

Novel targets for chronic inflammatory diseases: Focus on therapeutic drugs and natural compounds, volume II

Edited by

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Novel targets for chronic inflammatory diseases: Focus on therapeutic drugs and natural compounds, volume II

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Advances of the small molecule drugs regulating fibroblast-like synovial proliferation for rheumatoid arthritis

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Rheumatoid arthritis (RA) is a type of chronic autoimmune and inflammatory disease. In the pathological process of RA, the alteration of fibroblast-like synoviocyte (FLS) and its related factors is the main influence in the clinic and fundamental research. In RA, FLS exhibits a uniquely aggressive phenotype, leading to synovial hyperplasia, destruction of the cartilage and bone, and a pro-inflammatory environment in the synovial tissue for perpetuation and progression. Evidently, it is a highly promising way to target the pathological function of FLS for new anti-RA drugs. Based on this, we summed up the pathological mechanism of RA-FLS and reviewed the recent progress of small molecule drugs, including the synthetic small molecule compounds and natural products targeting RA-FLS. In the end, there were some views for further action. Compared with MAPK and NF- κ B signaling pathways, the JAK/STAT signaling pathway has great potential for research as targets. A small number of synthetic small molecule compounds have entered the clinic to treat RA and are often used in combination with other drugs. Meanwhile, most natural products are currently in the experimental stage, not the clinical trial stage, such as triptolide. There is an urgent need to unrelentingly develop new agents for RA.

KEYWORDS

rheumatoid arthritis, fibroblast-like synoviocytes, signaling pathways, small molecule drug, natural products

1 Introduction

Rheumatoid arthritis (RA) is a type of autoimmune joint disease. It often occurs in women and the elderly. RA might affect 0.5%–1% of the global population (Zhang et al., 2022). Among the multiple factors, genetic and autoimmune along with environmental factors might be the primary causes. It shows the clinical presentation of joint pain, thickening of the synovial membrane, pannus formation, and infiltration of various inflammatory cells in the joint space, leading to the damage of the cartilage as well as bone tissue, even remarkably joint deformity and dysfunction (Smolen et al., 2018). A lot of attention is paid to the treatment of RA because it has high morbidity, might lead to disability, and has poor prognosis (Davis et al., 2012; Almutairi et al., 2021). Currently, non-steroidal anti-inflammatory drugs (NSAIDs), disease-modifying anti-rheumatic drugs

(DMARDs) (synthetic or biologic agents), and glucocorticoids (Lampropoulos et al., 2015; Zhang et al., 2022) are popular in the treatment of RA. With the use of NSAIDs, the risk of cardiovascular disease might occur as well as gastrointestinal side effects, so a comprehensive evaluation is needed (O'Shea et al., 2013). DMARDs such as methotrexate (MTX), while suppressing inflammation and joint destruction, might cause nausea, anorexia, stomatitis, alopecia, myelosuppression, and even liver and pulmonary toxicity in severe cases, which requires careful monitoring. In addition, there are also problems of high expense and gastrointestinal adverse effects for DMARDs (Zhang et al., 2019). Biologic disease-modifying anti-rheumatic drugs (bDMARDs) show therapeutic effects for RA, but there are some individual differences because of different genetic backgrounds and environmental stimuli (Lampropoulos et al., 2015), and they do not cure the disease (Yamada, 2023). There is an urgent need to continuously develop new anti-RA drugs.

The synovium is considered to be a structure of connective soft-tissue membrane located in the joint cavity and the fibrocartilage, around arthrosis to provide nutrition and lubrication (Jay et al., 2000). The fibroblast-like synoviocytes (FLSs) are highly specialized mesenchymal cells found in the synovial membrane. In normal physiological regulation, FLS produces joint lubricants, for example, hyaluronic acid which nourishes the cartilage surface and shapes the synovial extracellular matrix (ECM). However, in RA, FLS exhibits a distinctive aggressive phenotype, with this aggressive behavior toward the ECM further exacerbating joint damage (Nygaard and Firestein, 2020). For this reason, one potential strategy for treating RA is the creation of medicines that target FLS (Bartok and Firestein, 2010). It is important to note that several of their monomers appear to have a positive impact on preventing arthritic synovial hyperplasia. They are mainly related to the induction of apoptosis and the inhibition of FLS proliferation. In this review, taking the state of FLS as a starting point, we summarize and discuss the literature on the small molecule drugs of FLS from PubMed, Embase, and other databases in the recent 3 years until 28 February 2023. Specific keywords used are "RA," "FLS," "MAPK," "NF- κ B," "JAK/STAT," "Wnt," and "signaling pathways." The small molecule drugs contain organic compounds with low molecular weights, typically ≤ 1000 Da. Also, these include both synthetic compounds and natural products derived mainly from plants and animals. Publications with incomplete data or conclusions and those not directly related to RA and small molecule compounds are excluded. Here, first, there is an introduction of the pathological mechanisms of RA-FLS. Second, according to the signaling pathways controlling the abnormal behavior of FLS, small molecule drugs of related pathways, especially drugs with high anti-RA-FLS potential, are analyzed in depth. Finally, we list our comments, which we hope will provide directions to developing targeted anti-rheumatic drugs for clinics.

2 FLS involved in the pathogenesis of RA

In RA, FLS proliferation releases several anti-inflammatory cytokines and growth factors, among which are tumor necrosis factor (TNF), interleukin (IL) (such as IL-6, IL-1 β , and IL-17), chemokines, and inflammatory enzymes [such as nitric oxide

synthase (NOS) and cyclooxygenase-2 (COX-2)]. Meanwhile, it provides the inflammatory microenvironment and potentially contributes to the initiation of chronic inflammation in the preliminary stage of RA. In addition, FLS produces large amounts of receptor activator of NF- κ B ligand (RANKL), vascular endothelial growth factor (VEGF), matrix metalloproteinases (MMPs), and so on, which causes synovial hyperplasia and arthritic joint destruction (Wang et al., 2012). Worse still, the activated FLS migrates to the cartilage and bone. This migration occurs not only at local sites but also through the bloodstream into distant areas and joints, destroying the cartilage, activating osteoclasts, and enhancing joint destruction in RA (Neumann et al., 2010; Hu et al., 2019). Here, we review the pathological mechanisms of RA from the three perspectives shown in Figure 1: synovial hyperplasia, joint damage, and immune inflammation.

2.1 Synovial hyperplasia

The synovium of RA exhibits endothelial hyperplasia and transformation into pannus tissue that destroys the articular cartilage and bone, with occasional lymphatic-like aggregates. A large number of inflammatory cytokines (IL-1 β , TNF- α , etc.) stimulate FLS to proliferate abnormally and exhibit anti-apoptosis. The imbalance between FLS anti-apoptotic and pro-apoptotic factors increases the number of FLS considerably, which directly leads to synovial hyperplasia. The FLS in the synovial lining layer is increased from the normal 1–3 to 10–15 cell layers (Neumann et al., 2010). The proliferated FLS develops into lymphoid-like structures, interacting with immune cells to form lymphoid organs and releasing pro-inflammatory factors and inflammatory mediators. Growth factors, such as platelet-derived growth factor (PDGF), transforming growth factor- β (TGF- β), and stimulatory cytokines in the synovial tissue, induce FLS proliferation through the activation of the signaling pathway. Along with the *in situ* proliferative capacity of FLS, the expression of anti-apoptotic molecules is also increased. The anti-apoptotic molecule FLICE inhibitory protein (FLIP) suppresses intracellular apoptosis-triggering cystatase-8, decreasing apoptosis and causing synovial proliferation (Bartok and Firestein, 2010).

2.2 Joint damage

Cartilage and bone destruction are hallmarks of RA. MMPs expressed by FLS degrade the chondral matrix, leading to impaired nutrient supply to the articular cartilage and tissue joint destruction.

2.2.1 Chondral matrix degradation

FLS mediates the overproduction of MMPs that interrupts the joint tissue, which contains a structure abundant in collagen and facilitates FLS infestation into the cartilage surface. Mediated by pro-inflammatory cytokines and toll-like receptors (TLRs), FLS upregulates the expression of MMPs, which activate osteoclasts and directly erode the bone, causing cartilage and bone destruction. Activated osteoclasts can reduce bone mass in the

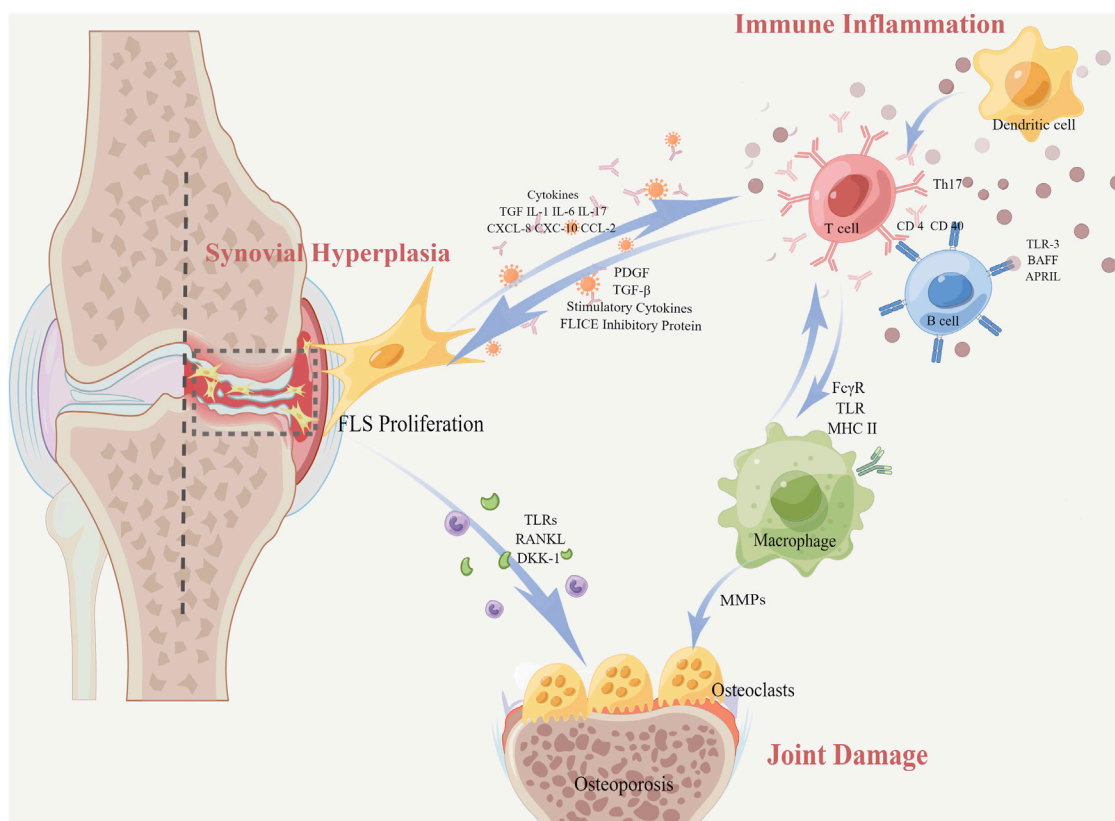


FIGURE 1

Pathological mechanisms of RA (In RA, the proliferation of FLS resulting from synovial hyperplasia releases various anti-inflammatory cytokines and growth factors. Meanwhile, the interaction between FLS and immune cells causes a transformation of regular FLS into an aggressive phenotype, resulting in an abnormal situation of T-cell and B-cell functions related to immune inflammation. Furthermore, FLS secretes pro-inflammatory cytokines into the joint space and invades the adjacent bone tissue through migration, inducing bone erosion and joint destruction. Macrophages also differentiate directly into mature osteoclasts).

periarticular bone early in the lesion, leading to osteoporosis. In addition, the extra expression of MMPs upregulates the levels of inflammatory factors and soluble mediators in the synovial tissue. Also, the factors are bound to receptors of MAPK, JAK/STAT, etc., signaling pathways, promoting and maintaining joint inflammation (Firestein, 2003).

2.2.2 Bone destruction

The migration of FLS is also the process of bone destruction. Due to the cytokines, FLS can migrate into the cartilage and bone, thus exacerbating cartilage destruction (Zeng et al., 2017). FLS produces RANKL in the cartilage or bone. Then, RANKL binds to the receptor activator of NF- κ B (RANK) on osteoclast precursors, inducing osteoclast differentiation, activation, and production. A large number of osteoclasts erode the surface of the adjacent articular cartilage membrane and induce bone destruction. Not only that, RA-FLS hinders the recovery process of bone erosion by hindering osteoblast activation through the secretion of dickkopf-1 (DKK-1). DKK-1 is a crucial regulatory molecule within the Wnt pathway, acting as an inhibitor of osteoclast function (Miao et al., 2013). Under specific microenvironmental conditions, macrophages can also differentiate directly into mature osteoclasts. In addition, inflammatory macrophages are a consistent source of matrix

metalloproteinases, such as MMP-1, MMP-3, MMP-7, MMP-10, MMP-12, MMP-14, and MMP-25, which participate in connective tissue transformation and joint surface erosion observed in RA.

2.3 Immune inflammation

FLS are known to contribute significantly to RA by secreting inflammatory chemokines that interact with synovial infiltrating cells. The chemokines secreted by FLS, including, CXC motif chemokine 8 (CXCL-8), CXCL-10, and CC motif chemokine ligand 2 (CCL2), can recruit a range of immune cells into the synovial tissue. Then, the inflammatory mediators, for example, IL, TNF- α , and TGF- β 1, from these immune cells in turn stimulate FLS activation, resulting in a vicious circle. Macrophages are constantly affected by inflammatory stimuli and participate in the development of chronic synovitis, bone erosion, and cartilage erosion. Macrophages express a lot of molecules on their surface, such as Fc-gamma receptors (Fc γ R), TLR, and the major histocompatibility complex class II (MHCII), which in turn, regulate their own activities, activate other cells in the local microenvironment, or attract immune cells outside the joint. TNF- α , IL-6, IL-1 β , IL-23, and a wide range of CXCL and CCL chemokines promote and maintain

inflammation by recruiting and activating polymorphonuclear leukocytes, T cells, B cells, or monocytes.

2.3.1 FLS and B cells

There is a bidirectional signaling between FLS and B cells. On one hand, FLS affects the maturation and growth of B cells by secreting cytokines. The etiology of autoimmune disorders involves both humoral immunity and B lymphocytes as significant contributors. The preservation of the B-cell pool and humoral immunity depend on the B-cell-activating factor of the TNF family (BAFF, also known as BLYS) and a proliferation-inducing ligand (APRIL). Taking TLR-3 as an example, TLR-3 triggers not only B-cell-activating BAFF but also APRIL. Both of them participate in the stimulation of B cells, thus prolonging B-cell survival (Bombardieri et al., 2011; Leah, 2011). On the other hand, B cells in turn induce the FLS inflammatory phenotype. In the FLS co-culture experiments with age-associated B cells (ABCs), ABCs induce FLS phenotype excitation through TNF- α inducing the activation of ERK1/2 and JAK-STAT1 signaling pathways, consequently promoting the persistence of RA (Qin et al., 2022).

2.3.2 FLS and T cells

T-cell infiltration and excessive proliferation of FLS are significantly upregulated in RA patients. Both interact during RA inflammation to perpetuate inflammation. RA-FLS can present peptides of inflammatory antigens to antigen-specific T cells, contributing to the auto-reactive immune response in RA (Tran et al., 2007). Then, FLS expresses adhesion molecules, transmitting signals to CD4 T cells, such as vascular cell adhesion molecule-1 (VCAM-1) and intercellular cell adhesion molecule-1 (ICAM-1). Finally, these adhesive molecules interact with integrins, for instance, lymphocyte function-associated antigen 1 (LFA-1), resulting in CD4 T-cell proliferation and IL-17 secretion and exacerbation of the inflammatory response (Mori et al., 2017). At the same time, macrophages express MHCII as antigen-presenting cells, thereby participating in the activation and recruitment of pathogenic T cells. So, there is also an interaction between T cells and FLS (Tran et al., 2008; Tu et al., 2022).

To sum up, FLS can secrete pro-inflammatory cytokines such as TNF- α , IL-1 β , IL-6, and MMP, in the joint space of RA patients and invade the adjacent bone tissue through migration, inducing bone erosion and joint destruction. The interaction between FLS and immune cells causes a transformation of regular FLS into an aggressive phenotype, resulting in abnormal T- and B-cell functions. Also, our body gradually loses its normal immune regulatory and protective ability (Ding et al., 2023). It is evident that FLS is the central effector cell in the pathogenesis. Given that there is no effective treatment targeted at FLS, the inhibition FLS-mediated pro-inflammatory response and subsequent tissue destruction seems to be a feasible strategy for RA (Nygaard and Firestein, 2020). In the next part, we summarize the results in the recent 3 years of small molecule drugs targeted at FLS.

3 Small molecule drugs regulating FLS

In the previous sections, we have clarified that RA-FLS are activated by multiple cytokines involved in the activation of FLS.

Targeted pathways of FLS might simultaneously block multiple signaling of cytokine receptors, inhibiting the activation, proliferation, and invasion of FLS and, thus, significantly controlling RA synovial inflammation and joint damage (Mavers et al., 2009; Wendling et al., 2010; Pan et al., 2016). Despite significant breakthroughs in RA therapy, many people with RA have persistent disease. The current RA therapy plans emphasize reducing T-cell and B-cell activity as well as cytokine signaling (Mahmoud et al., 2022). In RA, targeting signal transduction pathways is an emerging treatment option. According to the signaling pathway interacted with FLS, there are mainly MAPK, NF- κ B, JAK/STAT, PI3K/Akt, and Wnt signaling pathways in Figure 2. So, we present the drugs' research progress which regulates FLS function on the signaling pathways, including the small molecule compounds and natural products. It is aimed to explore promising novel drug development directions and broaden the path of novel targeted FLS.

3.1 Small molecule drugs targeting MAPK regulating FLS

The MAPK signaling pathway is associated with various kinases, such as P38, c-Jun N-terminal kinase (JNK), and extracellular regulated protein kinases (ERKs), which are involved in the proliferation, apoptosis, and migration of FLS, with the addition of cytokine secretion (Harigai et al., 2004; Tang et al., 2019). ERK is involved in the secretion of certain cytokines and cell proliferation and differentiation through the regulation of B-cell lymphoma 2 (Bcl-2). JNK decreases proteoglycan synthesis and enhances MMP-13 synthesis, which are necessary for bone deterioration and joint inflammation. p38 is associated with the cytokine secretion of MMP. Through inhibiting p38, MMP reduces cartilage degradation and inhibits osteoclast formation. Additionally, the MAPK pathway contributes to the FLS's increase in TNF- α expression, amplifying inflammatory signals, inducing FLS proliferation, aggravating inflammation, and damaging joints (Zuo et al., 2015; Kadkhoda et al., 2016). An increasing number of studies have shown that the MAPK pathway is activated in immune and autoimmune response conditions, regulating the cell responses of division, differentiation, apoptosis, inflammation, and stress and also participating in the activation of FLS (Müller-Ladner et al., 2007; Bustamante et al., 2017). In addition, MAPK activates downstream transcription factors that promote synovial cell proliferation and chondrocyte apoptosis. It also leads to high expression of multiple MMPs in synovial cells and chondrocytes and overhydrolysis of the extracellular matrix, resulting in joint damage. Therefore, MAPK is one of the most studied targets to inhibit RA-FLS (Wang et al., 2010).

Here, we review the synthetic small molecule compounds and natural products in the recent 3 years targeted to MAPK for FLS in Table 1, and the natural products regulating MAPK are shown in Figure 3. It is important to note that the majority of drugs affected numerous signaling pathways and multiple targets. As an MAPK downstream effector, p38 is considered

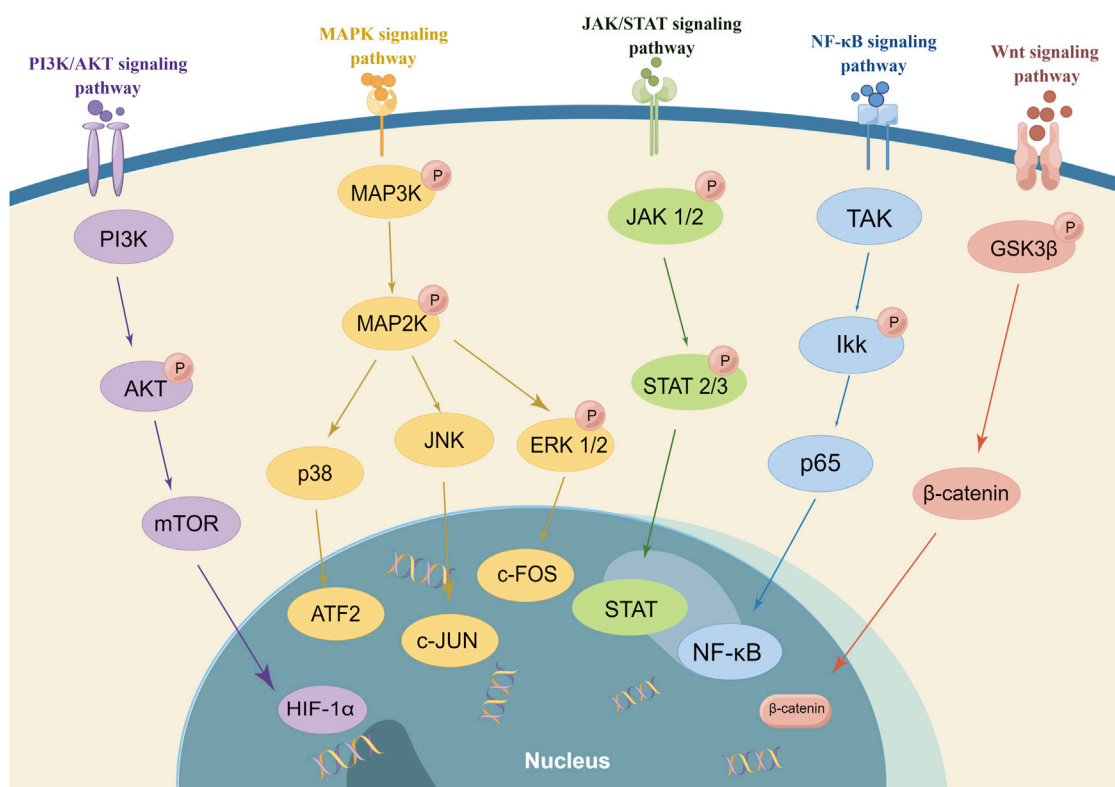


FIGURE 2

Signaling pathway regulating FLS (In RA, targeting signal transduction pathways is an emerging treatment option. The small molecule compounds and natural products interact with FLS in the different signaling pathways. There are mainly MAPK, NF-κB, JAK/STAT, PI3K/Akt, and Wnt signaling pathways. It is important to note that the majority of drugs affected numerous signaling pathways and multiple targets).

a possible target for RA, but only few p38 inhibitors have been tested in humans. Tacrolimus as a macrolide calcineurin inhibitor immunosuppressant drug decreased the production of angiotensin-1 (Ang1), tyrosine-protein kinase receptor (Tie-2), and VEGF in human FLS by preventing the activation of the IL-1β-mediated JNK and p38 MAPK pathways. Sugiura et al.'s (2020) study was very interesting. They found that glycogen synthase kinase 3 (GSK-3) inhibitors significantly reduced synovial fibroblast migration after 72 h and decreased Akt phosphorylation [Ser (473)] after 48 h *in vitro*, which might have therapeutic efficacy targeting the invasion and migration of synovial fibroblasts. Also, 3',3'-diindolylmethane exhibited the possibility of anti-RA-FLS activity *in vivo* and *in vitro* (Du et al., 2019). The small molecule compounds reported in recent years that could alter FLS *in vivo* and *in vitro* were elutriated extirpate, dasatinib, 4-phenylbutyric acid, and 3-(4-hydroxy-3-methoxyphenyl)-1-3-[1]-phenyl-propenone. Unfortunately, these medications are still in the laboratory stage. Because of their poor performance, p38 inhibitors have limited efficacy in RA treatment. Also, blocking p38's downstream had a compensatory effect on other kinases, so alternative options for p38 have been progressively explored (Guma et al., 2012). Regulation of MAPK kinases upstream of p38, the human mitogen-activated protein kinase kinase (MKK), such as MKK6 and MKK1, could selectively block the production of MMPs and pro-

inflammatory cytokines in FLS (Hammaker et al., 2012). In addition, ubiquitin D might be considered a possible therapeutic target for RA-FLS (Chen et al., 2023).

