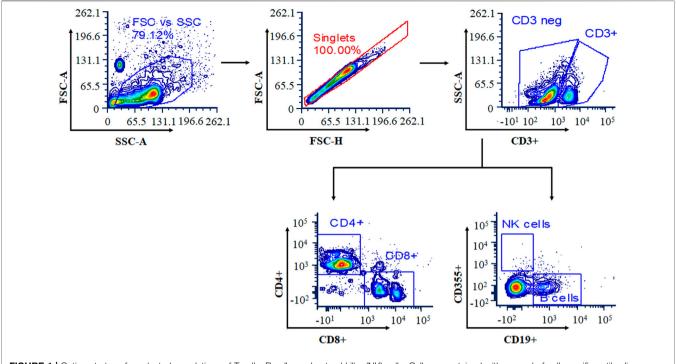


FIGURE 1 | Gating strategy for selected populations of T cells, B cells, and natural killer (NK) cells. Cells were stained with a panel of cell-specific antibodies conjugated with different fluorochromes: CD3e-FITC, CD4-PE, CD8-APC, CD19-APC, and CD335-PE.

region. ANOVA was used to justify the inadequacies of the models. After fitting the data to multiple models (linear, 2FI, quadratic, and cubic) and performing an ANOVA, it was found that the quadratic polynomial and 2FI models were the best fit for the splenocyte proliferation assay and pinocytic activity, respectively. The experimental values of the reactions were compared to the expected values quantitatively. MS-Excel was also used to create linear regression charts between the actual and predicted response values. The Box-Cox plot was used to describe the appropriate power transformation of the response data.

Principal component analysis (PCA) is a powerful statistical tool for data analysis and expression that can highlight the similarities and differences of sets. Raw data obtained from the UPLC-MS analysis were processed in the Progenies software (Waters, USA). Using this software, the maximum number of mass peaks can be captured and further identified by the library on the basis of their molecular weight. All detected metabolites are processed in the XLStat software to make a statistical difference between plants used to develop a polyherbal combination.

RESULTS

The plant materials used in the present study were authenticated according to the protocol of Indian Pharmacopoeia (Anonymous, 2010). The authenticated plant materials were extracted in three different solvents (aqueous, ethanol, and hydroethanol) by overnight maceration followed by reflux. We have evaluated aqueous, ethanolic, and hydroethanolic extracts from eight plants for their *in vitro* immunomodulatory activity. From eight plants, only

aqueous extracts of *P. emblica, T. cordifolia, W. somnifera*, and *P. nigrum* were found to be the best immunomodulators on the basis of their *in vitro* immunomodulatory activity and extractive yield.

Quantitative Estimation of Specific Markers

The aqueous extracts of four selected plants were chemically characterized by quantifying specific markers present in them. The linear regression calibration curves plotted between the peak area vs. concentration were linear for all standards, namely, gallic acid, berberine, piperine, and withaferin-A, with good linear relationships ($r^2=0.99$). Well-separated bands of gallic acid, berberine, piperine, and withaferin-A were visualized at $R_{\rm f}$ 0.44, 0.46, 0.69, and 0.35, respectively. HPTLC chromatograms of gallic acid, piperine, berberine, and withaferin-A in the optimized extract are shown in **Supplementary Figures S1–S4**. The percentages of gallic acid in *P. emblica*, piperine in *P. nigrum*, berberine in *T. cordifolia*, and withaferin-A in *W. somnifera* were found to be 5.01% \pm 0.07%, 1.62% \pm 0.01%, 1.04% \pm 0.02%, and 2.35% \pm 0.04%, respectively, of total weight (w/w).

Response Surface Methodology-Based Optimization of Extract Ratio for the Development of the Polyherbal Combination

The aqueous extracts of these four plants were optimized in ratios by RSM to develop a polyherbal combination. A BBD with three levels was used for all four extracts of *P. emblica* (A), *P. nigrum* (B), *W. somnifera* (C), and *T. cordifolia* (D) to finalize their ratio for the development of a polyherbal combination. The range of

TABLE 2 | ANOVA of the quadratic response surface model for splenocyte proliferation and response surface 2FI model for pinocytic activity in Box-Bhenken design experiments.