In natural products in Table 1 and Figure 3, alkaloids and flavonoids were more frequently reported and studied for their effects on the MAPK signaling pathway of FLS. Other categories, such as iridoids and saponins, were also found to have an impact. It is well known that flavonoids possess anti-oxidant and anti-inflammatory properties. Flavonoids can inhibit the inflammatory response and reduce the symptoms of inflammation while scavenging free radicals, reducing oxidative stress, and protecting cells from oxidative damage. Flavonoids usually inhibit FLS proliferation, migration, and invasion by inhibiting p38 and JNK. To our surprise, alkaloids also showed up significantly in the treatment of FLS. Preparations of berberine and paclitaxel were available for clinical use, but they have no indication for the treatment of RA.

Triptolide and tetrandrine from *Tripterygium wilfordii* Hook F. and *Stephania tetrandra* root, respectively, have anti-rheumatic effects in the classic sense. Tripterygium glycoside preparations have been clinically used for the treatment of RA. As the representative, we concentrate on triptolide, which has been studied more and has been proven to have multiple signaling pathways. The treatment with triptolide decreased the expression of phosphorylated JNK that TNF-α-produced, but it had no effect on the expression of phosphorylated p38 or

TABLE 1 Small molecule drugs targeting MAPK regulating FLS.

Name	Source	Targets/ signaling pathways	Estimate	References
The synthetic small molecule compounds				
GSK-3 inhibitors (6-bromoindirubin-3'-oxime and thiadiazolidinone-8)	Serine/threonine protein kinase	JNK, p38, NF-κB	Experimental: NF-κB ↓	Kwon et al. (2014); Sugiura et al. (2020)
			The phosphorylated JNK, c-Jun, ATF-2, p38 ↓	
			IL-6 ↓	
			IL-10 ↑	
Tacrolimus	Macrolide antibiotics from <i>Streptomyces</i>	JNK, p38	Clinical: showed higher retention rates combined with bDMARDs	Choe et al. (2012); Kaneko et al. (2021); Terabe et al. (2023)
			Adverse events stable in long-term observation	
			Effective with acceptable safety	
			Experimental: the expressions of Ang-1, Tie-2, VEGF ↓	
3'3-Diindolylmethane	The main product of indole-3-carbinol oligomerization catalyzed by acid	p38, JNK, Akt, mTOR	Experimental: proliferation, migration, and invasion of RA-FLS <i>in vitro</i> ↓	Du et al. (2019)
			MMP-2, MMP-3, MMP-8, and MMP-9 ↓ p-p38, JNK ↓	
			Akt, mTOR ↓	
			Pro-inflammatory cytokines and arthritis severity in mice ↓	
Telotristat etiprate	A tryptophan hydroxylase inhibitor	MAPK	Experimental: migration and invasion of RA-FLS <i>in vitro</i> ↓	Zhang et al. (2023)
			Targeting LGALS3	
Dasatinib	A Src kinase inhibitor	MAPK, STATs	Experimental: Src, Fyn, MAPK, STATs ↓	Yalcin Kehribar et al. (2021); Min et al. (2023)
			MMP-1, MMP-3, MMP-13 in FLS ↓	
4-Phenylbutyric acid	An HDAC inhibitor	MAPK, NF-κB	Experimental: p-MAPK, p-NF-κB ↓	Choi et al. (2021)
			MMP-1, MMP-3, COX-2 ↓	
			Endoplasmic reticulum stress ↓	
3-(4-Hydroxy-3-methoxy-phenyl)-1-3-[1]-phenyl-propenone	A benzylideneacetophenone derivative	MAPK	Experimental: IL-8, IL-6, PGE (2) ↓	Sur et al. (2020)
			Reducing the inflammation in the knee joints in C/K-arthritic rats	
The natural products				
Fangchinoline	A bisbenzylisoquinoline alkaloid from <i>Stephania tetrandra</i>	MAPK, NF-κB	Experimental: inflammatory cytokine secretion and ROS in human FLS ↓	Villa et al. (2020)
			Phosphorylation of the MAPK and NF-κB pathway in human FLS ↓	
Berberine	An alkaloid from <i>Coptis chinensis</i>	PI3K/Akt, Wnt, RAS/MAPK/FOXO/ HIF-1	Clinical: no indication for treatment of RA	Wang et al. (2019); Shen et al. (2020); Sujitha et al. (2020); Li et al. (2023); Li et al. (2023)
			Experimental: LRP5 protein ↓	
			β-Catenin transcription ↓ p38/ ERK ↓	
			Proliferation and adhesion of FLS ↓	
			MMP-1, MMP-3, RANKL, TNF-α ↓	

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TABLE 1 (Continued) Small molecule drugs targeting MAPK regulating FLS.

Name	Source	Targets/ signaling pathways	Estimate	References
Paclitaxel	An alkaloid from <i>Taxus chinensis</i>	MAPK, Akt/mTOR	Clinical: no indication for treatment of RA	Chen et al. (2021)
			Experimental: FLS migration dose dependently ↓	
			IL-6, IL-8, RANKL ↓	
			MMP-8, MMP-9 gene transcription ↓ p-ERK1/2 ↓	
			p-JNK ↓	
			Akt, p70S6K, 4EBP1, HIF-1α ↓	
Peimine	A steroidal alkaloid from <i>Fritillaria</i>	ERK, JNK, p38	Experimental: TNF-α induced destructive behaviors in MAPK for FLS↓	Zhou et al. (2022)
			RANKL-induced osteoclast formation ↓	
			Bone-resorption function ↓	
Tetrandrine	An alkaloid from <i>Stephania tetrandra</i> root	NF-κB, Ca ₂ (+), PI3K/Akt, MAPK	Experimental: Rac1, Cdc42, RhoA ↓	Lv et al. (2015); Zhong et al. (2019)
			MMP-2/9, F-actin, FAK↓	
			RANKL-induced osteoclastogenesis ↓	
Dehydroevodiamine	A quinazoline alkaloid from <i>Evodiae Fructus</i>	MAPK	Experimental: pro-inflammatory factors in AIA rats ↓	Dai et al. (2022)
			MMP-1, MMP-3 ↓ p-p38, p-JNK, and p-ERK ↓	
Tomatidine	A steroidal alkaloid from the Solanaceae family	MAPK, NF-κB	Experimental: proliferation and migration of FLS ↓	Yu et al. (2021)
			Synovial inflammation and joint destruction in CIA rats ↑	
			IL-1β, IL-6, TNF-α ↓	
			MMP-9, RANKL ↓	
Benzoylaconitine	An alkaloid from <i>Aconitum</i>	MAPK, Akt, NF-κB	Experimental: IL-6, IL-8 ↓	Yu et al. (2020)
			MAPK, p-Akt ↓	
			Degradation of IκB α↓ p-p65 and nuclear transposition ↓	
Kaempferol	A flavonoid from <i>Kaempferol galanga</i> L.	ERK-1/2, p38, JNK, NF-κB	Experimental: MAPK activation ↓, instead of altering TNF-α receptor activation	Yoon et al. (2013); Pan et al. (2018)
			Phosphorylation of ERK-1/2, p38, JNK ↓	
			NF-κB ↓	
Orientin	A flavonoid from <i>P. orientale</i>	p38, ERK	Experimental: viability, migration as well as invasion of FLS ↓	Ji and Xu (2022)
			TNFα-induced inflammatory makers ↓	

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TABLE 1 (Continued) Small molecule drugs targeting MAPK regulating FLS.

Name	Source	Targets/ signaling pathways	Estimate	References
Apigenin-4'-O- α -L-rhamnoside	A flavonoid from apigenin derivative	MAPK	Experimental: migration of FLS ↓	Cao et al. (2022)
			MMP-1, MMP3, RANKL, TNF- α ↓	
			MAPK1, HRAS, ATF-2, p38, JNK ↓	
Naringin	A flavonoid from citrus fruits	PI3K/Akt, ERK	Experimental: inflammation, MMPs ↓	Aihaiti et al. (2021)
			Apoptosis of FLS↑ the activation of caspase-3 ↑	
			Bax/Bcl-2 ↑ p- Akt, p-ERK ↓	
Liquiritin	A flavonoid from the roots of <i>Glycyrrhiza uralensis</i>	JNK, P38	Experimental: FLS proliferation ↓	Zhai et al. (2019)
			DNA fragmentation in the nucleus ↑	
			Altering the potential of the mitochondrial membrane	
			Bcl-2/Bax ratio ↓	
			VEGF ↓ p-JNK, p-p38 ↓	
Neohesperidin	A flavanone glycoside from citrus fruits	MAPK	Experimental: IL-1 β , IL-6, IL-8, TNF- α , MMP-3, MMP-9 and MMP-13 in FLSs ↓	Wang et al. (2021)
			MAPK ↓	
			ROS induced by TNF- α ↓	
Ononin	An isoflavone glycoside from the fruit of <i>Cnidium monnieri</i> (L.) cusson	NF- κ B, MAPK	Experimental: TNF- α mediated cells viability of FLS and MH7A ↓	Meng et al. (2021)
			Cell apoptosis ↑	
			IL-1 β , IL-6 ↓	
Cyanidin	An anthocyanidin from grapes, bilberry, blackberry, etc.	p38, STAT-3	Experimental: IL-17A induced the migration of monocytes from AA rats ↓	Samarpita and Rasool (2021); Samarpita et al. (2020)
			HSP27, CCR7, CXCR4 ↓	
			RANKL ↓	
			OPG ↑ p38 MAPK ↓	
Cyanidin-3-glucoside	An anthocyanin from berries	p38, ERK and JNK, NF- κ B	Experimental: TNF- α , IL-1 β , IL-6 ↓ p65 ↓	Sun and Li (2018)
			Phosphorylation of I κ B α , p38, ERK, JNK ↓	
Paris saponin VII Chonglou	A steroidal saponin from <i>Trillium tschonoskii</i> Maxim.	JNK, p38	Experimental: FLS invasion via managing the mitochondrial apoptosis, MAPK pathway	Meng et al. (2021)
			Improving histopathological changes	
			TNF- α , IL-1 β , IL-6 ↓	
			Modulating the expressions of apoptosis proteins in AIA rats	

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TABLE 1 (Continued) Small molecule drugs targeting MAPK regulating FLS.

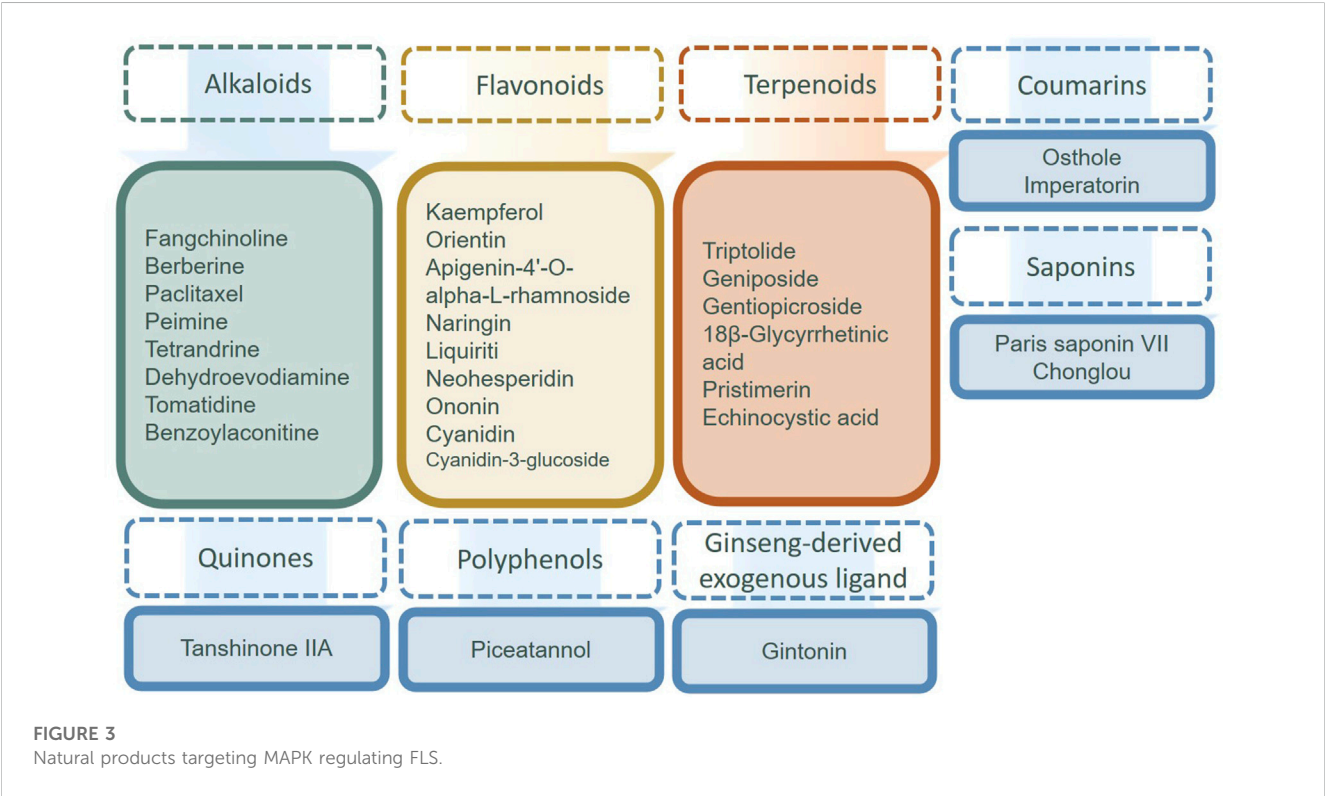
Name	Source	Targets/ signaling pathways	Estimate	References
Gintonin	A ginseng-derived exogenous ligand of lysophosphatidic acid	MAPK, NF-κB	Experimental: iNOS, IL-6, TNF-α, COX-2↓	Kim et al. (2021); Kim et al. (2021)
			NF-κB/p65 into the nucleus ↓	
Triptolide	An epoxide diterpene lactone from <i>Tripterygium wilfordii</i> Hook F.	JNK, MAPK8, PI3K/Akt	Experimental: p-JNK ↓	Yang et al. (2016); Xie et al. (2019); Song et al. (2020)
			The polymerization of F-actin ↓	
			The activation of MMP-9 ↓	
			Activating autophagy	
Geniposide	An iridoid glycoside from <i>Gardenia jasminoides</i> Ellis fruit	JNK, ERK1/2 and p38; PI3K; Akt	Experimental: proliferation of FLS ↓	Li et al. (2018); Bu et al. (2022)
			IFN-γ, IL-17 ↓	
			IL-4, TGFβ1↑ p-JNK, p-ERK1/2, p-p38 ↓	
			p-PI3K, p-Akt ↑	
Gentiopicroside	A secoiridoid glycoside from <i>Gentiana macrophylla</i> Pall.	CD147, p38, NF-κB	Experimental: proliferation of FLS ↓	Jia et al. (2022)
			MMP secretion↓	
			Regulating the CD147/p38/NF-κB pathway, p38, IκB α, and p65 ↓	
18β-Glycyrrhetic acid	A triterpene glycoside from <i>Glycyrrhiza</i>	MAPK, NF-κB	Experimental: IL-1β, IL-6, COX-2 in MH7A ↓	Feng et al. (2021)
			Cell viability	
			Cell apoptosis and G1 phase cell cycle arrest <i>in vitro</i> ↑	
			FOXO3 ↑	
			Liver damage caused by collagen or MTX <i>in vivo</i> ↓	
			Inflammation and proliferation in FLS ↓	
Pristimerin	A triterpenoid from Celastraceae and Hippocrateaceae families	MAPK/Erk1/2, PI3K/Akt	Experimental: viability and migration of FLS ↓	Lv et al. (2022)
			TNF-α, NO, p-Akt, p-ERK ↓	
Echinocystic acid	A pentacyclic triterpene from <i>Gleditsia sinensis</i>	MAPK, NF-κB	Experimental: arthritis symptoms in SKG mice ↓	Cheng et al. (2022)
			TNF-α, IL -6, IL-1β ↓	
			P-STAT3 ↓	
			MAPK, NF-κB	
Osthole	A coumarin from <i>Cnidium monnieri</i> and <i>Angelica pubescens</i>	NF-κB, MAPK	Experimental: IL-1β, TNF-α, IL-6 ↓	Xu et al. (2018); Lin et al. (2023)
			Proliferation and migration ↓	
			TGM2/Myc/WTAP-positive feedback circuit ↓	
Imperatorin	A coumarin from Umbelliferae	p38, ERK NF-κB	Experimental: proliferation and migration of FLS ↓	Lin et al. (2022)
			TNF-α, IL-6, and IL-8 ↓ p38, ERK ↓	
			p-IκBa ↓	

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TABLE 1 (Continued) Small molecule drugs targeting MAPK regulating FLS.

Name	Source	Targets/ signaling pathways	Estimate	References
Tanshinone IIA	A diterpene quinone from <i>Salvia miltiorrhiza</i> Bunge	MAPK, Akt/mTOR, HIF-1, and NF-κB	Experimental: FLS proliferation, migration, infiltration time, and dose dependently ↓	Du et al. (2020)
			MMPs, pro-inflammatory factors ↓	
Piceatannol	A derivative of resveratrol	MAPK, NF-κB	Experimental: Bax, cleaved caspase-3 ↑	Gao et al. (2022)
			PGE2, IL-6, IL-1β↓	
			COX-2 ↓	
			MMP-3, MMP-13 ↓	
			MAPK, NF-κB ↓	

↓: suppress, downregulate, inhibit, block, prevent, reduce, decrease; ↑: promote, upregulate, active, increase. mTOR, mammalian target of rapamycin; NFATc1, c-Fos and nuclear factor of activated T cells c1; ATF2, activating transcription factor-2; PGE2, prostaglandin E2; ROS, reactive oxygen species; HIF1, hypoxia-inducible factor 1; CIA, collagen-induced arthritis; IκB, inhibitor of κB; Bcl-2, B-cell lymphoma 2; Bax, Bcl-2-associated X; AA, adjuvant-induced arthritic; OPG, osteoprotegerin; MEKK, mitogen-activated protein kinase kinase; IKK, IκB kinase; TGM2, transglutaminase 2.



ERK (Yang et al., 2016) and reduced FLS migration and invasion by targeting the JNK/MAPK signaling pathway (Tang et al., 2020). Triptolide dramatically increased the p-Akt/Akt ratio, and inhibiting the PI3K/Akt signaling pathway in MH7A cells caused autophagy to be triggered, indicating that triptolide repressed autophagy via activating p-Akt/Akt (Xie et al., 2019). Other natural products, such as Paris saponin VII/Chonglou, geniposide, and gentiopicroside, shown in Table 1, also have the potential to regulate FLS against RA. However, it is currently in the experimental stage.

3.2 Small molecule drugs targeting NF-κB regulating FLS

As a major signaling transcription factor, NF-κB contributes to synovial inflammation, proliferation, and decay in bones in RA and regulates inflammatory gene expression and cell proliferation. Both innate and adaptive immune cells include NF-κB, which is a key mediator of the stimulation of pro-inflammatory genes (Liu et al., 2017). In a normal situation, NF-κB is bound to its repressor protein IκB and not activated. The nuclear-localization sequence (NLS) that

TABLE 2 Small molecule drugs targeting NF- κ B regulating FLS.

Name	Source	Targets/signaling pathways	Estimate	References
The synthetic small molecule compounds				
TAK-242	A TLR 4 antagonist	TLR4, TLR3; NF- κ B	Experimental: TLR4, TLR3 ↓	Samarpita et al. (2020)
			The migration of NF- κ B to the nucleus	
			IL-8, IL-1, MMP-7 ↓	
CKD-506	A HDAC inhibitor	NF- κ B	Experimental: MMP-1, MMP-3, IL-6, IL-8 ↓	Park et al. (2020)
			The proliferation of Teff ↓	
			Exerting a synergistic effect with MTX	
Oxymatrine hydrazone	Synthesized from oxidized bitter ginseng	MEK/1/2, NF- κ B	Experimental: IL-1 β , IL-6, IL-8 ↓	Zhang et al. (2021)
			MMP-1, MMP-13 ↓	
			MEK/1/2 and p65 phosphorylation ↓	
Paeoniflorin-6'-O-benzene sulfonate (CP-25)	A paeoniflorin derivative	NF- κ B, PI3K, GRK2	Experimental: the protein membrane expression and combination ↓	Wang et al. (2020); Wang et al. (2023)
Edaravone	Synthetic: 3-methyl-1-phenyl-2-pyrazolin-5-one	NF- κ B, MAPK	Clinical: no indication for the treatment of RA	Zhang et al. (2020); Liu et al. (2023)
			Experimental: altering the antioxidant factors, inflammatory mediators, and pro-inflammatory cytokines [NF- κ B, COX-2, and PGE (2)]	
			The level of cytokines and OPN, RANKL, and macrophage M-CSF ↓	
Roflumilast	An inhibitor of phosphodiesterase-4	NF- κ B	Clinical: no indication for the treatment of RA	Zhong et al. (2021)
			Experimental: ROS and MDA in MH7A cells ↓	
			IL-6, IL-8, TNF- α ↓	
			CCL5, CXCL9, CXCL10 ↓	
			MMP-1, MMP-13 ↓	
Sorafenib	A kinase inhibitor	NF- κ B, c-Jun	Clinical: no indication for treatment of RA	Wang et al. (2020)
			Experimental: apoptosis in AA FLSs ↓	
			Fas, caspase-3, Mcl-1 ↑	
			NF- κ B, C-Jun ↓	
Dexmedetomidine	A specific and selective alpha-2 adrenoceptor agonist	NF- κ B	Clinical: no indication for treatment of RA	Ji et al. (2020)
			Experimental: IL-1 β , IL-6, IL-17A, TNF- α , and P-P65 ↓	
			NLRCS ↓	
Alogliptin	An important selective dipeptidyl peptidase-4 inhibitor	NF- κ B	Clinical: no indication for the treatment of RA	Guo et al. (2020)
			Experimental: MMP-3, MMP-13, IL-6, IL-8, and TNF- α p- Jun, p-I κ B β , nuclear translocation of NF- κ B p65 ↓	

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TABLE 2 (Continued) Small molecule drugs targeting NF- κ B regulating FLS.