Parameters	For splenocyte proliferation	For pinocytic activ	
Regression			
Sum of square	0.136	0.0402	
Df	14	10	
Mean squares	0.0097	0.004	
F value	1.337	2.7203	
Р	0.297	0.0311	
Residual			
Sum of square	0.102	0.0266	
Df	14	18	
Mean square	0.0073	0.00147	
Lack of fit test			
Sum of square	0.0845	0.0126	
Df	10	14	
Mean squares	0.0084	0.0009	
F value	1.901	0.2601	
p-value	0.2805	0.973	
Coefficient correlation (r ²)	0.572	0.6017	
Coefficient of variation (CV %)	45.936	67.52	
Adequate precision value	4.965 (>4)	7.221(>4)	

variables, designs, and results obtained for splenocyte proliferation and pinocytic activity is presented in **Table 1**. The results were the average of three independent assays. The experimental results were modeled with a second-order quadratic and two-factor interaction (2FI) model to explain the dependence of *in vitro* immunomodulatory activity on different factors. The experimental data obtained from BBD to predict splenocyte proliferation and pinocytic activity are expressed by the following equation.

Splenocyte proliferation assay: 0.2292 + 0.04425 A - 0.009666667 B - 0.031833333 C - 0.0075 D - 0.05987 AB - 0.021125 AC - 0.0485 AD + 0.0395 BC - 0.024625 BD - 0.045375 CD - 0.080183333 A 2 - 0.042433333 B 2 + 0.005566667 C 2 + 0.013066667 D 2 .

Pinocytic activity: 0.056965517 + 0.029958333 A + 0.018291667 B + 0.002208333 C + 0.014791667 D + 0.04925 AB - 0.041375 AC - 0.011 AD + 0.0335 BC - 0.016375 BD - 0.00675 CD.

ANOVA for optimizing the ratio of four extracts to develop a polyherbal combination showed that the regression model was significant and the lack of fit was insignificant for both the splenocyte proliferation assay and pinocytic activity (**Table 2**).

The Model F-value of 2.72 of pinocytic activity implies that the model is significant. There is only a 3.11% chance that a "Model F-value" this large could occur due to noise. The "Lack of Fit F-value" of 0.26 implies that the lack of fit is not significant relative to the pure error. A nonsignificant lack of fit is good for the model. The "Adeq Precision 7.22" indicating the excellent signal-to-noise ratio and $^{3}4$ is desirable. This model is used to navigate the design space. However, for the splenocyte proliferation assay, the "Predicted R^{2} " of (-1.1524982) negative implies that the overall mean is a better predictor of the response than the current model. It showed Adeq precision of

4.96, indicating a good signal-to-noise ratio. **Figures 2**, **3** are the three-dimensional (3D) representation of the interacting effect of different plant extracts on the proliferation of splenocytes and pinocytic activity, respectively. A contour plot is a two-dimensional (2D) representation of the responses plotted against a combination of numerical factors and/or mixture components. It shows the relationship between the responses, the mixture components, and/or the statistical elements. **Supplementary Figures S5–S6** represent the interactions among the various factors on splenocyte proliferation and pinocytic activity, respectively.

The optimal ratio of four different extracts for the maximum pinocytic activity and splenocyte proliferation assay was 49.76%, 1.35%, 5.41%, and 43.33%. for *P. emblica, P. nigrum, W. somnifera*, and *T. cordifolia*, respectively. The defined polyherbal combination predicted an improvement in splenocyte proliferation up to 32.7% and pinocytic activity by 11.8%. These optimized values of the ratio of four extracts were validated by *in vitro* immunomodulatory activity. The statistically developed polyherbal combination exhibited a 34% increase in splenocyte cell proliferation and 10.7% pinocytic activity, indicating a 90%–115% validation of the predicted model.

Metabolomic Profiling of the Extract and the Developed Combination by Ultra-Performance Liquid Chromatography-Mass Spectrometry

UPLC-MS analysis files were processed through progenesis software to detect the maximum possible ions. Metlin, Massbank, and the chemical library were used to identify the ions and set tolerance levels below 10 ppm. In these four extracts and in combination, more than 5,000 ions were detected. These

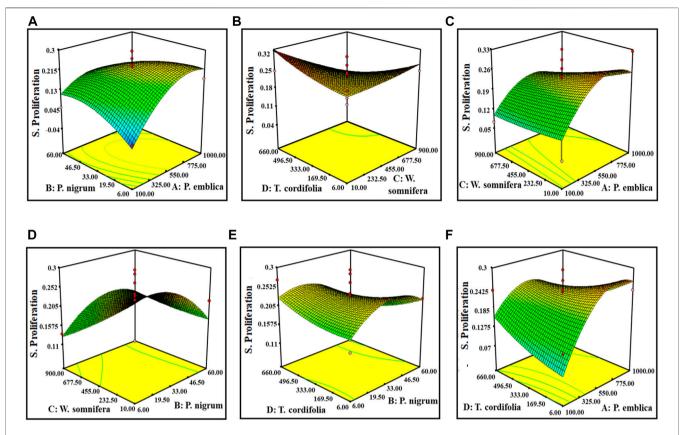


FIGURE 2 | Response surface graph showing the interaction among four extract concentrations and splenocyte proliferation activity. Interaction between **(A)** *P. emblica* and *P. nigrum*, **(B)** *P. emblica* and *W. somnifera*, **(C)** *P. emblica* and *T. cordifolia*, **(D)** *P. nigrum* and *W. somnifera*, **(E)** *P. nigrum* and *T. cordifolia*, and **(F)** *W. somnifera* and *T. cordifolia*.

ions were from molecular ion peaks and/or may be from the fragmentation of molecular ion peaks. All of these ions were detected and processed through progenesis software and identified by a database based on their m/z values. From the whole mass range, the detected ions were statistically differentiated through the S-plot, and the major metabolites causing differentiation between one extract and another were screened. The main abundant metabolites of the extracts and the combination are summarized in Supplementary Table S1. Most of the metabolites found are also reported in these plant extracts. Some common and major metabolites of P. emblica are phyllanemblin (Rt 1.25), gallic acid (Rt 2.08), quercetin (Rt 6.02), caffeic acid (Rt 4.59), ellagic acid (Rt 4.13), and punigluconin (Rt 8.05). Similarly, digallic acid (Rt 2.92), 7hydroxyflavanone (Rt 2.92), caffeic acid (Rt 4.59), schaftoside (R_t 4.56), syringin (R_t 4.59), jatrorrhizine (R_t 4.40), and sinapic acid (Rt 1.65) are found in T. cordifolia. Withaferin (Rt 5.25), withanolide (Rt 7.35), chlorogenic acid (Rt 4.16), and anaferine (R_t 6.30) were found in W. somnifera. Justicidin B (R_t 1.15), apiin (R_t 4.56), papaverine (R_t 4.78), piperazinamine (R_t 5.37), piperine (R_t 7.54), piperanine (R_t 9.78), and cubebin (R_t 7.69) are some metabolites found in P. nigrum. Some specific metabolites are found only in a single plant extract and a combination. The structure of major metabolites is summarized in **Supplementary**

Figure S7. However, the results of UPLC-MS analysis were processed through PCA. As per the PCA plots (**Supplementary Figure S8**), all the aqueous extracts show different types of metabolites, and it can be seen in the distribution of the aqueous extract in a different quadrant. All of these compounds are not being detected in combination due to their abundance in the extract. Several metabolites are also found in all extracts and in combination. Gallic acid (R_t 2.08), quercetin (R_t 6.02), ellagic acid (R_t 4.13), caffeic acid (R_t 4.59), kaempferitrin (R_t 5.02), and p-coumaric acid (R_t 1.25) are some common and significant metabolites also found in all the extracts and in combination.

Characterization of the Developed Polyherbal Combination

The optimized combination was characterized by determining their phenolic and flavonoid contents. Phenolic and flavonoid contents were expressed as gallic acid and rutin equivalent, respectively. The phenolic and flavonoid contents of the optimized combination were found to be 29.32% and 17.65% w/w of the polyherbal combination, respectively. The plants present in the polyherbal combination are the most abundant sources of phenolic and flavonoid metabolites, which may be

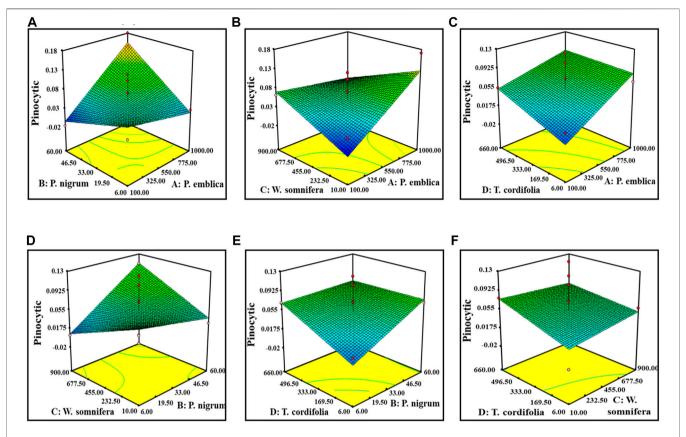


FIGURE 3 | Response surface graph showing the interaction among four extract concentrations and pinocytic activity. Interaction between (A) *P. emblica* and *P. nigrum*, (B) *P. emblica* and *W. somnifera*, (C) *P. emblica* and *T. cordifolia*, (D) *P. nigrum* and *W. somnifera*, (E) *P. nigrum* and *T. cordifolia*, and (F) *W. somnifera* and *T. cordifolia*.

responsible for their bioactivity (Mishra et al., 2013; Zhang et al., 2017; Tungmunnithum et al., 2018).