Name	Source	Targets/signaling pathways	Estimate	References
The natural products				
Diosmetin	A flavonoid from Rutaceae	NF- κ B	Experimental: proliferation of MH7A cells ↓	Chen et al. (2020)
			IL-1 β , IL-6, IL-8, MMP-1 ↓	
			and NF- κ B pathways activation ↓	
Mangiferin	A flavonoid of the bisphenirone family from mango leaves	ERK2, p38, NF- κ B	Experimental: MAPKs (ERK2 and p38), NF- κ B ↓	Luczkiewicz et al. (2014); Wang et al. (2021)
Icariin	A flavonoid glycoside from Epimedium Herba	NF- κ B	Experimental: TRIB1 ↑ by promoting Nrf2 expression regulating the TRIB1/TLR2/NF- κ B pathway	Wu et al. (2022)
Isoginkgetin	A biflavonoid from the leaves of the <i>Ginkgo biloba</i> tree	I κ B β , p65	Experimental: IL-1 β , IL-6, IL-8 ↓	Shao et al. (2022)
			Migration and invasion of FLS ↓ p-I κ B α , p-p65, MMP9 ↓	
Tectoridin	An isoflavone from dry rhizome of iris	TLR4/NLRP3/NF- κ B MAPK	Experimental: proliferation of FLS ↓	Huang et al. (2022); Niu et al. (2022)
			Cleaved caspase-3, Bax ↑	
			Bcl-2 ↓	
			Pro-inflammatory cytokines ↓	
			TLR4/NLRP3/NF- κ B ↓	
			ERK, JNK, p38 ↓	
Celastrol	A quinone-methylated triterpenoid from <i>Tripterygium wilfordii</i>	NF- κ B, Notch1, ERK, PI3K/Akt/mTOR	Experimental: NF- κ B pathway ↓	Gan et al. (2015); Yu et al. (2015); Doss et al. (2016); Fang et al. (2017); An et al. (2020); Yang et al. (2022)
			NLRP3 inflammasome activation ↓	
			ROS ↓	
			Changing some chemokine genes expression (CCL2, CXCL10, CXCL12, CCR2 and CXCR4)	
			SYK-MEK-ERK-NF- κ B signaling cascade ↓	
			Autophagy ↑	
			PI3K/Akt/mTOR ↓	
Aucubin	A monoterpenoid from asterids	NF- κ B	Experimental: inflammatory factors ↓	Zhang et al. (2022)
			Bone metabolism factors ↓ p-I κ B α , p-p65 ↓	
Heilaohuacid G	A triterpenoid from <i>Kadsura coccinea</i> /heilaohu	NF- κ B	Experimental: apoptosis and inflammatory reactions of FLS ↓	Yang et al. (2021); Yang et al. (2022)
Sinomenine	An alkaloid from <i>Sinomenium acutum</i>	NF- κ B	Experimental: adenosine receptor ↑	Zhou et al. (2017); Yi et al. (2021); Chen et al. (2011); Li et al. (2013); Zhou et al. (2015); Yao et al. (2017)
			NF- κ B activation via α 7nAChR ↓	
			Selective mPGES-1 expression ↓	
			TLR4/MyD88/NF- κ B signaling cascade ↓	

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TABLE 2 (Continued) Small molecule drugs targeting NF- κ B regulating FLS.

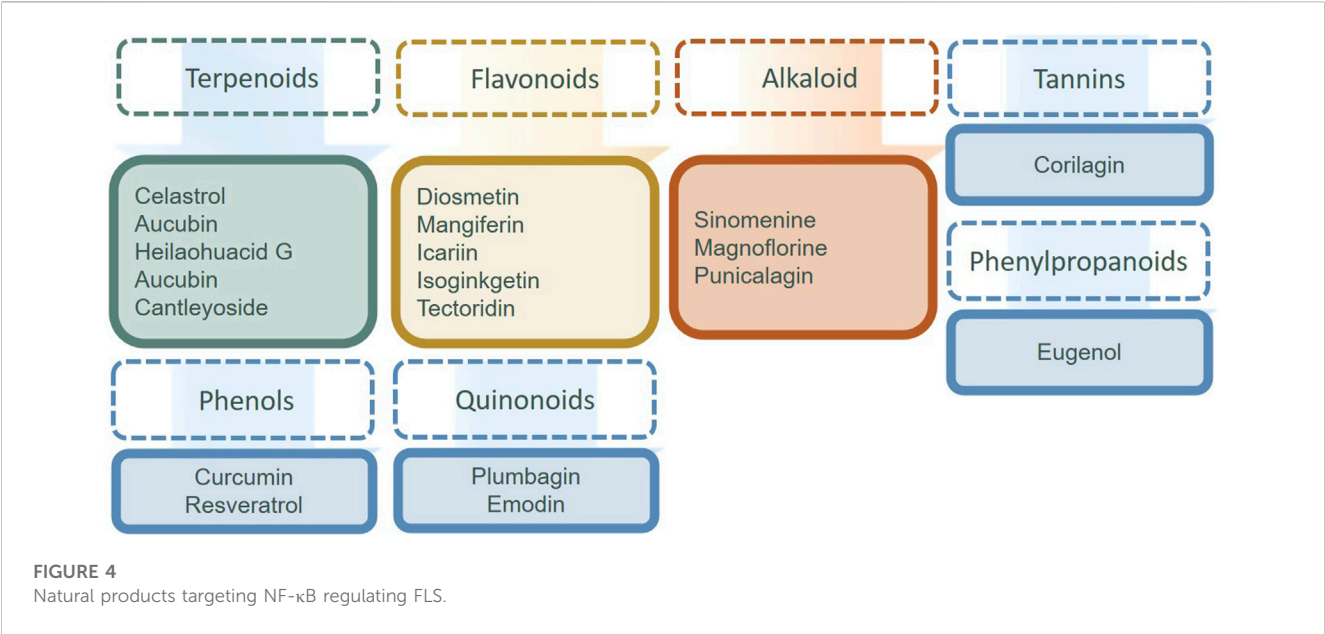
Name	Source	Targets/signaling pathways	Estimate	References
Magnoflorine	An alkaloid from <i>Clematis manshurica</i> Rupr.	PI3K/Akt/NF- κ B, Keap1-Nrf2/HO-1	Experimental: proliferation, migration, invasion, and reactive oxygen species levels of MH7A cells ↓	Shen et al. (2022)
			Bax ↑	
			Bcl-2 ↓ iNOS, COX-2, IL-6, IL-8, MMPs ↓	
			PI3K/Akt/NF- κ B ↓	
			Keap1-Nrf2/HO-1 ↑	
Curcumin	A polyphenol from turmeric, <i>curcuma longa</i>	NF- κ B, AP-1, and p38	Experimental: function of pro-inflammatory mediators ↓	Buhrmann et al. (2010); Shang et al. (2016); Mohammadian Haftcheshmeh et al. (2021); Xu et al. (2022)
			Osteoclastogenic potential	
			ERK1/2, p38, JNK ↓	
			RANK, c-Fos, NFATc1 levels ↓	
Punicalagin	A polyphenol from pomegranate juice	NF- κ B	Experimental: IL-1 β , IL-6, IL-8 and IL-17A ↓	Huang et al. (2021)
			MMP-1 and MMP-13 ↓	
			Proliferation and migration of RA FLSs ↓ phosphorylation of IKK and I κ Ba ↓	
Corilagin	A tannic acid from <i>Geranium wilfordii</i> Maxim.	NF- κ B p65, ERK, p38, JNK, I κ Ba	Experimental: Bcl-2, IL-6, IL-8, MMP-1, MMP-2, MMP-3, MMP-9, COX-2, iNOS ↓	Shen et al. (2022)
			Bax ↑	
			P-p65/p65, P-I κ Ba/I κ Ba, P-ERK/ERK, P-JNK/JNK, and P-p38/p38 ↓	
			NF- κ B p65 nuclear translocation ↓	
			Proliferation, migration, and invasion of FLS ↓	
Eugenol	A phenylpropanoid from a variety of aromatic herbal plants such as clove and tulsi	NF- κ B	Experimental: proliferation, migration, invasion, angiogenesis, and inflammatory response of FLS ↓	Wang et al. (2022)
			NF- κ B, COX-2 ↓	
Resveratrol	A phenol from grape	SIRT1, NF- κ B	Experimental: SIRT1 and downstream paths ↑	Wang et al. (2020); Sheng et al. (2022)
			The striking interplay between the SIRT1 and NF- κ B	
Plumbagin	A naphthoquinone from <i>Plumbago zeylanica</i> L.	p65	Experimental: viability of human FLS	Shu et al. (2022)
			Inflammatory cytokines, MMPs ↓	
			I κ B, NF- κ B, p65 into the nucleus ↓	
Emodin	An anthraquinone from rhubarb, buckthorn, etc.	MAPK, NF- κ B	Experimental: proliferation of the MH7A cell ↓	Cao et al. (2022)
			MAPK, PTGS2 ↓	
			CASP3 ↑	
Aucubin	An iridoid glycoside from <i>Eucommia ulmoides</i> Oliv.	NF- κ B	Experimental: migration and invasion of human FLS ↓	Zhang et al. (2022)
			NF- κ B -p65 activity of MC3T3-E1 cells ↓ p-I κ Ba β , p-I κ B, and p-p65 proteins ↓	

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TABLE 2 (Continued) Small molecule drugs targeting NF-κB regulating FLS.

Name	Source	Targets/signaling pathways	Estimate	References
Cantleyoside	An iridoid glycoside from <i>Ptercephalus hookeri</i> (C. B. Clarke) Hoeck	AMPK/Sirt 1/NF-κB	Experimental: proliferation of human FLS ↓	Bai et al. (2022)
			NO, TNF-α, IL-1β/6, MCP-1 and MMP-1/3/9 ↓	
			OCR, ECAR and real-time ATP generation rate p-NF-κB and translocation ↓	

↓: suppress, downregulate, inhibit, block, prevent, reduce, decrease; ↑: promote, upregulate, active, increase. HDAC, histone deacetylase; PGE (2), prostaglandin E (2); GRK2, G protein-coupled receptor kinase 2; M-CSF, macrophage colony stimulating factor; MDA, malondialdehyde; TRIB1, Tribbles pseudokinase 1; NFATc1, nuclear factor of activated T cells; NLRP3, NOD-like receptor protein 3; HO-1, heme oxygenase; SIRT1, silent information regulator 1; MCP-1, monocyte chemotactic protein-1; OPN, osteopontin; ATP, adenosine triphosphate; α7nAChR, α7 nicotinic acetylcholine receptor; mPGES-1, microsomal prostaglandin E synthase 1; AP-1, activated protein-1.



belongs to NF-κB is covered by the IκB unable to undergo nuclear translocation. However, in RA due to the activators (TNF-α, IL-17, etc.), IκB is phosphorylated, ubiquitinated by IκB kinase, and eventually degraded by the enzyme, releasing NF-κB. Following that, NF-κB p65 enters the nucleus and combines with target genes (Aupperle et al., 1999). The production of inflammatory mediators such as TNF-α, COX-2, and IL-1β increases as a result of this nuclear translocation in the synovium. Those activated sustaining states lead to massive abnormal activation of FLS (Saravanan et al., 2014). NF-κB p65 regulates apoptosis and inhibits protein expression, which has an antagonistic effect on apoptosis in FLS (Kadkhoda et al., 2016), leading to synovial hyperplasia and aggravating joint destruction (Yin et al., 2015). In addition, p38 mediates IκB phosphorylation, which is involved in regulating NF-κB activation (Carter et al., 1999; Kaminska, 2005).

The small molecule drugs and natural products targeted at NF-κB in recent 3 years are summarized in Table 2, and the classification of the natural products is in Figure 3. There have been many studies on small molecule compounds that modulate FLS in the NF-κB

signaling pathway, such as TAK-242 (Samarpita et al., 2020), CKD-506 (Park et al., 2020), and synthetic derivatives from natural products that also showed the activity of inhibiting proliferation. For example, oxymatrine hydrazone synthesized from oxidized bitter ginseng induced apoptosis and prevented TNF-α-mediated enhanced viability of RA-FLS (Zhang et al., 2021). Paeoniflorin-6'-O-benzene sulfonate (CP-25), a paeoniflorin derivative, had the ability to decrease membrane expression and the combination of these proteins (Wang et al., 2020; Wang et al., 2023). Edaravone, roflumilast, sorafenib, dexmedetomidine, and alogliptin have been used clinically, without the indication for the treatment of RA. The existing experiments showed that they have the anti-proliferation ability of FLS and were worthy of inclusion in the secondary development of drugs. In the natural products in Figure 4, flavonoids still predominated, such as diosmetin, icariin, isoginkgetin, and tectoridin. In a similar situation with the MAPK inhibitions for RA-FLS, these natural products were in the experimental stage. In addition, some inhibitors modulated both NF-κB and MAPK pathways to regulate FLS activity, such as tectoridin and corilagin.

TABLE 3 Small molecule drugs targeting JAK/STAT regulating FLS.

Name	Source	Targets/signaling pathways	Estimate	References
The synthetic small molecule compounds				
Peficitinib	A JAK inhibitor	JAK1, JAK2, JAK3, and Tyk2; STAT3	Clinical: phase II and III clinical trials and extension studies completed	Emori et al. (2020); Gutierrez-Urena et al. (2020); Kitanaga et al. (2020)
			Showed efficacy, safety, and tolerability in monotherapy or csDMARDs	
			Experimental: STAT3 phosphorylation by diversified cytokine concentration-dependently ↓	
			Growth factor-A, MMPs, IL-6, TNFSF11 ↓	
Filgotinib	A selective JAK1 inhibitor	JAK1	Clinical: under clinical trial pending approval for use in RA	Shimizu et al. (2023); Westhovens (2023)
			Dose-related effect was not observed for safety excepting for herpes zoster and the increases of lipids and creatine phosphokinase	
Takinib	A selective TAK1 inhibitor	TAK1, TAK3, JNK, NF-κB	Clinical: JAK-STAT pathways in RA patients ↓	Palmroth et al. (2021); Panipinto et al. (2021); Mardani et al. (2023)
			One case of liver failure	
			Experimental: p-TAK1, no effect for the TAK1 downstream factors ↑	
Baricitinib	A JAK 1 and 2 inhibitor	STAT1, JAK	Clinical: monocyte frequency and p-STAT1 in circulating monocytes served as potential early response markers to baricitinib treatment	Tucci et al. (2022); Weston et al. (2022); Taylor et al. (2023)
			Low-risk-related AESI	
			Low incidence with the dermatologic indications	
			Experimental: OSM-induced JAK signaling ↓	
			IL-6, MCP-1, IP-10 expression in the following stages ↓	
Upadacitinib	A selective JAK 1 inhibitor	JAK 1	Clinical: combination with MTX	Panchal et al. (2023); Taldaev et al. (2021)
			Maximum adverse events were reported at 12 mg twice daily	
Tofacitinib	A JAK/STAT inhibitor	STAT6/miR-425-5p/IGF1	Clinical: treatment of RA	Di Benedetto et al. (2021); Palmroth et al. (2021); Panipinto et al. (2021); Liu et al. (2022); Vomero et al. (2022); Ruscitti et al. (2022)
			Beneficial for RA patients who don't respond to TNF-inhibitors or methotrexate	
			Modulate autophagy of FLS	
			Experimental: pro-inflammatory cytokines ↓ collagen I and α-SMA of RA-FLS ↓	
Mometinib	A competitive JAK1/JAK2 inhibitor	IL-6/JAK1/STAT3	Clinical: no indication for treatment of RA.	Srivastava et al. (2022)
			Experimental: proliferative, migratory of FLS ↓	
			PRMT, survivin, HIF-1α ↓	
			JAK1 and STAT3 by IL-6/sIL-6R activation ↓	
			SOCS3 ↑	

(Continued on following page)

TABLE 3 (Continued) Small molecule drugs targeting JAK/STAT regulating FLS.

Name	Source	Targets/signaling pathways	Estimate	References
The natural products				
Matrine	An alkaloid from genus <i>Sophora</i>	JAK/STAT; PI3K/Akt/mTOR; TGF-β/Smad; Wnt	Experimental: Bcl-2 ↓	Yang et al. (2017); Ao et al. (2022); Lin et al. (2022)
			Bax, caspase-3↑	
			JAK2, STAT1, STAT3 phosphorylation ↓	
Vitexin	An apigenin flavone glycoside from passion flower, bamboo leaves, and pearl millet	JAK/STAT	Experimental: inflammatory enzyme markers ↓ iNOS ↓	Zhang et al. (2022)
			JAK/STAT expressions ↓	
			SOCS↑	
Isobavachalcone	A chalcone from <i>Psoralea corylifolia</i> Linn.	PI3K/Akt, JAK/STAT	Experimental: proliferation, migration, and invasion and promoted apoptosis of MH7A cells ↓ p-PI3K, p-STAT3, p-JAK1 SOCS3, p- Akt ↓	Wang et al. (2022)

↓: suppress, downregulate, inhibit, block, prevent, reduce, decrease; ↑: promote, upregulate, active, increase. csDMARDs, conventional synthetic disease-modifying anti-rheumatic drugs; TNFSF11, TNF Superfamily Member 11; AESI, adverse events of special interest; OSM, oncostatin M; α-SMA, smooth muscle alpha-actin; SOCS, suppressor of cytokine signaling; TAK, TGF β-activated kinase.

3.3 Small molecule drugs targeting JAK/STAT regulating FLS

JAK/STAT signaling has been instrumental in regulating immune and inflammatory responses. The JAK/STAT pathway can be segmented into three components: receptor-associated tyrosine kinase, JAK tyrosine kinase, and STAT transcription factor. The JAK kinase activates JAK upon receptor binding, leading to JAK-mediated phosphorylation of STAT. Among the STAT family, STAT1 and STAT3 serve as the primary activators (Kim et al., 2011). The expression and activity of STAT1 are elevated in the initial synovial tissue of RA, while STAT3 facilitates the survival of synovial fibroblasts. Elevated STAT3 expression contributes to the inhibition of programmed cell death-induced anti-apoptotic molecule expression, blocks apoptosis in RA-FLS, and promotes RA synovial thickening (Yang et al., 2017). The JAK/STAT pathway is also involved in regulating the response of RA-FLS to pro-inflammatory cytokines and plays an essential role in the pro-inflammatory response and invasive behavior of FLS (Diller et al., 2019).

Inhibitors of JAKs could block the activation of STATs in RA-LS in the synthesis of various drugs and in the study of natural products. We included the synthetic small molecule compounds and natural products in the last 3 years in Table 3. Tofacitinib is a Food and Drug Administration (FDA)- and European Medicines Agency (EMA)-approved JAK inhibitor that effectively treats RA (Vomero et al., 2022). The synthetic small molecule compounds of peficitinib, fingolitinib, takinib, tolvamycin, baricitinib, and abatinib all demonstrated monotherapy effectiveness in clinical trials in RA. The synthetic JAK inhibitors appeared to be an important treatment choice for difficult-to-treat RA patients and researchers (Kubo et al., 2023). Momelotinib had no indication for the treatment of RA in the clinic, but could inhibit the proliferation and migration of FLS (Srivastava et al., 2022). On the contrary, there are few research reports on the natural products in the JAK/STAT signal pathway.

3.4 Small molecule drugs targeting PI3k/Akt regulating FLS

The PI3K/Akt signaling pathway is involved in regulating cell growth, proliferation, differentiation, and survival and is associated with the production of pro-inflammatory cytokines, degrading enzymes of the extracellular matrix, and other factors in FLS. The activation of PI3K induces the phosphorylation of Akt and p-Akt. As a downstream effector, it can be involved in FLS invasion by regulating the transcriptional levels of MMPs. The Akt phosphorylation also activates downstream mTOR complex 1 (mTORC1). mTORC1 translates mRNA into proteins to regulate the cell activities of metabolism, growth, and differentiation and is involved in RA-FLS proliferation and survival (Wendel et al., 2004; Malemud, 2013).

Table 4 is a summary of the synthetic small molecules and natural drugs that have been developed recently that target PI3k/Akt. Metformin, a drug used to treat type 2 diabetes, has been shown to have a protective effect against the development of RA (Liang et al., 2023), and RA-FLS proliferation is inhibited by metformin in a dose- and time-dependent manner (Chen et al., 2019). The natural products targeted at PI3k/Akt regulating FLS came from a variety of sources. Against the development of inflammatory arthritis, ginger is a preventive substance. There was evidence that ginger helped reduce RA-related joint pain (Al-Nahain et al., 2014). The active ingredients of ginger, 6-shogaol, and 8-shogaol reduced the production of TNF-α, IL-1β, IL-6, etc., prevented migration, invasion, and population growth, and ameliorated joint destruction in mice (N. Li et al., 2023; Jo et al., 2022).

3.5 Wnt signaling pathway and relevant drugs regulating FLS

The Wnt signaling cascade participates in regulating the growth, differentiation, production, and apoptosis of osteoblasts. The conventional Wnt/β-catenin cascade, Wnt/Ca²⁺ signaling cascade, and Wnt/JNK signaling cascade coordinate with each other to

TABLE 4 Small molecule drugs targeting PI3k/Akt regulating FLS.