The developed polyherbal combination showed a potent DPPH radical scavenging potential, and IC $_{50}$ was recorded as 82.54 \pm 2.54 μ g/ml and was comparable to a standard antioxidant compound, ascorbic acid (IC $_{50}$ 55.37 \pm 1.25). The IC $_{50}$ of a compound is inversely proportional to its antioxidant activity, as it expresses the concentration of antioxidants required to decrease the concentration of DPPH by 50%. The presence of antioxidants in the herbal combination causes a reduction of Fe $^{3+}$ to Fe $^{2+}$ form. At 120 μ g/ml, the polyherbal combination showed the maximum reducing power, which is equivalent to 80 μ g/ml of ascorbic acid.

In Vitro Immunomodulatory Activity of the Developed Polyherbal Combination

The splenocytes isolated from the culture in RPMI medium for 72 h with or without polyherbal combination were counted for viability using the MTT assay. It was observed that splenocytes proliferate more when treated with the polyherbal combination compared to untreated cells. Here, five different concentrations (5–200 μ g/ml) of the polyherbal combination were tested for the splenocyte proliferation assay, and it was found that there was a dose-dependent increase in cell proliferation up to the

concentration of 150 µg/ml. In contrast, the concentration above 150 µg/ml showed no significant increment in the number of cells (Figure 4). However, all five concentrations of the combination showed dose-dependent pinocytic activity. Macrophages are the first-line defense against the antigen, and pinocytic activity is one of the distinguished methods to determine macrophage activation. We cultured mouse peritoneal macrophages in RPMI medium with or without supplementation of external stimuli and, after 48 h of incubation, used neutral red, which is readily taken up by macrophages to measure pinocytic activity. After the incubation with neutral red, the macrophages were lysed to measure the concentration of neutral red and determine the extent of pinocytic activity by macrophages. The enhancement of pinocytic activity by macrophages was expressed as the increase in neutral red concentration in cells treated with external stimuli as compared to untreated cells (Figure 4).

Effect of the Polyherbal Combination on Immunological Parameters

Hematological Parameters

Without affecting HGB content and RBC count, a significant reduction in lymphocyte, WBC, and platelet counts was observed

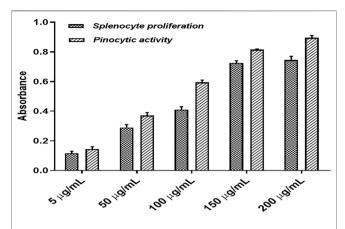


FIGURE 4 | Splenocyte proliferation assay and pinocytic activity of the developed polyherbal combination.

in cyclophosphamide-induced immunosuppressed mice. This change has been reversed and almost normalized upon administration of both doses of the polyherbal combination. **Table 3** shows the hematological parameters in mice from all groups. Healthy mice treated with the polyherbal combination showed a slight increase in favorable immune cells such as platelets, lymphocytes, and WBCs.

Immunomodulatory Parameters

The effect of the developed polyherbal combination on the immune system was measured by analyzing the percentage of increase or decrease in T cells, B cells, and NK cells. An increase in T-cell proliferation was observed in the cyclophosphamideinduced immunosuppressed mouse model when treated with the polyherbal combination (Figure 5). Cyclophosphamide treatment resulted in a significant reduction in CD4+ and CD8+ T cells, NK cells, and B cells. Two doses of the polyherbal combination (260 and 520 mg/kg) were administered orally to normal and immunosuppressed mice. Treatment with the developed polyherbal combination in cyclophosphamide-induced immunosuppressed mice resulted in a significant increase in the number of CD4⁺ and CD8⁺ T cells. Both doses, 260 and 520 mg/kg, increased CD4 cells by 18.25% and 22.56%, respectively, compared to 8.50% in the toxic control. A significant increase in the population of B cells

was observed; similarly, a significant increase in NK cells was recorded in immunosuppressed mice treated with the polyherbal combination. The polyherbal combination elicited a proportional enhancement of the immune cell population, with the maximum response being at 520 mg/kg dose (**Figure 5**). In normal mice administered the polyherbal combination, a slight but not significant increase in the number of the immune cell population was observed, such as CD4⁺ T cells (2%), CD8⁺ T cells (3%), NK cells (9%), and B cells (3%).

DISCUSSION

In the Indian traditional system of medicine, more than 30 plants have been used, individually or in polyherbal combinations, for immune disorders. On the basis of the reported literature, we have chosen eight plant materials and screened them for immunomodulatory activity. The aqueous, ethanolic, and hydroethanolic extracts of these plants were screened for their splenocyte proliferation assay and pinocytic activity. Based on their extractive values and in vitro immunomodulatory activities, the aqueous extracts of four plants were selected for the development of a polyherbal immunomodulator, although hydroethanolic extractive values of some plants were found to be higher compared to aqueous and ethanolic extracts. In the present investigation, we considered only aqueous extracts because they are preferred over other preparations of traditional formulations and are considered much safer as compared to other extracts (Mensah et al., 2019). The aqueous extracts of these four plants underwent ratio optimization for the development of the polyherbal combination.

The application of RSM allowed the simultaneous determination of the main and interaction effects of different concentrations of all the extracts on *in vitro* pinocytic and splenocyte proliferation assay (Shahab et al., 2020). The data pertaining to various models (linear, 2FI, quadratic, and cubic) and their subsequent ANOVA revealed that splenocyte proliferation assay and pinocytic activity were the most suitably defined with the quadratic polynomial and 2FI models, respectively.

The plot indicated that the residuals follow a normal distribution and approximately form a straight line (**Figure 6**). "Adequate Precision" is an index that measures the signal-to-

TABLE 3 | Effect of polyherbal combination on hematological parameters of mice after the end of treatment.

Hematological parameter	G-I	G-II	G-III	G-IV	G-V	G-VI	G-VII
HGB (g/dl)	11.22 ± 0.47	13.61 ± 0.77###	10.92 ± 0.64 ^{ns}	11.82 ± 0.45 ^{ns}	11.63 ± 0.98 ^{ns}	12.21 ± 1.11 ^{ns}	12.44 ± 0.54 ^{ns}
Neutrophil (×10 ³ /µl)	4.12 ± 0.08	$5.87 \pm 0.44^{\#}$	4.14 ± 0.01^{ns}	$5.74 \pm 0.22^{\#}$	4.27 ± 0.05^{ns}	4.88 ± 0.08^{ns}	4.34 ± 0.07^{ns}
Lymphocyte (×10 ³ /µl)	7.23 ± 0.07	8.11 ± 0.14 ^{ns}	9.33 ± 0.08##	4.25 ± 0.21###	5.45 ± 0.04^{ns}	$6.99 \pm 0.05***$	6.11 ± 0.14*
WBC (×10 ³ /µl)	6.24 ± 0.09	6.91 ± 0.09^{ns}	7.88 ± 0.07 #	3.33 ± 0.14###	5.33 ± 0.11**	6.74 ± 0.45***	6.14 ± 0.11***
RBC (×10 ⁶ /µl)	6.02 ± 0.12	6.47 ± 0.47^{ns}	6.98 ± 0.45^{ns}	6.06 ± 0.13^{ns}	5.84 ± 0.02^{ns}	6.94 ± 0.31^{ns}	7.09 ± 0.23^{ns}
PLT (×10 ⁵ /μl)	7.45 ± 0.12	8.44 ± 1.11 ^{ns}	12.36 ± 0.11###	5.93 ± 0.54^{ns}	10.70 ± 0.45**	10.24 ± 0.47***	11.32 ± 0.45***

HGB, hemoglobin; PLT, platelet; RBC, red blood cell; WBC, white blood cell; G-I, Normal control; G-II, Combination low dose sham; G-III, Combination high dose sham; G-IV, Toxic control; G-V, Combination low. Dose; G-VI, Combination high dose; G-VII, Standard treated group. The data were indicated as mean \pm SEM. Results were analyzed by two-way ANOVA, and the level of significant differences among different groups was determined by Bonferroni posttest using GraphPad Prism version 5.00 software. At 95% confidence interval, p < 0.05 was considered as statistically significant, ns p > 0.05, *p < 0.05, *p < 0.01, ***p < 0.01, ***p < 0.01; hash "#" denoted that data were compared to normal control, and asterisk "*" denoted that data were compared to toxic control.