Name	Source	Targets/signaling pathways	Estimate	References
The synthetic small molecule compounds				
Metformin	The biguanide hypoglycemic agents	IGF-IR/PI3K/Akt/m-TOR	Clinical: preventing RA	Liang et al. (2023); Chen et al. (2019); Gharib et al. (2021)
			Inflammation, disease severity, and quality of life with high safety ↑	
			Experimental: G2/M cell cycle phase arrest ↓	
			mTOR phosphorylation ↓	
			Adjusting the p70s6k and 4EBP1 phosphorylation	
The natural products				
Baicalein	A flavone from <i>Scutellaria baicalensis</i>	PI3K/Akt/mTOR	Experimental: apoptotic proteins ↑	Zhang et al. (2022)
			EMT-related proteins ↓	
			Cell apoptosis ↑	
			Cell migration phosphorylation ↓	
			The phosphorylation of PI3K, Akt, and mTOR dose dependently ↓	
Nobiletin	A polymethoxylated flavonoid from citrus peels	PI3K/Akt/HIF-1α	Experimental: enhanced the performance in synovial tissue combined with MTX	Liu et al. (2022)
			P-gp expression ↓	
			Contribute to MTX resistance	
Artemisitene	A derivatives of artemisinin from <i>Artemisia annua</i> L.	METTL3/ICAM2/PI3K/Akt/p300	Experimental: progression of FLS↓	Chen et al. (2022)
			N6-methyladenosine modification of ICAM2 mRNA ↓	
Shikonin	A naphthoquinone pigment from the root of <i>Lithospermum erythrorhizon</i>	PI3K- Akt -mTOR, MAPK	Experimental: migration, adhesion, and invasion of MH7A cells↓	Lian-Hua et al. (2020); Li et al. (2021)
			The phosphorylation levels of Akt, JNK, p38, ERK ↓	
Cinnamaldehyde	An aldehyde from the bark of <i>Cinnamomum cassia</i>	PI3K/Akt	Experimental: proliferation and metastasis ↓	Li and Wang (2020)
Daphnetin	A coumarin derivative from <i>Daphne odora</i>	PI3K/Akt/mTOR	Experimental: inflammatory response ↓	Deng et al. (2020)
			Cytokine expression ↓	
			IL-10 ↑	
6-Shogaol	An alkylphenol from ginger	PI3K/AKT/NF-κB	Experimental: proliferation, migration, and invasion of FLS and MH7A cells ↓	Li et al. (2023)
			IL-1β, IL-6, IL-8↓	
			MMP-2, MMP-9 ↓	
			PPAR-γ ↑	
8-Shogaol		TAK1, Akt, MAPK	Experimental: TAK1 activity selectively ↓	Jo et al. (2022)
			IKK, Akt, MAPK ↓	
			Reversing pathologies of joint structure	

↓: suppress, downregulate, inhibit, block, prevent, reduce, decrease; ↑: promote, upregulate, active, increase. METTL3, methyltransferase-like 3.

regulate the dynamic balance between osteoclasts and osteoblasts. Once the balance is disturbed, it might lead to bone erosion and bone destruction (Walsh et al., 2009; De, 2011; Deal, 2012). Studies

had shown that the growth Wnt3a/5a proteins could activate the Wnt signaling cascade as well as downstream genes, thus increasing fibronectin expression and promoting FLS function. The

forementioned processes also promoted the proliferation of RA synovial tissue without pro-inflammatory factors (Kim et al., 2010; Rabelo Fde et al., 2010; Maeda et al., 2013). Researchers (Cici et al., 2019) suggested that the inflammatory activation of the Wnt pathway might inhibit T-cell function and exacerbate the immune response [181]. In the recent 3 years, we inquired natural products, including paeoniflorin (Yang et al., 2022), 7-hydroxycoumarin (Umbelliferone) (Cai et al., 2022; Cai et al., 2022), and penta-acetyl geniposide (Cai et al., 2021).

4 Conclusion

In this review, we summarized as much as possible the involvement of FLS, covering the RA-FLS pathogenesis, synthetic small molecular compounds, and natural products targeting primary signaling pathways in the last 3 years. Natural products comprise a range of substances derived from diverse natural sources, such as plants, animals, and microorganism. These sources provided valuable resources for the design and development of drugs. From the results, the content of this paper could be continuously extended in the following aspects. 1) For the synthetic small molecule compounds, the popular targeting signaling pathways are still MAPK and NF- κ B in the current research stage. We cannot ignore that JAK/STAT has great potential for research studies, due to the fact that several drugs have appeared in the clinic. Moreover, modulation of Wnt signaling might not only repair articular bone damage but also inhibit the production of pro-inflammatory cytokines, showing a new strategy for RA treatment (Miao et al., 2013; Liu et al., 2019). Typically, these signaling pathways interacted with each other. A small molecule could act through multiple pathways. 2) For the natural products, there was great potential. Researchers have tried to explore drugs targeted to activate FLS to treat RA using traditional human experience and herbs. For example, triptolide has been a hot area of research for several years. Most of the results are currently in the experimental stage, not the clinical trial stage. Fortunately, the source plants of these natural products have been used for RA in clinical studies. 3) The natural products derived from herbal medicine that can regulate RA-FLS abnormalities are mainly

alkaloids, flavonoids, saponins, phenols, and quinones (Smolen et al., 2018). 4) In addition, we have found many reports on the mechanisms of herbal extract, Chinese herbal compound prescription, and traditional Chinese patent medicines in RA that were worthy of further research.

Author contributions

YT was responsible for writing and drawing by Figdraw. XL drafted the original framework and figures. QD collected and sorted materials. JS and YF provided guidance. LB reviewed writing and drawing. All authors contributed to the article and approved the submitted version.

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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

RA	Rheumatoid arthritis	TGF-β	Transforming growth factor- β
NFATc1	c-Fos and nuclear factor of activated T cells c1	NFATc1	Nuclear factor of activated T cells
FLS	Fibroblast-like synoviocyte	FLIP	Anti-apoptotic molecule FLICE inhibitory protein
ATF2	Activating transcription factor-2	NLRP3	NOD-like receptor protein 3
NSAIDs	Non-steroidal anti-inflammatory drugs	TLRs	Toll-like receptors
PGE (2)	Prostaglandin E (2)	HO-1	Heme oxygenase
DMARDs	Disease-modifying anti-rheumatic drugs	DKK-1	Dickkopf-1
ROS	Reactive oxygen species	SIRT1	Silent information regulator 1
MTX	Methotrexate	CXCL-8	CXC motif chemokine 8
HIF1	Hypoxia-inducible factor 1	MCP-1	Monocyte chemotactic protein-1
bdMARDs	Biologic disease-modifying anti-rheumatic drugs	CCL2	CC motif chemokine ligand 2
CIA	Collagen-induced arthritis	OPN	Osteopontin
ECM	Extracellular matrix	MHCII	Major histocompatibility complex class II
IκB	Inhibitor of κ B	ATP	Adenosine triphosphate
MAPK	Mitogen-activated protein kinase	FcγRs	Fc-gamma receptors
Bcl-2	B-cell lymphoma-2	α7nAChR	α 7-nicotinic acetylcholine receptor
NF-κB	Nuclear factor kappa-B	APRIL	A proliferation-inducing ligand
Bax	Bcl-2-associated X	mPGES-1	Microsomal prostaglandin E synthase 1
JAK	Janus kinase	ABCs	Age-associated B cells
AA	Adjuvant-induced arthritic	AP-1	Activated protein-1
STAT	Signal transducers and activators of transcription	VCAM-1	Vascular cell adhesion molecule-1
OPG	Osteoprotegerin	FDA	Food and Drug Administration
TNF	Tumor necrosis factor	ICAM-1	Intercellular cell adhesion molecule-1
MEKK	Mitogen-activated protein kinase kinase	EMA	European Medicines Agency
IL	Interleukin	LFA-1	Lymphocyte function-associated antigen
IKK	I κ B kinase	csDMARDs	Conventional synthetic disease-modifying anti-rheumatic drugs
NOS	Nitric oxide synthase	JNK	c-Jun N-terminal kinase
TGM2	Transglutaminase 2	TNFSF11	TNF Superfamily Member 11
COX-2	Cyclooxygenase-2	ERK	Extracellular regulated protein kinase
NLS	Nuclear-localization sequence	AESI	Adverse events of special interest
RANK	Receptor activator of NF- κ B	Bcl-2	B-cell lymphoma 2
HDAC	Histone deacetylases	OSM	Oncostatin M
RANKL	Receptor activator of NF- κ B ligand	Ang1	Angiopoietin-1
GRK2	G protein-coupled receptor kinase 2	α-SMA	Smooth muscle alpha-actin
VEGF	Vascular endothelial growth factor	Tie-2	Tyrosine-protein kinase receptor
M-CSF	Macrophage colony stimulating factor	SOCS	Suppressor of cytokine signaling
MMPs	Matrix metalloproteinases	GSK-3	Glycogen synthase kinase 3
MDA	Malondialdehyde	TAK	TGF β -activated kinase
PDGF	Platelet-derived growth factor	MKK	Mitogen-activated protein kinase kinase
TRIB1	Tribbles pseudokinase 1	mTORC1	mTOR complex 1
		mTOR	Mammalian target of rapamycin



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Ursolic acid reduces oxidative stress injury to ameliorate experimental autoimmune myocarditis by activating Nrf2/HO-1 signaling pathway

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Background: Oxidative stress is crucial in experimental autoimmune myocarditis (EAM)-induced inflammatory myocardial injury. Ursolic acid (UA) is an antioxidant-enriched traditional Chinese medicine formula. The present study aimed to investigate whether UA could alleviate inflammatory cardiac injury and determine the underlying mechanisms.

Methods: Six-week-old male BALB/c mice were randomly assigned to one of the three groups: Sham, EAM group, or UA intervention group (UA group) by gavage for 2 weeks. An EAM model was developed by subcutaneous injection of α -myosin heavy chain derived polypeptide (α -MyHC peptide) into lymph nodes on days 0 and 7. Echocardiography was used to assess cardiac function on day 21. The inflammation level in the myocardial tissue of each group was compared using hematoxylin and eosin staining (HE) of heart sections and Interleukin-6 (IL-6) immunohistochemical staining. Masson staining revealed the degree of cardiac fibrosis. Furthermore, Dihydroethidium staining, Western blot, immunohistochemistry, and enzyme-linked immunosorbent assay (ELISA) were used to determine the mechanism of cardioprotective effects of UA on EAM-induced cardiac injury, and the level of IL-6, Nrf2, and HO-1.

Results: In EAM mice, UA intervention significantly reduced the degree of inflammatory infiltration and myocardial fibrosis while improving cardiac function. Mechanistically, UA reduced myocardial injury by inhibiting oxidative stress (as demonstrated by a decrease of superoxide and normalization of pro- and antioxidant enzyme levels). Interestingly, UA intervention upregulated the expression of antioxidant factors such as Nrf2 and HO-1. *In vitro* experiments, specific Nrf2 inhibitors reversed the antioxidant and antiapoptotic effects of

Abbreviations: UA, ursolic acid; EAM, experimental autoimmune myocarditis; Nrf2, Nuclear factor erythroid-related factor 2; HO-1, Heme oxygenase-1; NQO1, NAD(P)H quinone dehydrogenase 1; GSH-Px, Glutathione peroxidase; Elisa, enzyme-linked immunosorbent assay; DHE, Dihydroethidium; MDA, Malondialdehyde; ROS, Reactive oxygen species; AREs, antioxidant response elements; EF, ejection fraction; FS, fractional shortening; LV, left ventricle; cTnI, cardiac troponin I; BNP, brain natriuretic peptide.

ursolic acid, which further suggested that the amelioration of EAM by UA was in a Nrf2/HO-1 pathway-dependent manner.

Conclusion: These findings indicate that UA is a cardioprotective traditional Chinese medicine formula that reduces EAM-induced cardiac injury by up-regulating Nrf2/HO-1 expression and suppressing oxidative stress, making it a promising therapeutic strategy for the treatment of EAM.

KEYWORDS

experimental autoimmune myocarditis, ursolic acid, oxidative stress, Nrf2, HO-1

Introduction

Myocarditis is an inflammation of the myocardium caused by viruses, bacteria, or parasites, as well as non-infectious causes such as autoimmunity, hypersensitivity, and cardiotoxicity (Frustaci et al., 2009; Caforio et al., 2015). It can result in sudden cardiac death or dilated cardiomyopathy (Felker et al., 2000). Currently, most myocarditis treatments are based on supportive and immunosuppressive therapy (Jensen and Marchant, 2016). However, effective therapies against myocarditis are lacking. The prevailing view indicates that oxidative stress exacerbates the autoimmune process in myocarditis (Tada and Suzuki, 2016). Moreover, long-term oxidative stress and antioxidant system suppression may result in cardiac remodeling in inflammatory cardiomyopathy (Tada and Suzuki, 2016). Oxidative stress is considered a potential therapeutic target to treat myocarditis. One of the hallmark changes in the myocarditis heart is increased oxidative stress, which leads to cardiac apoptosis. Nuclear factor erythroid-related factor 2 (Nrf2) is a transcription factor that activates under conditions of high oxidative stress and regulates many antioxidant and detoxification genes (Dinkova-Kostova et al., 2018). An imbalance between active oxidants and antioxidants causes oxidative stress. Under oxidative conditions, Nrf2 is released upon dissociation from kelch like ECH associated protein 1 (Keap1) and translocated to the nucleus (Kobayashi et al., 2006). In the nucleus, it binds to antioxidant response elements (AREs), the promoter regions of its target genes. All of these genes, including Heme oxygenase-1 (HO-1), NAD(P)H quinone dehydrogenase 1 (NQO1), and Glutathione peroxidase (GSH-Px), have AREs in their promoter regions.

Traditional Chinese medicine has long been uniquely effective in treating inflammatory diseases. Ursolic acid (UA) is a pentacyclic triterpenoid compound found in many natural plants, such as apple peels, herbal medicines, and other edible plants (Cui et al., 2006; Seeram, 2008; Tannock, 2011). UA has numerous biological properties, including anti-tumor, anti-oxidation, anti-inflammation, anti-fibrosis, and anti-atherosclerosis, and can be used to treat various diseases (Wang et al., 2011; Silva et al., 2016). Some of these effects of UA are determined by its potent antioxidant properties (López-Hortas et al., 2018). Moreover, mounting evidence suggests the versatile roles of UA in the cardiovascular system (Saravanan, Pugalendi, 2006). Previous studies have confirmed that UA is a cardioprotective compound due to its antioxidant properties (Liobikas et al., 2011). However, whether UA can improve experimental autoimmune myocarditis (EAM) is unknown.

Several works have demonstrated the modulation of Nrf2 by UA as one of the main mechanisms behind their beneficial effects in pathological models like cigarette smoke-induced emphysema (Lin et al., 2017) and renal tubular epithelial cell damage induced by calcium oxalate monohydrate. Nevertheless, the regulation of this antioxidant pathway in cardiac pathology remains to be further investigated (Jia et al., 2021). The Nrf2 pathway has been shown to play a critical role in EAM as it reduces DNA damage induced by oxidative stress in EAM mice (Jaén et al., 2020). However, it is unknown whether UA can alleviate inflammation and oxidative injury in EAM through Nrf2/HO-1 signaling pathway.

In the present study, an EAM murine model was developed to investigate the regulatory role of UA in anti-inflammatory and cardiac antioxidant pathways. The present study investigated whether UA can reduce EAM-induced oxidative stress injury and whether this effect is mediated through Nrf2 and HO-1 signaling pathways. The present study provides new insights for developing therapeutic targets to improve the prognosis and treatment of myocarditis patients.

Materials and methods

Experimental animals and EAM model

Male BALB/c mice aged 6–7 weeks (weighing 18–20 g) were obtained from Beijing Vital River Laboratory Animal Technology Co., LTD. (China) and housed at 25°C ± 2°C with free access to water and food on a 12 h light/dark cycle. The Animal Ethics Committee of Tongji Medical College, Huazhong University of Science and Technology (China) approved all experimental procedures that complied with the National Institutes of Health Guidelines on the Use of Laboratory Animals (Approval code: S3136; The validity of approval is from 01/01/2022–12/31/2024).

All mice were anesthetized using 1.5% isoflurane before the procedure to minimize animal stress. Mice were immunized with a cardiac-specific peptide (α -MyHC peptide: Ac-RSLKLMATLFSTYASADR-OH) purchased from GL Biochem Ltd (China). The peptide was dissolved in saline and emulsified in a 1:1 ratio with Complete Freund's Adjuvant (Sigma, United States) (n = 30). On day 0, 200 μ g peptide in 0.2 mL of the emulsion was injected subcutaneously into one side of the axillary and inguinal lymph node region. On day 7, the same dose was injected subcutaneously into the opposite side. Sham group (n = 12) was injected with a physiological saline solution instead of myosin. Mice immunized with cardiac peptide were randomly divided into UA treatment (n = 16) and PBS (n = 14).

groups. From day 7–21, mice were given intragastric gavage of UA ((U6753, Sigma, United States), 100 mg/kg) (UA intervention group) or PBS containing 7.5% DMSO (D2650, Sigma, United States) (sham group and peptide-immunized mice without UA). Therefore, three experimental groups were formed: 1) a sham group, 2) an EAM group, and 3) an EAM + UA group. On day 21, all mice underwent echocardiography. The blood was then obtained through cardiac puncture. Body weight (BW) and tibial length (TL) were measured. Finally, hearts were removed from the chest and subjected to subsequent experiments.

Transthoracic echocardiography

On day 21, the cardiac function was assessed using an echocardiographic imaging system (Vevo 1,100, Canada) with a transducer MS400 (30 MHz). The mice were anesthetized with 1.5% isoflurane, and two-dimensional echocardiographic views of the mid-ventricular short axis at the papillary muscle tips below the mitral valve were obtained. The Vevo 1,100 software calculated the left ventricular ejection fraction (EF) and fractional shortening (FS).

Measurement of cytokines by enzyme-linked immunosorbent assay (ELISA)

Tissue (10 mg) was homogenized in PBS on ice for ELISA. The samples were centrifuged for 10 min at $5,000 \times g$ to remove any insoluble material. Plasma samples were collected by cardiac puncture. Interleukin-6 (IL-6), cardiac troponin I (cTnI), and brain natriuretic peptide (BNP) levels were measured using ELISA kits (mlbio, China) according to the manufacturer's instructions.

Malondialdehyde (MDA) assay

MDA was measured using the MDA assay kit (Beyotime, China) as directed by the manufacturer. Plasma (100 μ L) or homogenized cells (1×10^6) samples were added to 200 μ L MDA Lysis Buffer. The samples were incubated at 100°C for 15 min before being cooled in an ice bath to room temperature. The samples were centrifuged at 1,000 g for 10 min at room temperature to remove any insoluble material. Then, 200 μ L of supernatant was pipetted into a 96-well plate, and the absorbance was measured at 532 nm (A_{532}).

Cell culture and *in vitro* experimental protocols

H9c2 cells were obtained from the cell bank of the Chinese Academy of Sciences (China). The cells were cultured in dulbecco's modified eagle medium (DMEM) (high glucose) medium (Gibco, United States) supplemented with 10% fetal bovine serum (FBS) (Gibco, United States) and 1% of penicillin-streptomycin (Gibco, United States) in a humidified atmosphere of 5% CO₂ at 37°C. Cells were maintained in a proliferative state (i.e., undifferentiated state). To induce inflammation, cells were rendered quiescent by serum

TABLE 1 RT q-PCR primer sequences.

	Primer sequences (5'-3')
GAPDH	Forward: 5'-ACTCCAACCTCAGGCAAAATTCA-3'
	Reverse: 5'-GGCCTCACCCCATTTGATG-3'
IL-6	Forward: 5'-ACAACCACGGCTTCCTACT-3'
	Reverse: 5'-CTCATTTCACGATTCCAG-3'
Col1a1	Forward: 5'-AATGGCACGGCTGTGTGCGA-3'
	Reverse: 5'-AGCACTCGCCCTCCCGTCTT-3'
Col3a1	Forward: 5'-CCTGGCTCAAATGGCTCAC-3'
	Reverse: 5'-GACCTCGTGTCCGGGTAT-3'

starvation for 12 h prior to stimulation with rIL-6 (25 ng/mL) for 1 h (Shi et al., 2020). In order to study the antioxidant effect of ursolic acid, 10 μ M, 20 μ M, 30 μ M, 40 μ M, and 50 μ M of UA was added to the cells culture 4 h after the addition of rIL-6. For Nrf2 inhibitor experiments, cultures were co-incubated by 30 μ M UA and 5 μ M ML385 for 4 h (HY-100523, MCE, United States) (Chen et al., 2021). The cells were split into four groups: 1) Sham group; 2) IL-6 group; 3) UA group (IL-6 + UA); 4) ML385 group (IL-6 + UA + ML385).

Cell viability assay

Cell viability was determined using the Cell Counting Kit-8 (CCK-8) (Biosharp, China) assay following the manufacturer's instructions. The cells were seeded at a density of 5,000 cells/well in the 96-well plates. After 24 h, cells were treated with different concentrations of UA. The CCK-8 solution was added to each well, and the cells were incubated at 37°C for another 2 h. The absorbance was measured at 450 nm (A_{450}). Each sample was replicated thrice. The cells that stained positive for CCK-8 solution was thought to be viable. The results are presented as a percentage compared with sham group.

Histopathology and immunohistochemistry

Myocardial tissues from left ventricle (LV) of mice at the papillary muscle level were harvested, fixed in fresh 4% paraformaldehyde, embedded in paraffin, and serially sectioned (5–6 μ m). Dewaxed and hydrated heart sections were stained with hematoxylin and eosin staining (HE) for general morphology or with Masson trichrome stain kit for fibrosis detection. The blue stained area (collagen deposition) was quantified and normalized to the total section area using ImageJ (1.8.0, National Institutes of Health) software to determine cardiac fibrosis.

Immunofluorescence staining

The paraffin sections were baked for 1 h in a 65°C oven. The sections were dewaxed and antigen repaired before incubating in 3% H₂O₂ for 10 min to remove endogenous enzymes. After 1 h of

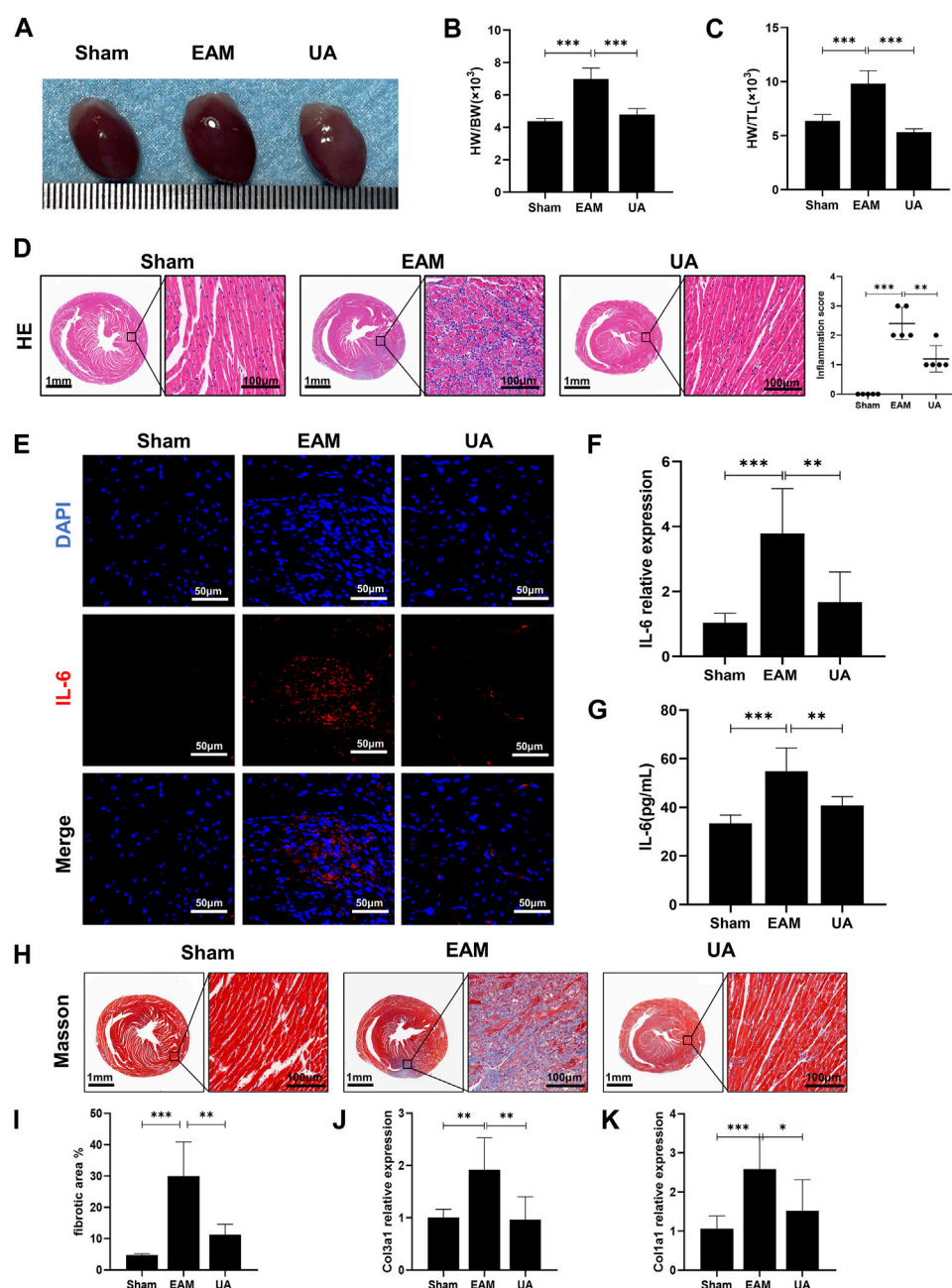


FIGURE 1

UA mitigated EAM-induced cardiac inflammation and fibrosis. (A) Heart images representing each experimental group. (B) Heart weight to body weight ratio (HW/BW). (C) Heart weight to tibial length ratio (HW/TL) from all experimental groups. (D) Representative histological images of immune cell infiltration in cardiac tissue from the indicated groups and the corresponding quantification ($n = 5$). Scale bars: left 1mm, inset 100 μ m. (E) Representative immunofluorescence images of cardiac tissue stained red with IL-6 and blue with DAPI. Scale bars: 50 μ m. (F) RT-qPCR detected the mRNA levels of IL-6 in cardiac tissue. (G) ELISA detected IL-6 levels in cardiac tissue from all experimental groups at day 21. (H, I) Representative Masson staining images indicating collagen fiber deposition in blue and the corresponding quantification ($n = 8$). Scale bars: left 1 mm, inset 100 μ m. (J, K) Col1a1 and Col3a1 mRNA expression levels in cardiac tissue from the indicated groups at day 21 ($n = 9$). (Data were shown as the mean \pm SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test and Games-Howell's multiple comparisons test; ns = not significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

blocking with goat serum at room temperature, heart slides were incubated overnight at 4°C with the following primary antibodies: α -Smooth Muscle Actin (α -SMA) (1:100) (#7817, Abcam, United Kingdom), IL-6 (1:50) (#290735, Abcam, United Kingdom). Samples were incubated with secondary

antibodies combined with Alexa Fluor 488 and 555 (Beyotime, China) for 1 h at 1:500, followed by 4',6-diamidino-2-phenylindole (DAPI) (Beyotime, China) for 15 min at room temperature. Finally, the sections were washed with PBS 1x and covered with coverslips.