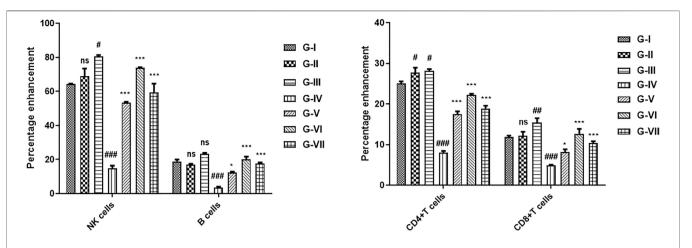


FIGURE 5 | Effect of the developed polyherbal combination on cyclophosphamide-induced immunosuppressed mice. Data were obtained from FACS analysis, (A) natural killer (NK) cells and B cells, and (B) CD4 and CD8 cells. The data were indicated as mean ± SEM. Results were analyzed by two-way ANOVA, and the level of significant differences among different groups was determined by Bonferroni posttest using GraphPad Prism version 5.00 software. At 95% confidence interval, p < 0.05 was considered as statistically significant, ns p > 0.05, *p < 0.05, *p < 0.01, ***p < 0.001; hash "#" denoted that data were compared to normal control, and asterisk "*" denoted that data were compared to toxic control. G-I (Normal control), G-II (Sham low dose), G-III (Sham high dose), G-IV (Toxic control), G-V (Combination low dose), G-VI (Combination high dose), and G-VII (Standard).

noise ratio. A ratio of greater than 4 is desirable. In this study, the computed ratio of 4.96 and 7.21 for splenocyte proliferation assay and pinocytic activity, respectively, indicated an adequate signal. These results are indicative of maximum predictive responses with constant variance and quadratic model accuracy demonstrating a good reproducibility of the data. The optimum conditions were determined using RSM with a fourfactor, two-level BBD. It was also estimated using regression equation for finding the best range of parameters achieving maximum splenocyte proliferation and pinocytic activity. To describe the suitable power transformation of response data, the Box–Cox plot was used (Vélez et al., 2015), since lambda (λ) is the most appropriate power transformation to apply the response data (**Figure 6B**).

From the point prediction tools, we have checked the effect of different doses of the extract. Upon increasing the dose of P. emblica up to 730 mg (100-730 mg), it increased the proliferation of the splenocytes and the pinocytic activity of macrophages, but after that point, the proliferation of splenocytes decreased but no significant change in the pinocytic activity. At an optimal level of P. emblica (750 mg), the increased dose of P. nigrum up to 22.2 mg was directly proportional to the in vitro immunomodulatory activity in both the assays. Furthermore, inverse proliferation was observed. At an optimal level of P. emblica (750 mg) and P. nigrum (20.59 mg), the concentration of W. somnifera was found inversely proportional to the in vitro immunomodulatory activity. At a low concentration of T. cordifolia, increased splenocyte proliferation and lower pinocytic activity were predicted when the levels of P. emblica, P. nigrum, and W. somnifera was at the optimal level. Individually, a dose of P. nigrum up to 41 mg increased splenocyte proliferation and decreased pinocytic activity, while, after this level, splenocyte proliferation was decreased, but no changes in pinocytic activity were measured. W. somnifera

individually did not cause any change in pinocytic activity but was directly proportional to the proliferation of splenocytes. Similarly, *T. cordifolia* on a lower dose caused an increase in the proliferation of splenocytes and *vice versa* for pinocytic activity.

The combination has shown a better antioxidant potential compared to individual extracts. A lower value of IC₅₀ (82.54 \pm 2.54 µg/ml) indicates a higher antioxidant activity of the combination. The plant extracts used in the polyherbal combination contained a higher amount of phenolics and flavonoids and may be responsible for antioxidant activity (Liu et al., 2009). The antioxidant potential exhibited by the developed combination might be due to the presence of secondary metabolites from selected plants. In particular, P. emblica contains hydrolyzable tannins with low molecular weight having a very strong antioxidant action (Ghosal et al., 1996; Singh et al., 2015), whereas W. somnifera contains withanolides, naturally occurring steroidal lactones having strong antioxidant properties (Devkar et al., 2014; Zahiruddin et al., 2020). Similarly, a strong antioxidant potential was also reported for the aqueous extract of T. cordifolia (Premanath and Lakshmidevi, 2010) and P. nigrum (Gülçin, 2005). Our findings strongly suggest that these plant materials are promising sources of natural antioxidants.

The developed polyherbal combination showed not only immunomodulatory activity in vitro but also potential immunomodulatory activity against cyclophosphamide-induced immunosuppressed mice. Cyclophosphamide is known to cause a significant reduction in WBC and lymphocyte count (Huyan et al., 2011), and in this study, the effects of the polyherbal combination was tested on cyclophosphamide-induced immunosuppressed mice. The impact of the developed polyherbal combination was evaluated on HGB, neutrophils, lymphocytes, WBC, RBC, and platelet counts in cyclophosphamide-induced immunosuppressed mice.

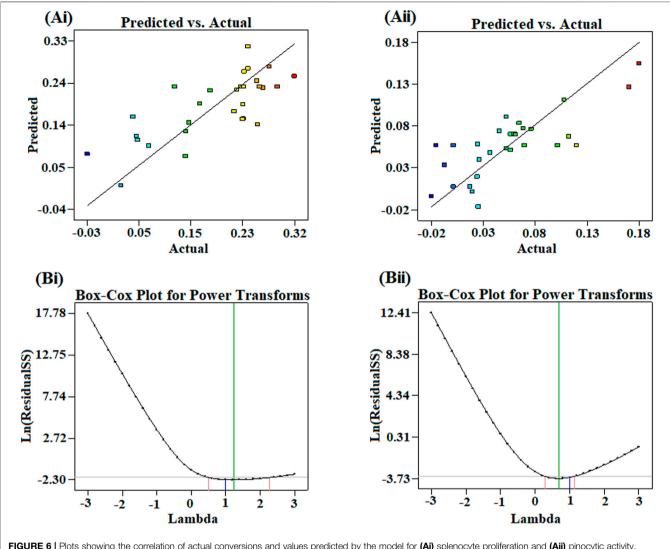


FIGURE 6 | Plots showing the correlation of actual conversions and values predicted by the model for (Ai) splenocyte proliferation and (Aii) pinocytic activity. Box-Cox plot showing optimized lambda for the transformation of (Bi) splenocyte proliferation and (Bii) pinocytic activity.

Lymphocyte, WBC, and platelet counts were significantly decreased upon cyclophosphamide treatment but reversed upon the treatment with the polyherbal combination. Even in healthy mice treated with the polyherbal combination, a slight increase in these cells was recorded.

WBCs are produced from the bone marrow, which is the most affected organ during immunosuppression therapy, as indicated by WBC and platelet counts (Vigila and Baskaran, 2008). Mice treated with cyclophosphamide showed a significant reduction in total platelet and WBC counts and recovered on treatment with both doses of combination. These results indicate that the herbal combination can modulate bone marrow activity, mainly suppression and stimulation, to counteract cyclophosphamide-induced myelosuppression. On the other hand, lymphocytes are a type of WBCs that are of fundamental significance. They regulate the specificity of the immune response to infectious microorganisms and other foreign bodies. Total lymphocyte counts were increased

significantly in mice of all groups treated with the developed polyherbal combination compared to negative control mice. Our results also showed that there was no significant change in the RBC count in any group of mice. For a proper immune system, there should be harmony in RBC and WBC counts (El Bishlawy, 1999), and the developed polyherbal combination maintained the harmony. The results indicated that the developed polyherbal combination is highly efficient in augmenting the immune responses by enhancing the population of T cells and B cells but not NK cells. Since T cells play an important role in regulating the immune response, being responsible for cell-mediated immunity, in a balanced immune system, rapid T-cell proliferation following antigen stimulus is governed by subsequent differentiation of T cells into effectors cells (Luckheeram et al., 2012). Modifications of WBCs and differential counts are important signs of immune response and were supported by enhanced CD4 and CD8 cell counts.

The results of the developed polyherbal combination supported the traditional claims of plants used for an immunomodulatory activity. Previously, aqueous extracts of these four plant materials were tested for their immune enhancing potential. For example, the aqueous extract of T. cordifolia can modulate the immune system by increasing the count of WBC, and the aqueous extract is superior to the alcoholic extract (Manjrekar et al., 2000). Similarly, the root extract of W. somnifera also proved its T-cell enhancement, splenocyte cell proliferation, and stimulation of phagocytosis of macrophages (Davis and Kuttan, 2000). It has been also proven that the aqueous extract of *P. nigrum* causes splenocyte proliferation in a dose-dependent manner (Majdalawieh and Carr, 2010), and this report agrees with our in vitro results. The aqueous extract of these plant materials contains phenolic and flavonoids as the major group of constituents. These phenolic metabolites can promote nonspecific immune function, proliferate splenocytes, and enhance humoral immune responses and NK cell activity (Liu

We have screened this developed polyherbal combination and the individual extracts for the identification of major metabolites. Of the identified metabolites, several metabolites were previously tested for immunomodulatory activity. Among different metabolites, cordifolioside A and tinocordiside present in the extract of *T. cordifolia* showed immunomodulatory activity (Sharma et al., 2012), and these compounds are also found in our developed polyherbal combination.