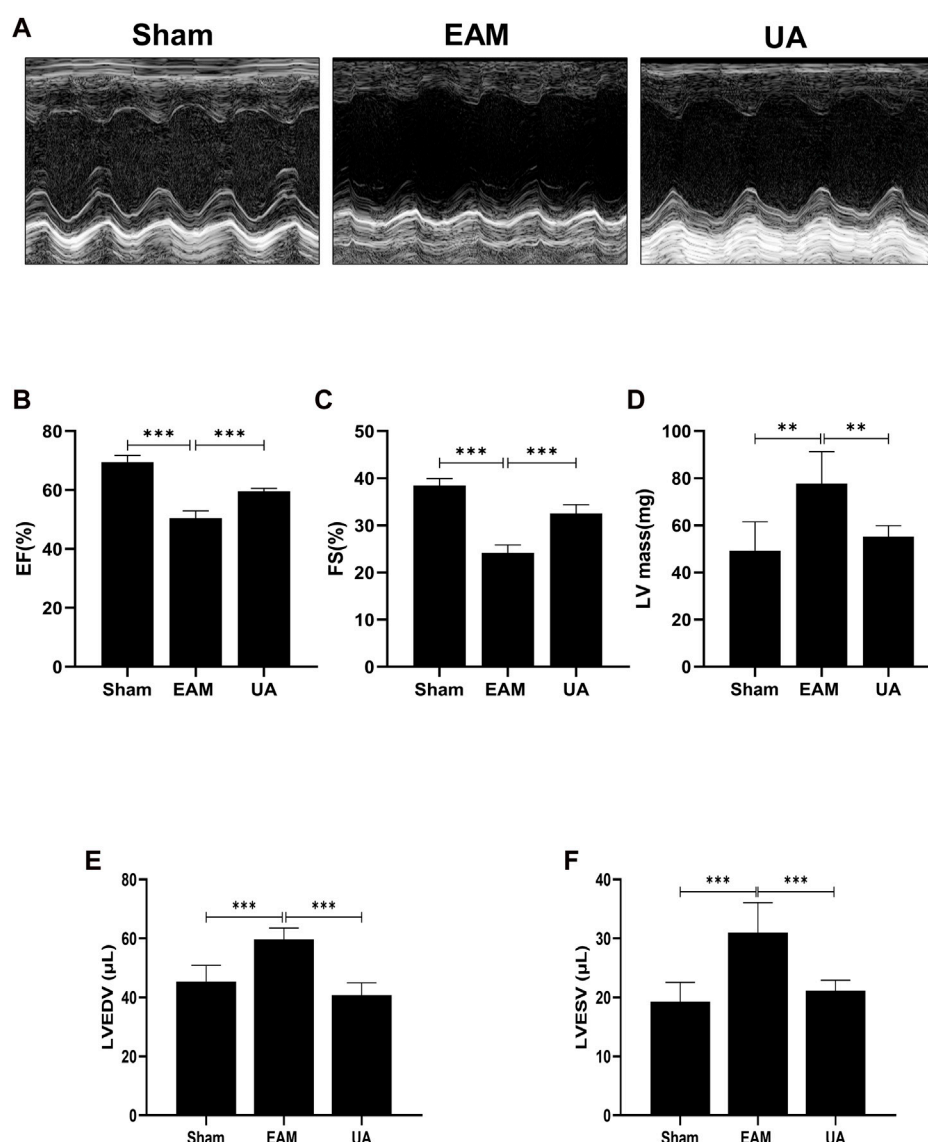


FIGURE 2

UA improved EAM-induced left ventricular dysfunction. (A) Representative echocardiography M-mode images from the indicated groups on day 21. (B, C) Statistical analysis of ejection fractions (EF) and fractional shorting (FS) in indicated groups. (D, E, F) Left ventricular function-related ultrasonic parameters in each group ($n = 6$). (Data were shown as the mean \pm SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test; ns = not significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

TUNEL assay

Myocardial apoptosis was determined by terminal deoxynucleotidyl transferase dUTP nick-end labeling (TUNEL) staining by TUNEL Apoptosis Assay Kit with fluorescein (Beyotime, China) following the manufacturer's instructions. Green fluorescein staining was used to identify apoptotic nuclei, while DAPI stained total nuclei. The apoptotic index was expressed as the percentage of apoptotic nuclei to total nuclei.

Western blot analysis

Cardiac tissues or cells were homogenized in ripa lysis buffer (include protease and phosphatase Inhibitor) with a sonicator on

ice, and the total protein concentrations were measured using the BCA Protein Assay Kit (Beyotime, China). As previously reported, cytosolic and nucleic proteins were separated for analysis of Nrf2 release. Depending on the molecular weight of target proteins, equal amounts of protein lysates (20–40 μ g/lane) were subjected to 10%–12% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and immunoblotted to PVDF membranes (MerckMillipore, Germany). After blocking with 5% skim milk for 1 h at room temperature, the membranes were incubated at 4°C overnight with respective primary antibodies against Nrf2 (1:1,000) (16,396, proteintech, China), HO-1 (1:1,000, ab52947), LaminB1 (1:1,000, ab133741), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (1:2000, CST#5174), β -actin (1:

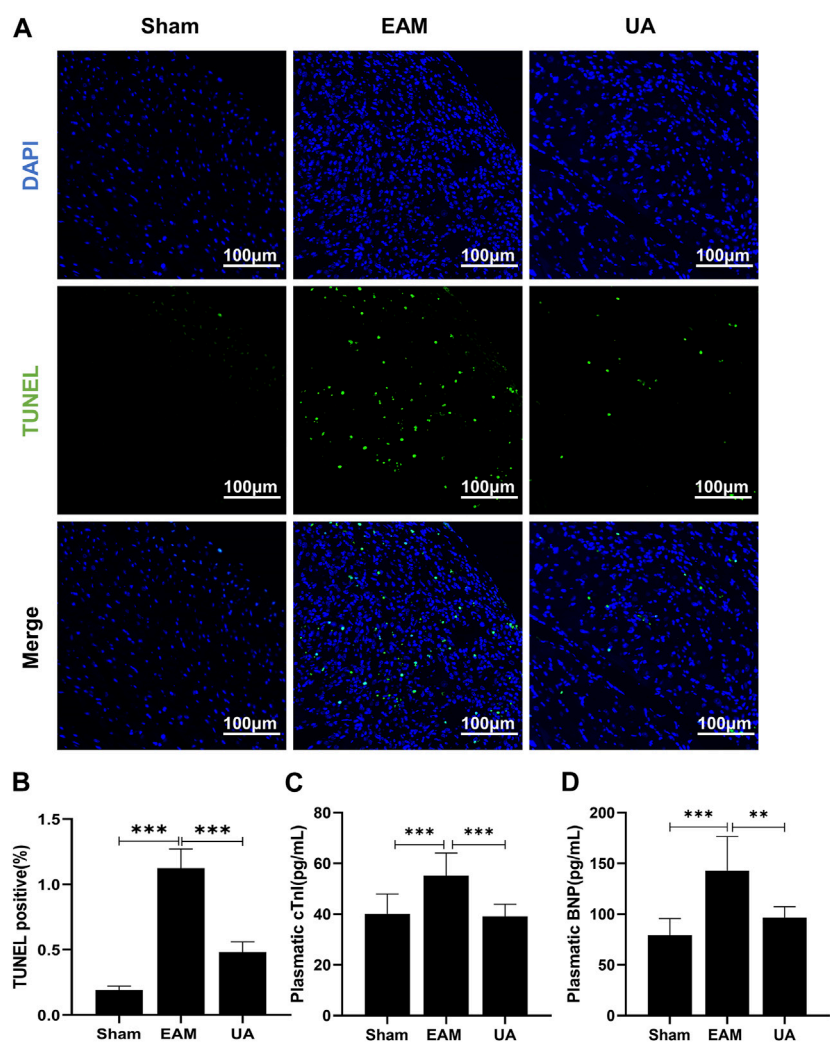


FIGURE 3 UA reduced EAM-induced cardiomyocyte apoptosis. **(A)** TUNEL staining images of cardiac tissue stained with TUNEL-positive nuclei in green and DAPI in blue. Scale bars: 100 μm. **(B)** Quantitative analysis of apoptotic index among the indicated groups (n = 5). **(C, D)** cTnI and BNP levels detected by ELISA in cardiac tissue from the indicated groups (n = 9). (Data were shown as the mean ± SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test and Games-Howell's multiple comparisons test; ns = not significant, **p* < 0.05, ***p* < 0.01, ****p* < 0.001).

TABLE 2 Cardiac function parameters obtained from echocardiography.

	Sham	EAM	UA
Heart rate (bpm)	401 ± 86	410 ± 21	382 ± 26
Ejection fraction%	69.5 ± 2	50 ± 2.5***	59.5 ± 1.5###
Fractional shortening%	38 ± 1.5	24 ± 2***	32 ± 1.5###
LVEDV (μL)	46 ± 6	60 ± 4***	41 ± 4###
LVESV (μL)	19 ± 3	31 ± 5***	21 ± 2###
LV mass (mg)	49 ± 12	78 ± 14**	55 ± 4.5##

Data are presented as mean ± SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test.
**p* < 0.05.
***p* < 0.01.
****p* < 0.001 vs. Control.
#*p* < 0.05.
##*p* < 0.01.
###*p* < 0.001 vs EAM. LVEDV, Left ventricular end-diastolic volume; LVESV, left ventricular end-systolic volume.

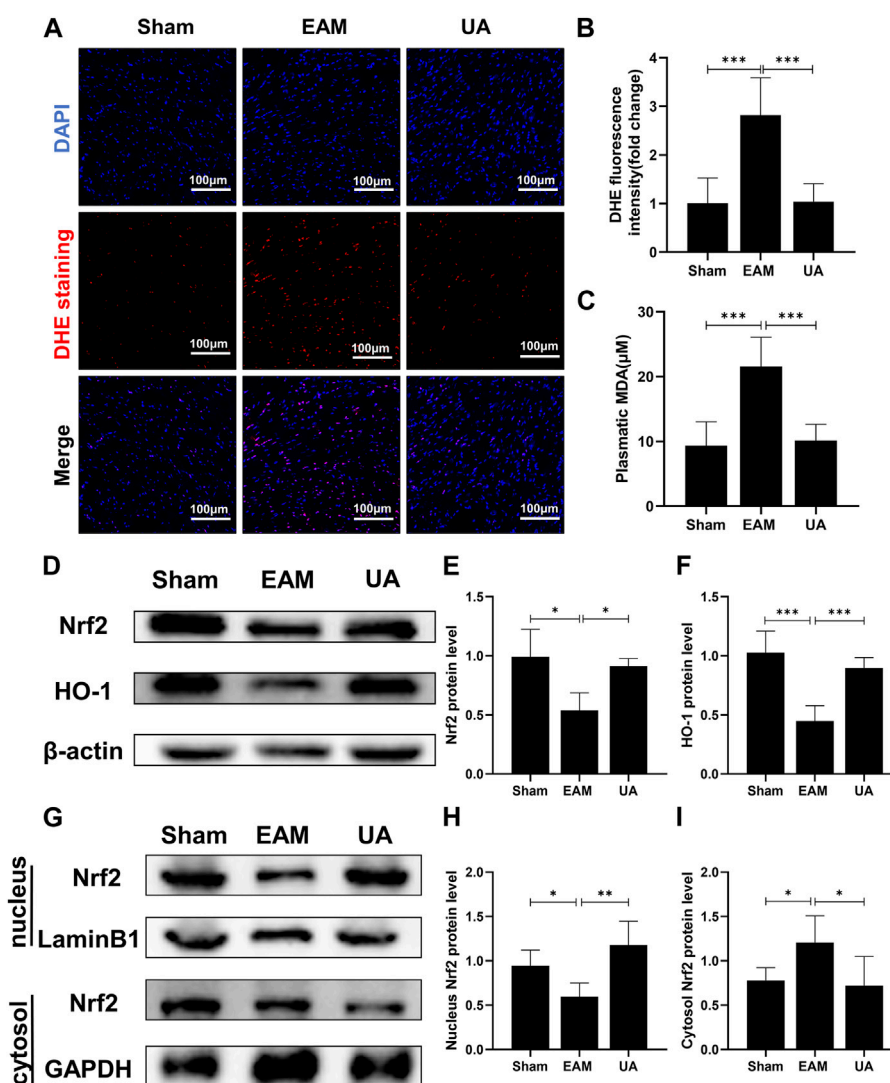


FIGURE 4

UA reduced the EAM-induced cardiac oxidative stress by regulating Nrf2 levels. (A) Heart images of DHE staining in the indicated groups. Scale bars: 100 μm. (B) The fluorescence intensity of DHE staining was measured and expressed as a fold change ($n = 3$). (C) An MDA assay measured serum MDA levels in each group. (D, E, F) The total cellular Nrf2 and HO-1 protein expression levels in each group were measured with Western blot and the representative quantification ($n = 6$). (G, H, I) Protein expressions of Nrf2 in cytoplasmic and nuclear cell lysates in mouse hearts of the different groups. (Data were shown as the mean \pm SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test and Games-Howell's multiple comparisons test; ns = not significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

1,000, ab8226) and washed. The protein bands were visualized using enhanced chemiluminescence (Pierce, United States) after incubation with the corresponding secondary HRP-conjugated antibodies. Densitometry values were determined using ImageJ software (1.8.0, National Institutes of Health).

Real-time quantitative polymerase chain reaction (RT q-PCR)

TRIzol Reagent (Invitrogen, United States) was used to isolate total RNA from flash-frozen myocardial tissues or H9c2 cells. cDNA was synthesized using a reverse transcription reagent kit (Takara Biotechnology, Japan) and

then amplified in the Bio-rad CFX CONNECT Detector system using the SYBR® Premix Ex Taq™ Perfect Real Time Kit (Takara Biotechnology, Japan). Relative expression was computed using the CT method. Table 1 lists the SYBR Green real-time PCR primers for mouse gene expression.

Molecular docking

The crystal structure of Nrf2 protein (PDB ID: 7O7B) has been obtained from the RCSB protein data bank. For protein preparation, the natural ligand was extracted and the resulting crystal structure was then freed of the water molecules and added the polar hydrogen atoms. The 3D structure of ursolic acid has

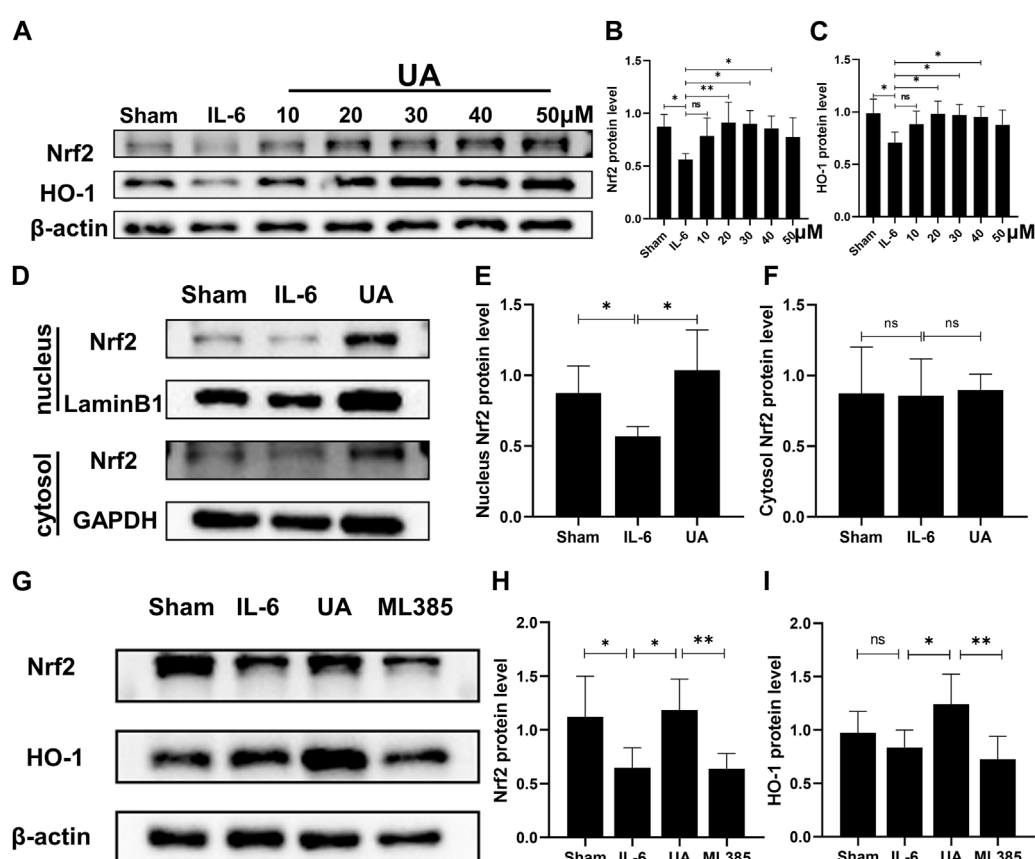


FIGURE 5

UA upregulated Nrf2/HO-1 signaling pathway *in vitro*. (A, B, C) Representative Western blot images and quantification of Nrf2 and HO-1 protein levels of H9c2 cells treated with UA at various concentrations ($n = 6$). (D, E, F) Protein expression of Nrf2 in cytoplasmic and nuclear cell lysate from different groups of H9c2 cells (UA = 30 μ M). (G, H, I) The Nrf2 and HO-1 protein expression in H9c2 cells were measured with Western blot and the representative quantification ($n = 6$). (Data were shown as the mean \pm SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test and Games-Howell's multiple comparisons test; ns = not significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

been obtained from pubchem database. This structure was optimized and polar hydrogen atoms are added. Subsequently, the docking procedure was conducted by using Autodock software and its conformation was optimized by using a genetic algorithm based on the principle of minimizing docking energy.

Statistical analysis

The data were analyzed with GraphPad Prism software (version 8.0 for Windows, San Diego, CA, United States). All data are normally distributed. The multiple-group comparisons were performed using one-way analysis of variance (ANOVA), followed by Tukey's multiple comparison test for homogeneity of variance and Games-Howell's multiple comparisons test for heterogeneity of variance. All values were presented as mean \pm SD. The differences were considered statistically significant with a p -value < 0.05 .

Results

Ursolic acid ameliorated myocardial damage in EAM mice

The ratios of heart weight/body weight (HW/BW) and heart weight/tibia length (HW/TL) were elevated and heart was enlarged in EAM mice compared to sham group, which was alleviated by UA treatment (Figures 1A–C). H&E-stained EAM heart sections revealed a high inflammation score, which was reduced by UA treatment (Figure 1D). Immunofluorescence staining was used to characterize the immune cells in the infiltrated area. Compared with sham group, IL-6 was significantly increased in EAM group, while other inflammatory factors IL-1 β and TNF- α had no significant difference (Figure 1E; Supplementary Figure S1A,B). In addition, UA could partially normalize IL-6 mRNA expression and the secretion level of IL-6 in EAM mouse heart tissues (Figures 1F,G).

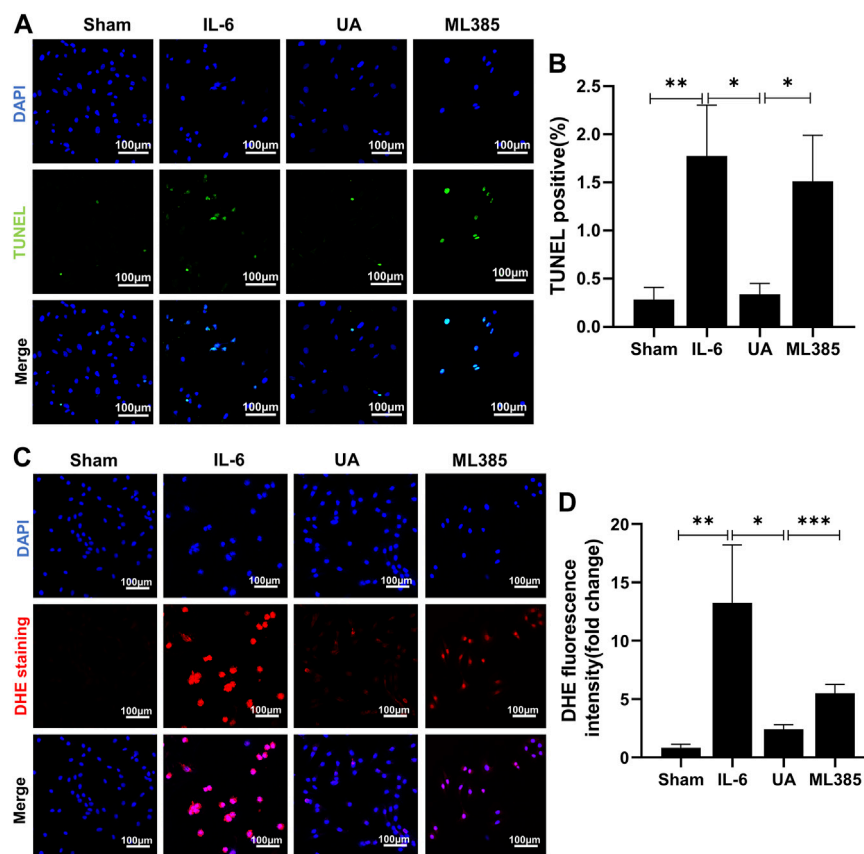


FIGURE 6

ML385 counteracted the anti-apoptosis and antioxidant effects of Ursolic Acid. (A) TUNEL staining images of H9c2 cells stained with TUNEL-positive nuclei in green and DAPI in blue. Scale bars: 100 μ m. (B) Quantitative analysis of apoptotic index among the indicated groups ($n = 5$). (C) Representative images of DHE staining in H9c2 cells. Scale bars: 100 μ m. (D) Fluorescence intensity of DHE staining was measured, and the results were expressed as a fold change ($n = 6$). (Data were shown as the mean \pm SD, ordinary one-way analysis of variance, Tukey's multiple comparisons test and Games-Howell's multiple comparisons test; ns = not significant, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$).

In EAM model, heart sections stained with Masson's trichrome to detect collagen fiber deposition revealed some peripheral fibrotic areas in EAM mice that were reduced by UA administration (Figures 1H,I). Immunofluorescence staining with α -SMA, a fibroblast activation marker, was also increased in EAM animals, whereas it was decreased in UA-treated mice (Supplementary Figure S1C). The fibrosis analysis was supplemented by estimating mRNA levels of mediators involved in the development of cardiac fibrosis. In the present study, EAM mice had higher levels of collagen 1 (Col1a1) and 3 (Col3a1) cardiac mRNA that significantly reduced in UA-treated EAM mice (Figure 1J,K). Ursolic acid intervention alleviated myocardial inflammation and fibrosis in mice with EAM.

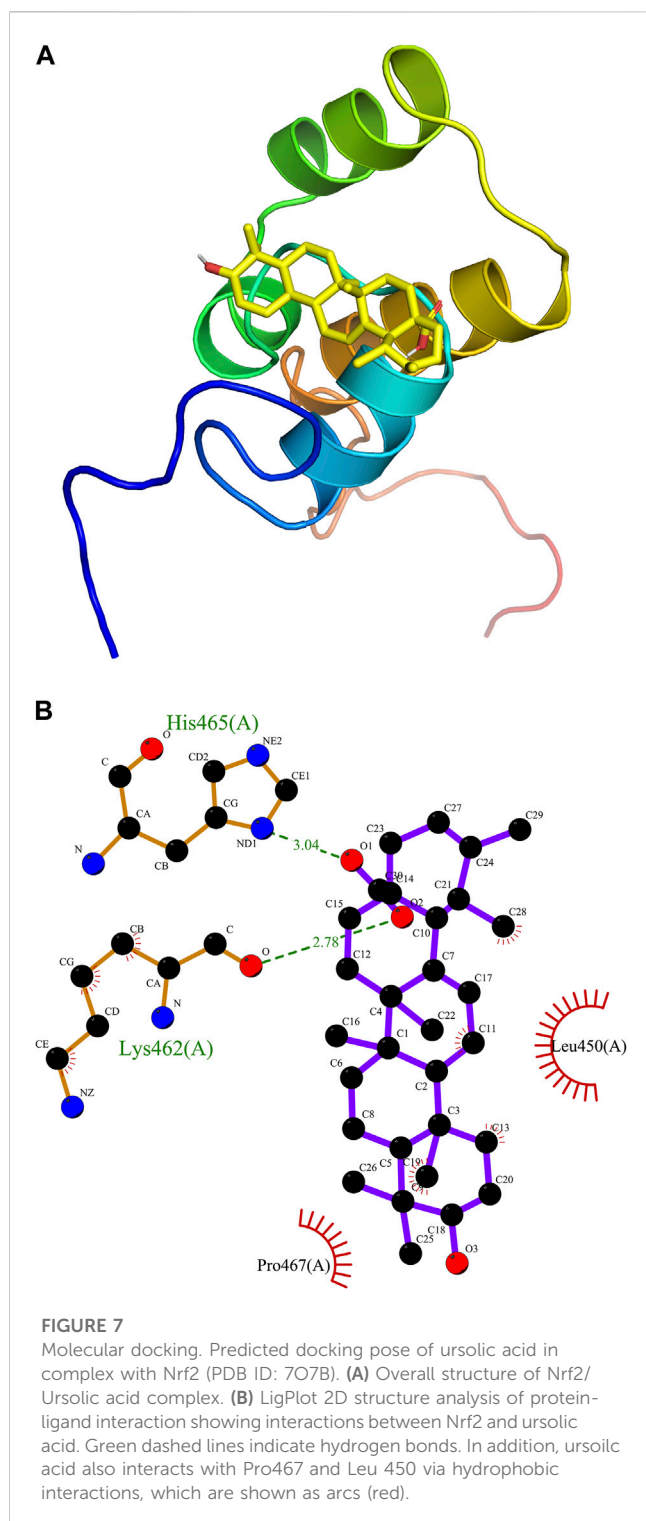
Ursolic acid treatment mitigated EAM-Induced systolic dysfunction

On day 21, echocardiography was performed to assess cardiac function in each group (Figure 2; Table 2). Figure 2A depicts the representative M-mode echocardiograms for each group. Cardiac systolic dysfunction, as indicated by left ventricular EF and FS,

decreased significantly in the EAM group but not in the UA-treated group (Figures 2B,C). When compared to sham group, the EAM group had substantially higher levels of left ventricular end-diastolic volume (LVEDV), left ventricular end-systolic volume (LVESV), and left ventricular mass (LV Mass), which was mitigated in the UA-treated group (Figures 2D–F). Other factors, such as heart rate (HR), did not differ between the groups (Table 2). Ursolic acid reduced left ventricular dysfunction induced by EAM.

Ursolic acid treatment reduced cardiac apoptosis

Cardiac dysfunction has been associated with increased cardiomyocytes death, which eventually debilitates the contractile capacity of the heart. Findings indicated that the proportion of TUNEL-positive nuclei increased significantly in EAM group (Figures 3A,B). In addition, increased plasmatic levels of the cardiac damage marker cTnI (Figure 3C) and BNP (Figure 3D) were found in EAM mice. However, both parameters were significantly lower in UA-treated EAM mice.



Effects of ursolic acid in the cardiac oxidative stress development: Nrf2 signaling pathway

Hearts from EAM animals were also exposed to elevated levels of oxidative stress that overwhelms the capacity of antioxidant systems to cope with this severe inflammatory scenario. Therefore, cytosolic reactive oxygen species (ROS) sensor DHE was used to characterize intracellular ROS, and MDA content was measured to assess lipid

peroxidation end products. The findings revealed that EAM mice had higher ROS levels and lipid peroxidation levels than sham group, while UA-treated mice had lower levels (Figure 4A–C).

Nrf2 is an important transcriptional factor and the Nrf2/HO-1 axis is an important antioxidative stress pathway in the body. The present study identified that EAM reduced Nrf2/HO-1 protein expression of mice while UA could restore it (Figure 4D–F). Furthermore, UA treatment activated total cellular and nuclear Nrf2 in mouse heart but not cytoplasmic Nrf2 (Figure 4G–I). These findings demonstrate that UA's cardio-protective effect is partially due to the induction of the antioxidant response via the Nrf2 pathway activation.

Ursolic acid upregulated Nrf2/HO-1 signaling pathway *in Vitro*

To further confirm the molecular mechanism of UA in the inflammatory injury of cardiomyocytes, H9c2 cell was used *in vitro* experiments. To investigate the role of Nrf2 in the UA-mediated beneficial effects, we performed a set of experiments in which we exposed IL-6-stimulated cells to UA (10 μ M, 20 μ M, 30 μ M, 40 μ M, and 50 μ M) for 4 h and quantified Nrf2 total protein levels in H9c2 cell (Figure 5A–C). To investigate the toxicity of UA to cells, we examined cell survival at various concentration points after 24 h of UA intervention (Supplementary Figure S1D). Findings revealed that cell survival was significantly reduced after 24 h of treatment with 50 μ M UA. However, the cell survival rate did not change significantly when the concentration of UA less than 50 μ M. In conclusion, 30 μ M UA was selected for further experiments. The inflammatory cells stimulated by IL-6 were separated nucleoprotein from cytoplasmic protein by nuclear protein extraction kit. In IL-6-stimulated cells, the expression level of Nrf2 in nucleoprotein increased significantly after UA treatment. Meanwhile, there were no significant differences in the expression of Nrf2 in the cytoplasm between the groups (Figure 5D–F).

To further testify that the effects of UA were Nrf2/HO-1 pathway-dependent, specific Nrf2 inhibitor ML385 was utilized *in vitro*. Protein expression of both Nrf2 and HO-1 was reduced after co-incubation of ML385 with UA in cardiomyocytes (Figure 5G–I; Supplementary Figure S1E–G).

ML385 counteracted the anti-apoptosis and antioxidant effects of ursolic acid

Inflammation increased the percentage of apoptotic cells and intracellular ROS. UA attenuated inflammation-induced apoptosis and ROS accumulation, which were nearly abrogated by administration of ML385 (Figure 6). It suggested that the anti-apoptotic and antioxidant effects of UA were mainly achieved by activating Nrf2.

Docking analysis

For a better understanding of the correlation between ursolic acid and Nrf2 domain, AutoDock Vina (Molecular Graphics Lab at the Scripps Research Institute) was employed for the receptor and

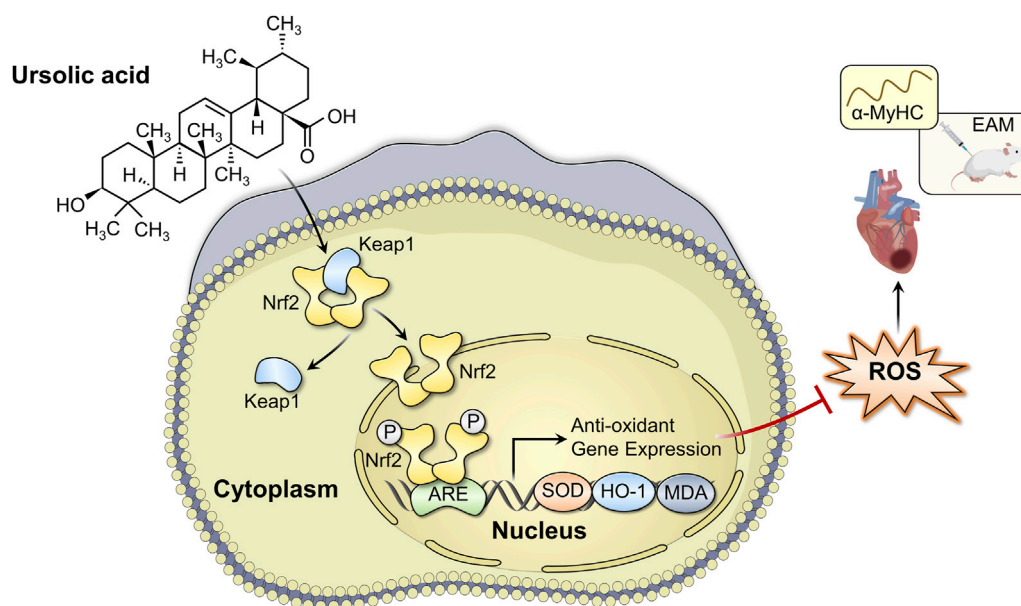


FIGURE 8

Schematic diagram of the mechanism of ursolic acid in the treatment of experimental autoimmune myocarditis.

ligand docking analysis. An interacting complex of Nrf2 and ursolic acid was obtained after docking the molecular proteins with different conformations and poses. The 3D molecular simulation illustrate the binding modes of ursolic acid with Nrf2 via the hydrogen bond and other interactions (Figure 7A). The binding energy between Nrf2 and ursolic is -6.9 kCal/mol. In Figure 7B, Nrf2 primarily relied on hydrogen bonds to interact with ursolic acid, ursolic acid forms a hydrogen bond (2.78 Å) with Lys462 and a hydrogen bond (3.04 Å). In addition, ursolic acid also interacts with Pro467 and Leu 450 via hydrophobic interactions, which are shown as arcs (red) in Figure 7B.

Discussion

In the present study, we found that UA could reduce EAM-induced myocardial injury through the oxidative stress pathway. UA ameliorated EAM-induced myocardial injury by scavenging ROS and activating the Nrf2/HO-1 pathway.

Despite the host-activated immune response, many studies have confirmed the presence of multiple anti-myocardial antibodies in patients with myocarditis and DCM, the most common of which are anti-cardiac myosin antibodies (Caforio et al., 2008). In the present study, the EAM model in mice is induced by immunizing mice with myocardial self-antigens, which simulates the autoimmune process of acute myocarditis (Pando et al., 2010; Zempo et al., 2015). An autoimmune response is a common pathological process of myocarditis caused by various pathogenic factors. The EAM model has been used in many studies to investigate the pathogenesis of clinical myocarditis and post-myocarditis cardiac dysfunction (Tada and Suzuki, 2016). Therefore, we select the EAM model to further investigate the role and potential mechanisms of UA in protection against myocarditis.

In an abnormal immune response in the myocardium, antigen presence stimulates the differentiation and proliferation of many T cells in the peripheral immune organs, which migrates from the blood circulation to the heart. Lymphocytes infiltrate the myocardium and release inflammatory cytokines such as IL-6, IL-17, and IL-23, causing cardiomyocyte hypertrophy or death, resulting in myocardial hypertrophy or fibrosis and cardiac systolic or diastolic dysfunction (Vdovenko and Eriksson, 2018; Chang et al., 2019). IL-6 plays an important role in the inflammatory storm of myocarditis. Yamashita et al. demonstrated that blocking IL-6 receptors prior to immunization inhibited the development of autoimmune myocarditis in mice. In a study of autoimmune myocarditis in IL-6-deficient mice, it was found that the prevalence and severity of myocarditis were markedly reduced in the absence of IL-6. These may provide evidences for our selection of IL-6 as the primary inflammatory agent. Therefore, in the present study, we provide experimental evidence that IL-6 stimulation of H9c2 cells causes ROS production and cell apoptosis (Figure 6).

In recent years, Nrf2 has been shown to have a protective role in major cardiovascular diseases (CVDs) in murine models. It can improve cardiac function and reduce efferocytosis and the release of pro-inflammatory cytokines, thereby improving the pathological phenotype (Gu et al., 2017; Shen et al., 2019; Chen et al., 2021). Nrf2 is the master regulator of antioxidant responses. The activation of the Nrf2-dependent antioxidant system is important in cellular defense against oxidative stress damage, and the deficiency of the Nrf2 system may pose a significant risk to the cardiovascular system (da Costa et al., 2019). Curcumin, a natural Nrf2 activator, inhibits oxidative stress and inflammation caused by free fatty acid treatment of cardiomyocytes, implying that Nrf2 is closely associated with the risk of obesity-related metabolic cardiovascular disease (Zeng et al., 2015). In experimental diabetic cardiomyopathy, reduced Nrf2 activity was

observed, as was antioxidant enzyme activity downstream and increased oxidative stress (Wang et al., 2017). In addition, numerous studies have demonstrated that Nrf2 protects against atherosclerosis by reducing vascular smooth muscle cell (VSMC) migration, proliferation, calcification, and vascular remodeling (Duckers et al., 2001; Ashino et al., 2013; Ashino et al., 2016), although it has not been thoroughly studied that Nrf2-ARE may play a regulatory role in myocarditis (Tada and Suzuki, 2016). Our findings revealed that EAM downregulates the Nrf2 protein expression and reduces the nuclear entry of Nrf2. Moreover, EAM downregulates Nrf2 transcription regulation of phase II antioxidant enzyme HO-1, increases the oxidative stress-induced lipid peroxidation index Malondialdehyde (MDA) and cell apoptosis in heart. Under oxidative conditions, Nrf2 translocates from the cytoplasm to the nucleus, which binds to AREs to regulate downstream genes, such as HO-1, in the present study. These findings are consistent with a previous study that describe the role of Nrf2 upregulation in protecting the EAM-induced cardiomyocyte from oxidant stress damage (Jaén et al., 2020). We determined that UA can reduce damage associated with oxidative stress in the EAM model by activating the Nrf2 pathway and its antioxidant targets. To further validate this view, in the present study, we identified Nrf2 as the primary target of UA through the inhibition of Nrf2 by ML385, which nearly reversed the beneficial effects of UA on apoptosis and oxidative stress damage.

Currently, the prevailing view is that oxidative stress exacerbates the dysfunction and structural remodeling of myocarditis. There are also many studies for the effects of antioxidants. Meanwhile, more and more molecular targets and new drugs have been discovered. However, due to the difficulty of manufacturing the drugs and safety, clinical translation cannot be achieved. In contrast, ursolic acid has following advantages, which make it promising as an antioxidant to assist in EAM treatment: 1) UA is a natural product ingredient that can be extracted from natural plants (e.g., apple peels) in plentiful quantities and at a relatively cheap price; 2) UA probably provides a better safety profile in clinical use, even people with a high risk of myocarditis may benefit from taking UA as a health supplement. Furthermore, the findings of the present study on the regulatory role of UA in EAM broaden our understanding of the multiple functions of UA in the heart. These findings could serve as a model for drug development in autoimmune myocarditis. The results, along with previous studies on the role of UA in myocardial infarction and atherosclerosis, suggest that UA may be useful for various clinical indications in CVDs.

However, there are several limitations to present study. To further validate the role of Nrf2/HO-1 signaling pathway in H9c2, we selected Nrf2 inhibitor, ML385, rather than Nrf2 siRNA, which is relatively less persuasion. Furthermore, the antioxidant mechanisms of ursolic acid are complex and still need further study.

Conclusion

In conclusion, we have demonstrated that UA administration could alleviate EAM-induced myocardial injury, as evidenced by improvements in cardiac functions, cardiac inflammation, and

structural remodeling, partially by attenuating oxidative stress in a Nrf2/HO-1 pathway-dependent manner (Figure 8). The present study indicates that UA may be a therapeutic candidate drug for the treatment of myocarditis.

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 Institutional Animal Care and Use Committee, Huazhong University of Science and Technology.

Author contributions

YF, TL and JW designed this research; YF, SH, YB and JQ performed the experiments; YF, YZ, YT and JS analyzed and interpreted the results; YF drafted manuscript; TL, QJ and WD revised the manuscript; YC, JW and MX determined the final version of manuscript. All authors contributed to the article and approved the submitted version.

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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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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fphar.2023.1189372/full#supplementary-material>

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Commentary: Identification of cuproptosis hub genes contributing to the immune microenvironment in ulcerative colitis using bioinformatic analysis and experimental verification

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inflammatory bowel disease, ulcerative colitis, cuproptosis, bioinformatics, FDX1

A Commentary on

Identification of cuproptosis hub genes contributing to the immune microenvironment in ulcerative colitis using bioinformatic analysis and experimental verification

by Yang C, Wang W, Li S, Qiao Z, Ma X, Yang M, Zhang J, Cao L, Yao S, Yang Z and Wang W (2023) *Front. Immunol.* 14:1113385. doi: 10.3389/fimmu.2023.1113385

Cuproptosis is an entirely novel copper-dependent regulated cell death that differs morphologically, biochemically, and genetically from apoptosis, autophagy and ferroptosis (1). Yang et al. (2) and Chen et al. (3) conducted studies that suggested a potential therapeutic role of cuproptosis in inflammatory bowel disease (IBD). They reached this conclusion by employing bioinformatics analysis and experimental validation using dextran sodium sulfate (DSS)-induced mouse models. Yang et al. confirmed the therapeutic effects of three cuproptosis-related genes (*DLAT*, *DLD*, and *PDHA1*) on immune infiltration in patients with ulcerative colitis (UC). Similarly, Chen et al. found that Crohn's disease (CD), UC, celiac disease (CEL), and IBD-induced cancer (IBD-CA) had common cuproptosis-related differentially expressed genes, including *DLAT*, *LIAS*, *DBT*, and *PDHA1*. Both these studies had positive implications for mechanism exploration; however, further analyses of their results are warranted.

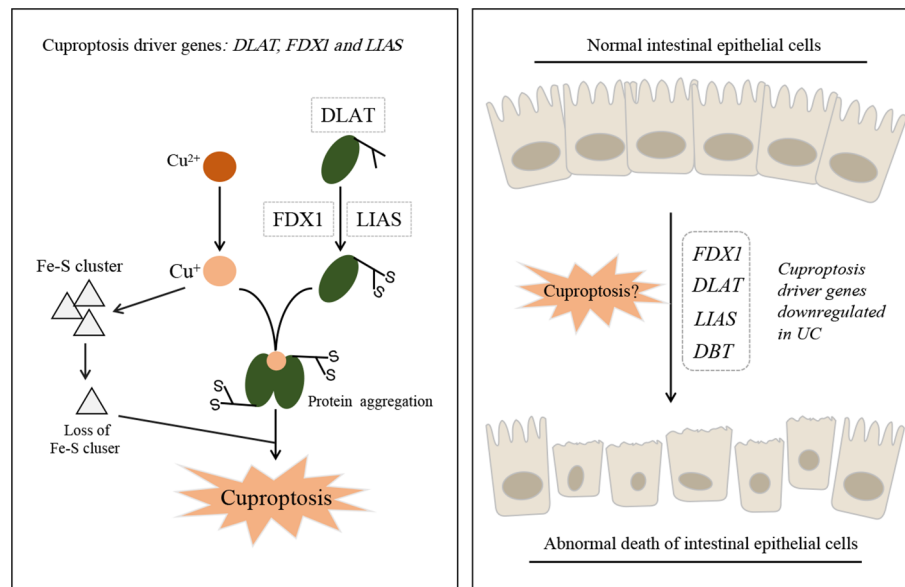


FIGURE 1

Schematic model of cuproptosis and ulcerative colitis. Cu^{+} binds to lipoylated mitochondrial enzymes DLAT and induced the aggregation of these proteins. Mitochondrial ferredoxin (FDX1) and lipoyl synthase (LIAS) are key driver genes of cuproptosis (Left). Abnormal death of intestinal epithelial cells can lead to the occurrence of ulcerative colitis, but the cuproptosis driver genes were identified as down-regulated in UC patients (Right).