Gallic acid (Rt 2.08) and ellagic acid (Rt 4.13) have been reported to stimulate immune cells and can improve the immune cell population damaged by cyclophosphamide. Moreover, these compounds were both found in the extracts and also in the developed combination. Withaferin A $(R_t 5.25)$ and withanolide $(R_t 9.09)$ are the major metabolites found in the aqueous extract of W. somnifera and in the developed combination (Furmanowa et al., 2001). These two compounds activated phagocytosis and peritoneal macrophages, increased the secretion of lysosomal enzymes, and selectively enhanced the CD4 and CD8 counts (Bani et al., 2006). Asperuloside (Rt 9.47) increased the T-cell count, followed by increased secretion of interferon (IFN)-y and tumor necrosis factor (TNF)-α, thereby enhancing the function of immune effector cells via induction of inflammatory cytokines (Chan et al., 2020). Asperuloside was found in P. emblica and W. somnifera extracts as well as in the developed polyherbal combination. Caffeic acid phenethyl ester (Rt 2.92) was found in all the extracts except P. nigrum. It increased T-lymphocyte production and enhanced the T cell-mediated immune response (Park et al., 2004). While caffeic acid (Rt 4.59) was present in all the extracts and also in the developed combination, it can increase NK cell activation and proliferate splenic T cells (Kilani-Jaziri et al., 2017).

Several formulations composed of these plant materials are available in the market claiming immunomodulatory activity. We have compared their activity with the results of the proposed combination on the basis of the reported literature. Gnanasekaran et al. (2015) reported that Chyawanprash could increase the total leukocyte in cyclophosphamide-induced immunosuppressed mice but not up to the normal level. Treatment with the developed cyclophosphamide-induced combination of immunosuppressed mice resulted in complete normalization of the total leukocyte count. Septilin, a well-known and widely used compound formulation in India, is composed of two powders and six plant extracts, in which T. cordifolia and P. emblica are the major ones. This formulation does cause the proliferation of splenocytes and increase in the lymphocyte count (Daswani and Yegnanarayan, 2002). But the level of significance is lower than the results obtained using our polyherbal combination. However, a real comparative analysis is ongoing in our laboratory. From these preliminary results, we can say that the developed polyherbal combination is better in terms of both in vitro and in vivo immune stimulating activity. The developed combination has been characterized by measuring the metabolomic content, thereby identifying the active constituents.

CONCLUSIONS AND PERSPECTIVES

The developed polyherbal combination containing P. emblica, P. nigrum, W. somnifera, and T. cordifolia exhibited potent immunomodulatory activity through stimulating pinocytosis and splenocyte proliferation. It also enhanced the subsets of various immune cells, mainly NK cells, B cells, CD4, and CD8 T cells, in cyclophosphamide-induced immunosuppressed mice. This immunomodulatory potential may be attributed to the presence of a group of metabolites in the polyherbal combination such as phenols, flavonoids, tannins, alkaloids, and glycosides exhibiting multiple mechanisms. The metabolomic profiling of the extracts and polyherbal combination through UPLC-MS revealed the presence of more than 180 metabolites, and PCA showed a wide array of metabolites, which are distributed in different quadrants. The polyherbal combination studied can be explored for its protective potential against various immunosuppressing clinical conditions and microbial attacks. Further research for its complete efficacy evaluation, development of its dosage form for its utilization in health care, and its in-depth metabolic characterization are in progress. It would be also interesting to check the pharmacokinetic profiling of the developed polyherbal combination with respect to specific marker constituents present in it.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation, to any qualified researcher.

ETHICS STATEMENT

The animal study was reviewed and approved by IAEC, Jamia Hamdard, New Delhi, India (Registration No. 173/GO/RE/S/2000/CPCSEA).

AUTHOR CONTRIBUTIONS

SZ contributed to conceptualization, literature review, experimental studies, data curation, data interpretation, and writing the original drafts. AP and MI contributed to experimental studies and data curation. WK contributed to the interpretation of data and article preparation. MW contributed to statistical analysis. RP contributed to the investigation and article

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SUPPLEMENTARY MATERIAL

The supplementary material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphar.2021.647244/full#supplementary-material

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