Tsvetkov P et al. first discovered cuproptosis in 2022 (1), and since then, 12 cuproptosis-related genes, namely *FDX1*, *LIAS*, *DLAT*, *DLD*, *PDHA1*, *PDHB*, *MTF1*, *GLS*, *CDKN2A*, *LIPT1*, *ATP7B*, and *SLC31A1*, have been validated. This gene set is currently used in many disease studies using bioinformatics analysis. Especially, *DLAT*, *DLA*, *PDHA1*, *LIAS*, and *DBT* are known to promote cuproptosis (Figure 1); hence, the downregulation of these genes prevents cuproptosis. Of note, the promotion of tumor cell death and inhibition of non-tumor cell death are opposing treatment strategies. For example, ferroptosis inhibition alleviates experimental colitis (4) while ferroptosis promotion in tumor cells is a novel therapeutic approach for cancer (5). However, in the above-mentioned studies, the expression of these genes in the intestinal mucosa samples of IBD was found to be downregulated compared to individuals without IBD (Figure 1). According to Tsvetkov P et al. (1), *FDX1* is a key cuproptosis regulator that reduces Cu^{2+} to the more toxic Cu^{+} , thus promoting abnormal oligomerization of thioacylated proteins in the tricarboxylic acid cycle. However, Yang et al. (2) found *FDX1* expression to be downregulated in patients with IBD compared to normal individuals. This seems contradictory if we assume that cuproptosis occurs in the intestinal mucosa of patients with IBD. The contradictory results suggest two things: (I) the downregulation of these genes may not be related to cuproptosis, and may only be as a result of the disease itself; (II) The regulatory mechanism of cuproptosis in normal intestinal mucosal cells could be opposite to that in tumor cells. These hypotheses require further validation.

UC is characterized by recurring inflammatory episodes limited to the colon's mucosal layer (6). Promoting mucosal healing, even at the cell level, has been a potential strategy for

IBD, including UC, treatment (7). Therefore, inhibiting abnormal intestinal epithelial cell death to maintain intestinal mucosal homeostasis is a potential intervention strategy. Both studies validated their results using DSS-induced colitis mouse models. Yang et al. conducted a quantitative analysis of four cuproptosis genes using western blot, which further validated the results from their bioinformatics analysis; however, whether the samples used in the experiment were whole colon tissue or intestinal mucosal cells has not been mentioned. The use of intestinal mucosal cells alone for validation will provide more accurate results, as the bioinformatics analysis samples were also from the intestinal mucosa of patients with IBD.

More studies are still needed to verify whether cuproptosis occurs in the intestinal mucosal cells of patients with IBD. Additionally, the detection of cell copper is also necessary.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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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Baricitinib treatment for refractory skin changes in POEMS syndrome: a case report

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Polyneuropathy, organomegaly, endocrinopathy, monoclonal plasma cell disorder, and skin changes (POEMS) syndrome is a multisystem disorder that has limited treatment options. Here, we described a case of a 55-year-old female subject who was treated for multiple drugs, but the skin symptoms continued to progress; the patient responded well to baricitinib. This suggests that JAK/STAT signaling pathways play an essential role in the pathological process of POEMS syndrome.

KEYWORDS

POEMS syndrome, Janus kinase inhibitor (JAKI), JAK/STAT signaling, skin changes, case report

1 Introduction

Polyneuropathy, organomegaly, endocrinopathy, monoclonal plasma cell disorder, and skin changes (POEMS) syndrome is a multisystem disorder that has limited treatment options (Brown and Ginsberg, 2019). Majority of patients with POEMS syndrome present with hyperpigmentation, hemangiomas, and hypertrichosis. However, most patients do not benefit from the current approaches available for the treatment of these cutaneous symptoms. Herein, we report the case of a patient with POEMS syndrome who presented with six types of skin changes and responded well to baricitinib, with all skin lesions resolving over the treatment period.

2 Case report

The patient is a 55-year-old female subject, who, in 2014, was initially diagnosed with systemic sclerosis due to pulmonary fibrosis and skin changes, including hypertrichosis of the limbs and jaws, thickening and swelling of the skin, hyperpigmentation, hemangiomas, Raynaud's phenomenon, and swelling of the back and lower limbs. Skin biopsy of the right leg revealed hyperkeratosis of the epidermis, mild hyperplasia of the dermis, and sparse collagen fibers in the middle without dermal vascularization. In 2016, the patient complained of bilateral lower limb pain, numbness, and paresthesia. An electrophysiological examination suggested multiple peripheral neuropathies. Ultrasonography revealed bilateral lymphadenopathy in the neck and supraclavicular, axillary, inguinal, mesenteric, and retroperitoneal regions. Laboratory tests revealed diabetes mellitus and mild renal dysfunction, as well as serum vascular endothelial growth factor (VEGF) levels of 7,924 pg/mL (normal range: 0–600 pg/mL). Furthermore, serum protein electrophoresis revealed a monoclonal band of IgA lambda +. Consequently, the patient was diagnosed with



FIGURE 1

Prior to the treatment with baricitinib, hyperpigmentation, skin thickening on the face, upper and lower limbs with hypertrichosis and hemangiomas in the extensor lateral forearms, and swollen lower limbs were observed (A). The skin changes have partially dissipated after 3 months of treatment (B) and have been almost fully reversed after 1 year (C).

POEMS syndrome due to multiple peripheral neuropathy symptoms, skin changes, and a high level of VEGF, based on the current diagnostic criteria for POEMS syndrome, i.e., the Dispenzieri diagnostic criteria (Miest et al., 2013).

The patient refused bortezomib; therefore, an alternative treatment regimen was adopted. Despite treatment with multiple drugs, including thalidomide, cyclophosphamide, glucocorticoids, and Kunxian capsules, supplemented with the usual dose, the skin symptoms continued to progress, while other non-skin symptoms improved. Hence, the treatment plan was modified, and oral baricitinib (2 mg/day) was administered. The cutaneous symptoms improved after 3 months of baricitinib treatment, and full recovery was noted after 1 year (Figure 1). The patient showed sustained improvement in the skin symptoms over 18 months of follow-up, and serum VEGF levels decreased considerably to 50.62 pg/mL.

3 Discussion

The Janus kinase (JAK)/STAT pathway is involved in various skin disorders, including alopecia areata, atopic dermatitis, lupus erythematosus, dermatomyositis, psoriasis, and vitiligo (Solimani et al., 2019). Vitiligo is an autoimmune skin disease in which melanocytes are reduced in association with the activation of the interferon- γ (IFN- γ) and CXCL-10 signaling pathways (Frisoli et al., 2020). The JAK inhibitor baricitinib, which has been shown to block IFN- γ signaling and contribute to re-pigmentation, has been approved for treatment of patients with vitiligo (Qi et al., 2021; Yan et al., 2022). Interestingly, in the present case, hyperpigmentation was treated with baricitinib, which is in contrast to the skin symptoms of vitiligo.

To the best of our knowledge, this is the first report on the successful use of baricitinib to treat skin symptoms associated

with POEMS syndrome. The pathogenic mechanisms underlying the skin symptoms associated with POEMS syndrome are poorly understood. However, VEGF has been identified as a key cytokine involved in the pathogenesis of this disorder and is known to reflect the disease activity (Dispenzieri, 2017). Du et al. reported that VEGF expression is associated with JAK/STAT signaling in psoriasis (Du et al., 2020). The role of JAK/STAT in rheumatoid arthritis and new vessel formation has also been reported. Paola et al. explored the anti-angiogenic role of tofacitinib, another JAK inhibitor, in experimental arthritis, which was attributed to inhibition of the pro-angiogenic effects of VEGF (Di Benedetto et al., 2021). Further evidence has confirmed that among the tyrosine kinase cell receptor (VEGFR) 2-mediated signaling pathways, the JAK/STAT signaling pathway, especially the STAT3 signaling pathway, is a critical target and biomarker of angiogenesis (Zhang et al., 2011). Given these findings and our observation with the present case, we propose that angiogenesis is the primary process involved in the pathogenesis of cutaneous changes in patients with POEMS syndrome.

4 Conclusion

Baricitinib is a promising treatment for skin symptoms in patients with POEMS, which can be attributed to the targeting of JAK/STAT signaling to inhibit angiogenesis. However, further studies are required to better understand the pathogenic mechanisms underlying POEMS syndrome, specifically the role of JAK/STAT3 signaling and angiogenesis.

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

Written informed consent was obtained from the individual(s) for the publication of any potentially identifiable images or data included in this article. Written informed consent was obtained from the participant/patient(s) for the publication of this case report.

Author contributions

JX, ZL, and YJ prepared the study documents. DT, XQ, and EJ were responsible for patient contact and data collection. JX and JZ drafted the manuscript. All authors contributed to the article and approved the submitted version.

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Tangeretin attenuates bleomycin-induced pulmonary fibrosis by inhibiting epithelial-mesenchymal transition via the PI3K/Akt pathway

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Background: Pulmonary fibrosis (PF) is a terminal pathological change in a variety of lung diseases characterized by excessive deposition of extracellular matrix, for which effective treatment is lacking. Tangeretin (Tan), a flavonoid derived from citrus, has been shown to have a wide range of pharmacological effects. This study aimed to investigate the role and potential mechanisms of Tan on pulmonary fibrosis.

Methods: A model of pulmonary fibrosis was established by administering bleomycin through tracheal drip, followed by administering Tan or pirfenidone through gavage. HE and Masson staining were employed to assess the extent of pulmonary fibrosis. Subsequently, Western blot, enzyme-linked immunosorbent assay (ELISA), RNA sequencing, and immunohistochemistry techniques were employed to uncover the protective mechanism of Tan in PF mice. Furthermore, A549 cells were stimulated with TGF- β 1 to induce epithelial-mesenchymal transition (EMT) and demonstrate the effectiveness of Tan in mitigating PF.

Results: Tan significantly ameliorated bleomycin-induced pulmonary fibrosis, improved fibrotic pathological changes, and collagen deposition in the lungs, and reduced lung inflammation and oxidative stress. The KEGG pathway enrichment analysis revealed a higher number of enriched genes in the PI3K/Akt pathway. Additionally, Tan can inhibit the EMT process related to pulmonary fibrosis.

Conclusion: Taken together, the above research results indicate that Tan suppresses inflammation, oxidative stress, and EMT in BLM-induced pulmonary fibrosis via the PI3K/Akt pathway and is a potential agent for the treatment of pulmonary fibrosis.

KEYWORDS

pulmonary fibrosis, tangeretin, PI3K/Akt signaling pathway, epithelial-mesenchymal transition, bleomycin

1 Introduction

Pulmonary fibrosis (PF) is a chronic and lethal lung disease that is characterized by the excessive deposition of extracellular matrix (ECM), resulting in impaired gas exchange and lung function (Moss et al., 2022; C; Wang and Yang, 2022; J; Yang et al., 2023a). The most prevalent form of PF is idiopathic pulmonary fibrosis, which has a bleak prognosis and a median survival rate of 2.5–3.5 years following diagnosis (Strongman et al., 2018). Pulmonary fibrosis is associated with multiple risk factors, such as genetic predisposition, exposure to radiation and environmental toxins, adverse drug reactions, and age and gender (Mathai and Schwartz, 2019). Additionally, various respiratory viruses, including the common influenza virus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and respiratory syncytial virus, have been identified as potential causative agents of pulmonary fibrosis (Wang et al., 2017; Chiou et al., 2023; W; Yang et al., 2022). Currently, pulmonary fibrosis is treated with pirfenidone (PFD) and nintedanib, which have limited efficacy in halting the progression of fibrosis and are associated with varying degrees of adverse effects, thereby hindering their widespread use (Trachalaki et al., 2021). Consequently, novel therapeutic approaches are warranted for the prevention and management of pulmonary fibrosis.

The pathogenesis of pulmonary fibrosis remains uncertain; however, current consensus suggests that it initiates with anomalous tissue restoration following injury (Sun et al., 2023; H; Li, Zhao, Tian, et al., 2020). Following lung injury, alveolar type II (AT2) cells participate in the repair process through self-renewal and differentiation into alveolar type I epithelial cells (AT1) (L. Shao et al., 2021; P; Wang, Yan, et al., 2022; Tan et al., 2021). Furthermore, AT2 cells may acquire a mesenchymal phenotype via epithelial-mesenchymal transition (EMT), stimulate fibroblast activation and differentiation, and generate a substantial quantity of extracellular matrix (ECM) molecules implicated in pulmonary fibrosis (Olajuyin et al., 2019; Zhou et al., 2022). Transforming growth factor- β 1 (TGF- β 1) is acknowledged as a pro-fibrotic factor in various organs (Meng et al., 2016). Its mechanism of action involves binding to the TGF- β type II receptor on the AT2 cell membrane and recruiting the TGF- β type I receptor to the plasma membrane, resulting in the formation of a heterotrimer that activates the downstream Smads signaling pathway and the expression of EMT-related transcription factors Snail, Slug, and Twist1 (P. Wang, Yan, et al., 2022; Garg, 2013). Additionally, TGF- β 1 can induce EMT through a non-Smad-dependent pathway, whereby it stimulates the expression of the PI3K subunit p110 and phosphorylation of Akt to promote EMT (Y.E. Zhang, 2017; Saito et al., 2017). The activation of Akt is facilitated through the regulation of its downstream proteins, such as GSK-3 β , mTOR, HIF-1 α , and NF- κ B, which are implicated in the pathogenesis of pulmonary fibrosis (Qin et al., 2021; Peng et al., 2022; Xu et al., 2022).

Tangeretin (Tan) is a naturally occurring flavonoid mainly found in the peel of citrus plants. It exhibits various pharmacological properties, such as antioxidant and anti-inflammatory effects (Xin, et al., 2019; Sedik and Elgohary,

2023). Tan is absorbed by the gastrointestinal tract and primarily metabolized to 4'-demethyltangeretin by CYP1A1 and CYP1A2 enzymes (Surichan et al., 2018). Tan has the potential to mitigate acute lung injury induced by LPS through the inhibition of the Th17 response, TNF- α , and MPO activity via the Notch signaling pathway (M. Li, Zhao, Qi, et al., 2020). Previous studies have demonstrated that Tan is able to prevent podocyte injury and renal fibrosis by effectively blocking glucose-induced oxidative stress and hypoxia-induced EMT in podocytes (Kang et al., 2020). In addition, Tan effectively suppressed the activation of JAK2/STAT3, Wnt, and EGFR signaling pathways, as well as lung fibroblast activation (F. Yang J. et al., 2023; D; Shao et al., 2022). However, the potential mechanism of Tan in the treatment of pulmonary fibrosis remains incompletely understood. In this study, we employed network pharmacology to predict the potential biological pathways of Tan in the management of pulmonary fibrosis. Additionally, we conducted experimental investigations to investigate the function of Tan in pulmonary fibrosis.

2 Materials and methods

2.1 Chemicals and reagents

Tan was purchased from Chengdu Must Biotechnology Co., Ltd. (purity \geq 98%, Chengdu, China). Bleomycin sulfate (BLM) was obtained from Macklin (Shanghai, China). Pirfenidone was purchased from Solarbio (Beijing, China). The primary antibodies against E-cadherin, N-cadherin, MMP9, and collagen I were purchased from Immunoway (Plano, TX, United States). p-PI3K, PI3K, p-Akt1, and Akt1 were from Affinity Bioscience (Changzhou, China). TGF- β 1, TGFBR2, α -SMA, β -actin, and all the secondary antibodies were from the Proteintech Group (Wuhan, China).

2.2 Animal model and treatment

Thirty-six 6–8 weeks old male C57BL/6 mice (weight 18–22 g) were purchased from Liaoning Changsheng Biotechnology Co., Ltd. and randomly divided into 6 groups: control, BLM, BLM + Tan (10 mg/kg, Tan 10), BLM + Tan (20 mg/kg, Tan 20), BLM + Tan (40 mg/kg, Tan 40), and BLM + pirfenidone (PFD). The pulmonary fibrosis mice model was constructed by intra-tracheal drip with 5 mg/kg of BLM at day 0. The control mice received an equal amount of saline intravenously. The following day after BLM treatment by gavage, once daily for 21 days: the positive drug group was given pirfenidone by gavage (200 mg/kg/d), Tan powder dissolved in 0.5% sodium carboxymethylcellulose (CMC-Na) solution by gavage (10 mg/kg/d, 20 mg/kg/d, 40 mg/kg/d), and the control and BLM groups were given equal volumes of 0.5% CMC-Na. Body weights were measured every 7 days. On the last day, the mice were euthanized and lung tissues were collected for subsequent experiments. All experiments were conducted in strict accordance with the Jilin University Guide for the Use and Welfare of Laboratory Animals and were approved by the Jilin University Animal Testing Ethics Committee (approval number: SY202212001).

TABLE 1 Primers sequences used for qPCR.

Gene Name	Forward primer (5'to 3')	Reverse primer (5'to 3')
GAPDH	GAATGGGCAGCCGTTAGGAA	AGGAGAAATCGGGCCAGCTA
IL-1 β	TGCCACCTTTTGACAGTGATG	TGATGTGCTGCTGCGAGATT
IL-6	TGGTCTTCTGGAGTACCATAGC	TGTGACTCCAGCTTATCTCTTGG
TNF- α	GAGGCCAAGCCCTGGTATG	CGGGCCGATTGATCTCAGC
TGF- β 1	ACAATTCTGGCGTTACCTT	AGCCCTGTATTCCGTCTCC
collagen I	GTGTTCCCTACTCAGCCGTC	ACTCGAACGGGAATCCATCG
MMP9	AACCTCCAACCTCACGGAC	CAGCGTGGTGTTCGAATGG
E-cadherin	CAGGTCTCTCATGGCTTTGC	CTTCCGAAAAGAAGGCTGTCC
N-cadherin	AGGCTTCTGGTGAAATTGCAT	GTCCACCTTGAAATCTGCTGG
α -SMA	AGCGGGCATCCACGAAAC	TTGATCTTCATGGTGTGGGT

2.3 Cell culture and treatment

A549 cells were bought from the Cell Bank of the Chinese Academy of Sciences (Shanghai, China). Cells were cultured at 37°C under 5% CO₂ in Dulbecco's Modified Eagle Media (DMEM; HyClone) with 10% fetal bovine serum (Biological Industries) and 100 U/mL penicillin and 100 μ g/mL streptomycin. The cytotoxicity of Tan to A549 cells was determined by the CCK-8 assay. An *in vitro* pulmonary fibrosis model was established using 5 ng/mL TGF- β 1 stimulated A549 cells as described previously (Weng et al., 2018; W; Liu et al., 2022). Briefly, A549 cells were seeded into 6-well plates and starved for 24 h following co-culture for 24 h at different Tan concentrations with or without TGF- β 1 (Peprotech, New Jersey, United States).

2.4 Histopathological analysis of lung tissues

The left lung was fixed in 4% paraformaldehyde for 24 h, embedded in paraffin, and cut to 4 μ m. The sections were then stained with hematoxylin-eosin (H&E) and Masson's trichrome stain. Fibrosis scoring and pulmonary fibrosis area assessment were performed as described previously (Hübner et al., 2008; C.-Y; Chen et al., 2010). Briefly, the area of blue collagen fibers in the whole Masson stained scanned section was quantified using ImageJ software in a 2 \times field of view, with the degree of pulmonary fibrosis expressed as a percentage of collagen fiber area. The area fraction of fibrosis = collagen fiber area/lung tissue area \times 100%.

2.5 Determination of hydroxyproline, oxidative stress, and inflammatory cytokines in lung tissues

The hydroxyproline, SOD, CAT, and MDA (Nanjing Jiancheng, Nanjing, China) contents in the mice lung tissues were detected according to the manufacturer's instructions. The levels of IL-1 β , IL-6, and TNF- α (BioLegend, United States) in lung tissue homogenates were measured using ELISA kits according to the manufacturer's instructions.

2.6 Quantitative real-time polymerase chain reaction

Total RNA was extracted using TRIzol® Reagent (Magen) and then reverse transcribed into cDNA using a TransScript® Uni All-in-One First-Strand cDNA Synthesis SuperMix kit (TransGen Biotech, China). The gene expression was detected by qPCR with FastStart universal SYBR Green Master (Roche, United States) using QuantStudio 1 (Thermo Fisher, United States). GAPDH was used as an internal control. The target genes' relative mRNA expression level was quantified with the 2^{- $\Delta\Delta$ CT} method. The primers used (Sangon Biotech, China) are shown in Table 1.

2.7 RNA sequencing analysis

Total RNA was extracted from the lung tissues using TRIzol® Reagent according to the manufacturer's instructions (Magen). RNA samples were detected based on the A260/A280 absorbance ratio with a Nanodrop ND-2000 system (Thermo Scientific, United States), and the RIN of RNA was determined by an Agilent Bioanalyzer 4150 system (Agilent Technologies, CA, United States). Only qualified samples will be used for library construction. Paired-end libraries were prepared using a ABclonal mRNA-seq Lib Prep Kit (ABclonal, China) following the manufacturer's instructions. The mRNA was purified from 1 μ g total RNA using oligo (dT) magnetic beads followed by fragmentation carried out using divalent cations at elevated temperatures in ABclonal First Strand Synthesis Reaction Buffer. Subsequently, first-strand cDNAs were synthesized with random hexamer primers and Reverse Transcriptase (RNase H) using mRNA fragments as templates, followed by second-strand cDNA synthesis using DNA polymerase I, RNaseH, buffer, and dNTPs. The synthesized double stranded cDNA fragments were then adapterligated for preparation of the paired-end library. Adaptor-ligated cDNA were used for PCR amplification. PCR products were purified (AMPure XP system) and library quality was assessed on an Agilent Bioanalyzer 4150 system. Finally, the

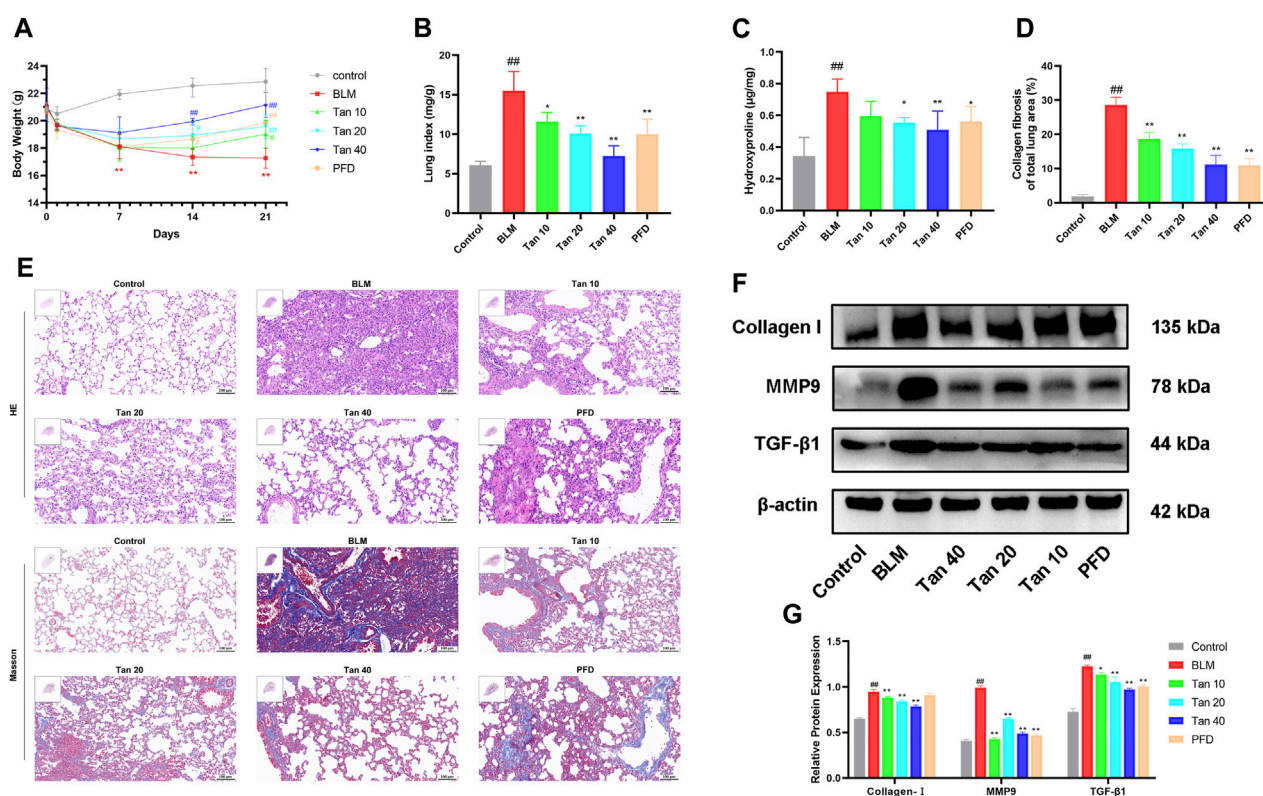


FIGURE 1

Tan attenuated BLM-induced pulmonary fibrosis in mice. (A) Body weight changes in various groups of mice at different time points ($n = 6$). (B) Lung index on day 21 ($n = 6$). (C) The hydroxyproline content in the mice lung tissues ($n = 6$). (D) Area statistics of blue collagen fibers in lung tissue as indicated in Materials and methods. (E) The images of H&E and Masson staining, scale bar, 100 μm . (F) Western blotting of collagen I, MMP9, and TGF- β 1 proteins in mice lung. (G) Quantification of Western blot bands using ImageJ ($n = 3$). The data represent the mean \pm SD. $^*p < 0.05$, $^{**}p < 0.01$, compared with the control group. $^{\#}p < 0.05$, $^{\#\#}p < 0.01$, compared with the model group.

library preparations were sequenced on an Illumina Novaseq 6000 and 150 bp paired-end reads were generated. The data generated from Illumina platform were used for bioinformatics analysis. All of the analyses were performed using an in-house pipeline from Shanghai Applied Protein Technology. FeatureCounts (<http://subread.sourceforge.net/>) was used to count the reads numbers mapped to each gene. And then FPKM of each gene was calculated based on the length of the gene and reads count mapped to this gene. Differential expression analysis was performed using the DESeq2 (<http://bioconductor.org/packages/release/bioc/html/DESeq2.html>), DEGs with $|\log_2\text{FC}| > 1$ and $\text{Padj} < 0.05$ were considered to be significantly different expressed genes.

2.8 Immunohistochemistry

The lung tissue sections underwent de-paraffinization and hydration, followed by antigen retrieval in 3% H_2O_2 for 10 min. Subsequently, the sections were incubated with goat serum and then exposed to α -SMA antibody (1:1500) or E-cadherin antibody (1:500) at 4°C overnight. The sections were then incubated with goat anti-rabbit IgG, followed by incubation with 0.05% diaminobenzidine and restained with hematoxylin.

2.9 Western blot analysis

Total proteins from lung tissue and cells were extracted using RIPA lysis buffer (Thermo Fisher, United States) supplemented with a phosphatase and protease inhibitor cocktail. Then, the samples were lysed on ice for 20 min and centrifuged at 12,000 rpm for 10 min. The total protein concentrations in the supernatant were measured by the BCA protein kit (Thermo Fisher, United States). The proteins were separated by SDS-PAGE and transferred onto PVDF membranes (Millipore, United States). After blocking the membranes with 5% skimmed milk for 2 h, the membranes were sealed with different primary antibodies against TGF- β 1, TGFBR2, α -SMA, E-cadherin, N-cadherin, collagen I, p-PI3K, PI3K, p-Akt1, Akt1, and β -actin at 4°C overnight. The membranes were then incubated for 2 h at room temperature with horseradish peroxidase (HRP)-coupled goat anti-mouse or goat anti-rabbit IgG secondary antibody. The protein bands were visualized using the ECL luminescence detection kit, and the grayscale values of the protein bands were analyzed using ImageJ software.

2.10 Statistical analysis

All data were presented as mean \pm standard deviation (SD). GraphPad Prism 8.0 software was used to perform One-way

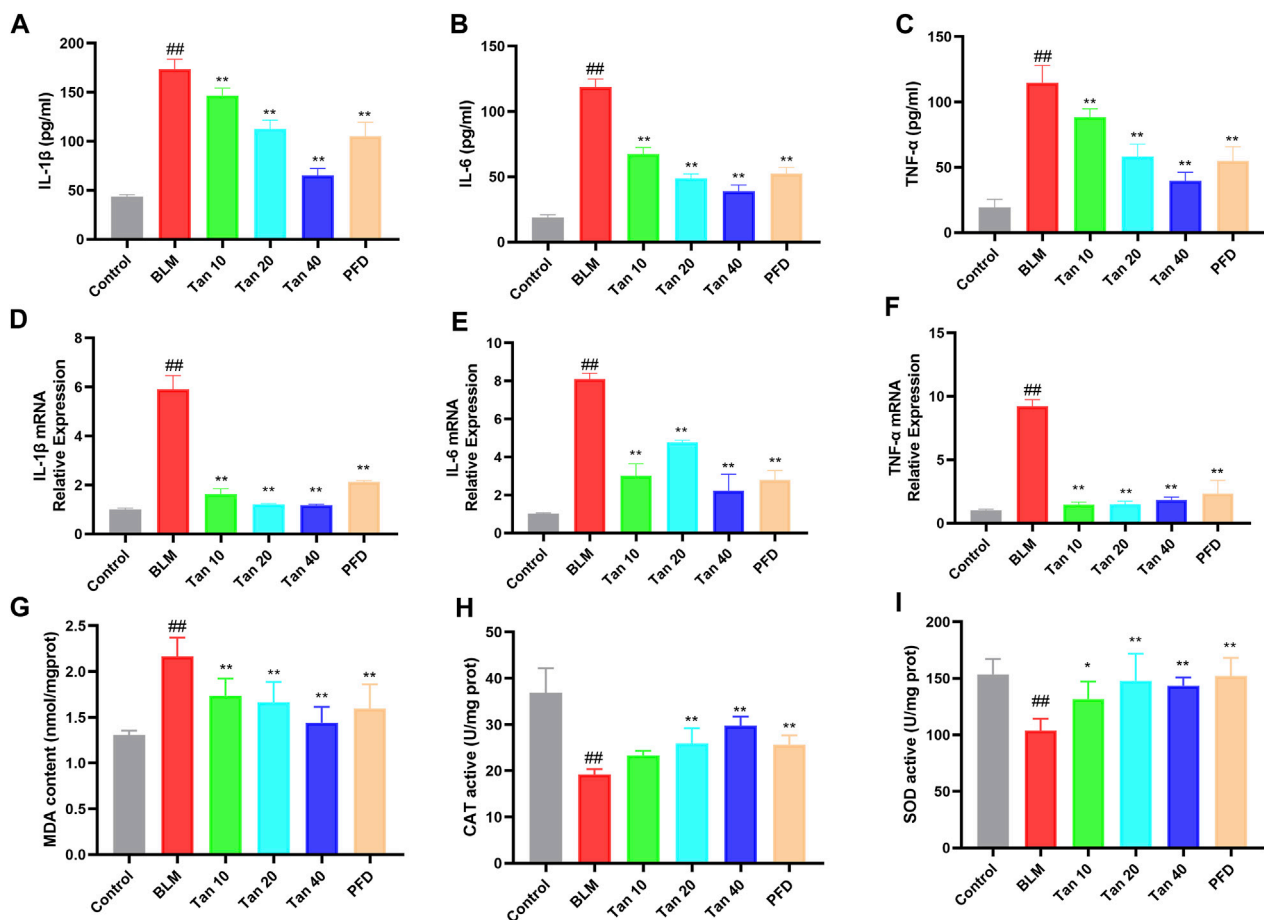


FIGURE 2

Tan reduced inflammation and oxidative stress in mice lung tissues. The secretion of IL-1 β (A), IL-6 (B), and TNF- α (C) in lung tissue homogenates were measured by ELISA ($n = 6$). The mRNA levels of IL-1 β (D), IL-6 (E), and TNF- α (F) in lung tissue were measured by qPCR ($n = 3$). The MDA content (G), CAT (H), and SOD (I) activity were determined in the mice lung tissues ($n = 6$). ## $p < 0.01$, compared with the control group. * $p < 0.05$, ** $p < 0.01$, compared with the model group.

ANOVA analysis and to graph. $p < 0.05$ was considered statistically significant.

3 Results

3.1 Tan attenuated bleomycin-induced pulmonary fibrosis in mice

To investigate the role of Tan in pulmonary fibrosis, a pulmonary fibrosis mouse model was established by tracheal drip injection of BLM. The results showed that the weight of BLM-treated mice decreased significantly, while Tan or PFD could increase the weight of the mice (Figure 1A). Meanwhile, Tan or PFD could effectively reduce the lung index and the hydroxyproline content of the lung tissue (Figures 1B,C). H&E and Masson staining results showed that, compared with the control group, the BLM group mice had severely damaged alveolar structures with massive inflammatory cell infiltration, alveolar wall thickening, and blue collagen deposition. These effects were significantly reduced by treatment with Tan or PFD

(Figure 1E). Furthermore, Tan or PFD treatment reduced the Ashcroft score and the area of collagen fibers in the lung tissue of mice with pulmonary fibrosis (Figure 1D, Supplementary Figure S1A). Then, we measured the expression of collagen I, TGF- β 1 and the core protein MMP9, markers of pulmonary fibrosis, by Western blotting. The data showed that BLM induced the expression of collagen I, TGF- β 1, and MMP9, and Tan or PFD treatment significantly reduced this increase (Figures 1F,G). Consistent with the Western blotting results, qPCR results indicated that Tan intervention significantly reduced collagen I, TGF- β 1, and MMP9 mRNA levels (Supplementary Figures S1B–D). Collectively, these results suggest that Tan could mitigate BLM-induced pulmonary fibrosis.

3.2 Tan reduced inflammation and oxidative stress in mice lung tissues

Studies have found that inflammation and oxidative stress also play an important role in the development of pulmonary fibrosis (Cameli et al., 2020; Q; Zhang et al., 2023). Hence, to evaluate the

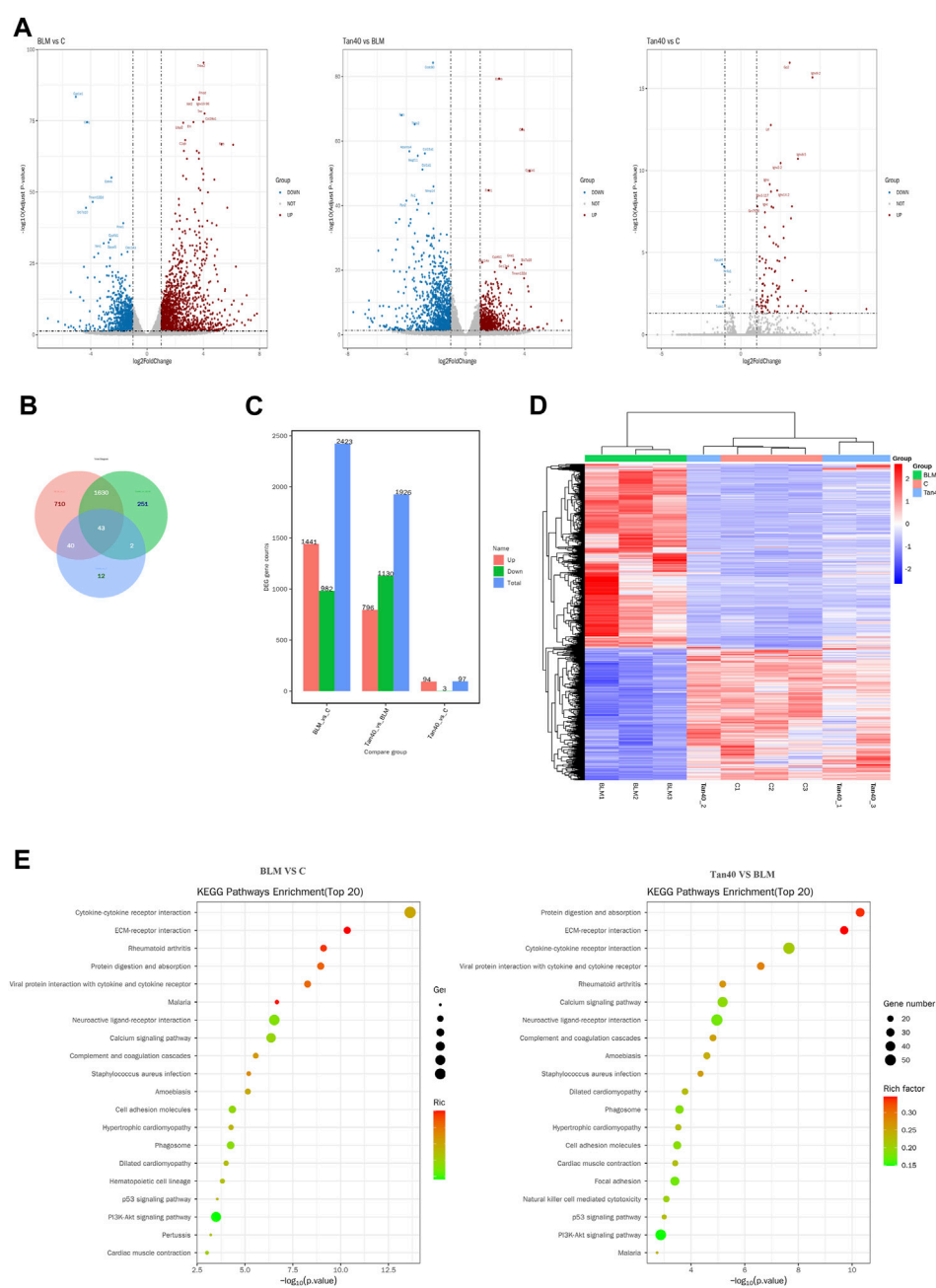


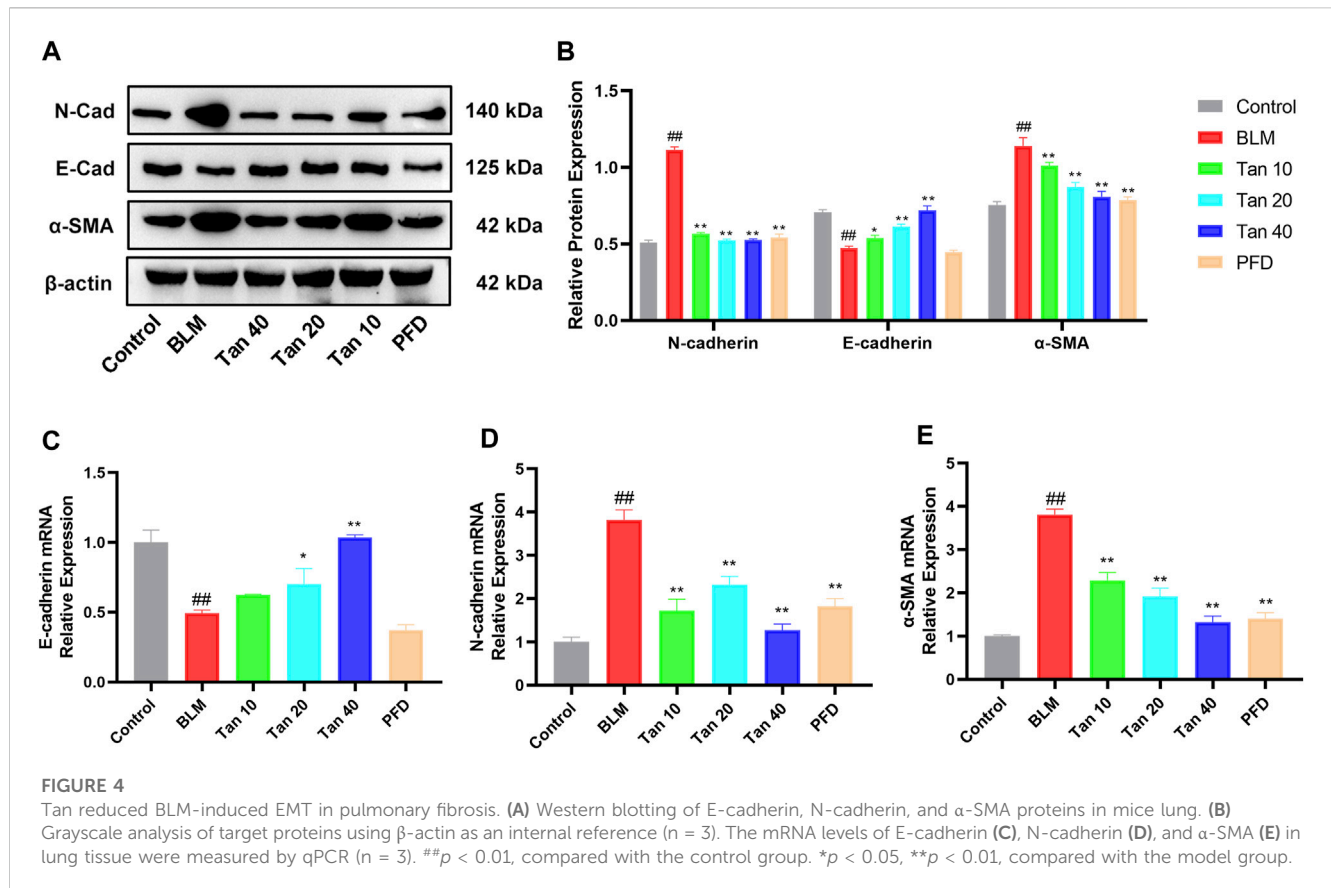
FIGURE 3

Transcriptomic effects of Tan on the lungs of mice with pulmonary fibrosis ($n = 3$). **(A)** Volcano plot of mRNA expression in each group of lung tissue. **(B)** Venn diagram of differentially expressed mRNAs between the three groups. **(C)** Number of DEGs (Differential Expressed Genes) in each group. **(D)** Heatmap showing the hierarchical clustering of mRNAs in the lung tissues of different groups. **(E)** The top 20 KEGG pathway enrichment analysis in control vs BLM, BLM vs Tan 40.

anti-inflammatory and antioxidant effects of Tan, we measured inflammation and oxidative stress-related indicators in mice lung tissues. The secretion and mRNA expression of IL-1 β , IL-6, and TNF- α were significantly higher in the lung tissue of BLM-treated mice compared to the control group, and Tan decreased them in a dose-dependent manner (Figures 2A–F). In addition, the Tan intervention significantly reduced MDA levels and increased CAT and SOD activities (Figures 2G–I).

3.3 Transcriptomic analysis of Tan treating pulmonary fibrosis

We used DESeq2 for differential analysis, with the screening being $|\log_2FC| > 1$ and $\text{Padj} < 0.05$. Volcano plot showing changes in expression of different genes between the three groups (Figure 3A). Compared with the control group, a total of 2423 DEGs were identified in the BLM group, of which 1441 were upregulated



and 982 were downregulated. After treatment with Tan, a total of 1926 DEGs were identified. Among them, 796 genes were upregulated, while 1130 genes were downregulated (Figure 3B). The Venn diagram showed 43 DEGs between the groups, which may be the critical DEG for the Tan treatment of pulmonary fibrosis (Figure 3C). As shown in Figure 3D, heat map clustering analysis was performed on the DEGs. In addition, the KEGG pathway enrichment analysis showed that Tan treatment of pulmonary fibrosis mice mainly affected ECM-receptor interaction, PI3K/Akt signaling pathway, P53 signaling pathway and other related pathways. The top 20 KEGG pathways were showed in Figure 3E.

3.4 Tan inhibited BLM-Induced epithelial-mesenchymal transition process *in Vivo*

EMT is a critical pathological process in pulmonary fibrosis, manifested mainly in the transformation of epithelial cells into fibroblasts, leading to a downregulation of the expression of the epithelial marker E-cadherin and an upregulation of the mesenchymal phenotypic markers N-cadherin and α-SMA (Rout-Pitt et al., 2018; Miao et al., 2022). As shown in Figures 4A,B, the expression of E-cadherin was reduced and the expression of N-cadherin and α-SMA was increased in the lung tissue of BLM-treated mice compared to the control group. The qPCR results were consistent with the Western blotting results, which showed that Tan intervention significantly upregulated E-cadherin gene expression and downregulated N-cadherin and α-SMA gene expression (Figures 4C–E). Immunohistochemical staining revealed a significant

increase in α-SMA expression and decrease in E-cadherin expression in the BLM group. However, intervention with Tan reversed these changes (Figures 5A, B).

3.5 Tan alleviated TGF-β1-induced epithelial-mesenchymal transition process in A549 cells

To further elucidate the mechanism of Tan in pulmonary fibrosis, we examined the effect of Tan on TGF-β1-induced EMT in A549 cells. The CCK-8 results showed no cytotoxic effect of Tan on A549 cells in the concentration range of 0–10 μM (Figure 6A). Tan effectively reduced the upregulation of TGFBR2 induced by 5 ng/mL TGF-β1 stimulation (Supplementary Figure S2). The results presented in Figures 6B–F indicate a significant increase in the protein expression of collagen I, N-cadherin, and α-SMA, along with a decrease in E-cadherin expression in A549 cells following TGF-β1 stimulation. In contrast, Tan administration decreased the expression of collagen I, N-cadherin, and α-SMA and increased the expression of E-cadherin. In conclusion, Tan can inhibit TGF-β1 induced EMT process to alleviate pulmonary fibrosis.

3.6 Tan inhibited PI3K/Akt signaling pathway *in Vitro* and *in Vivo*

Transcriptomic results showed that the PI3K/Akt signaling pathway was enriched with more DEGs. To investigate the potential

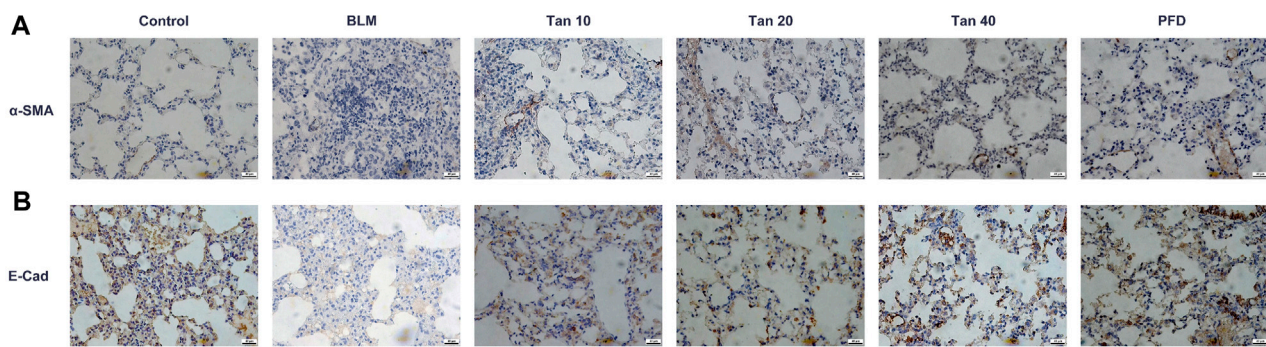


FIGURE 5
Immunohistochemical results of α -SMA (A) and E-cadherin (B) in lung tissue, scale bar, 40 μ m.

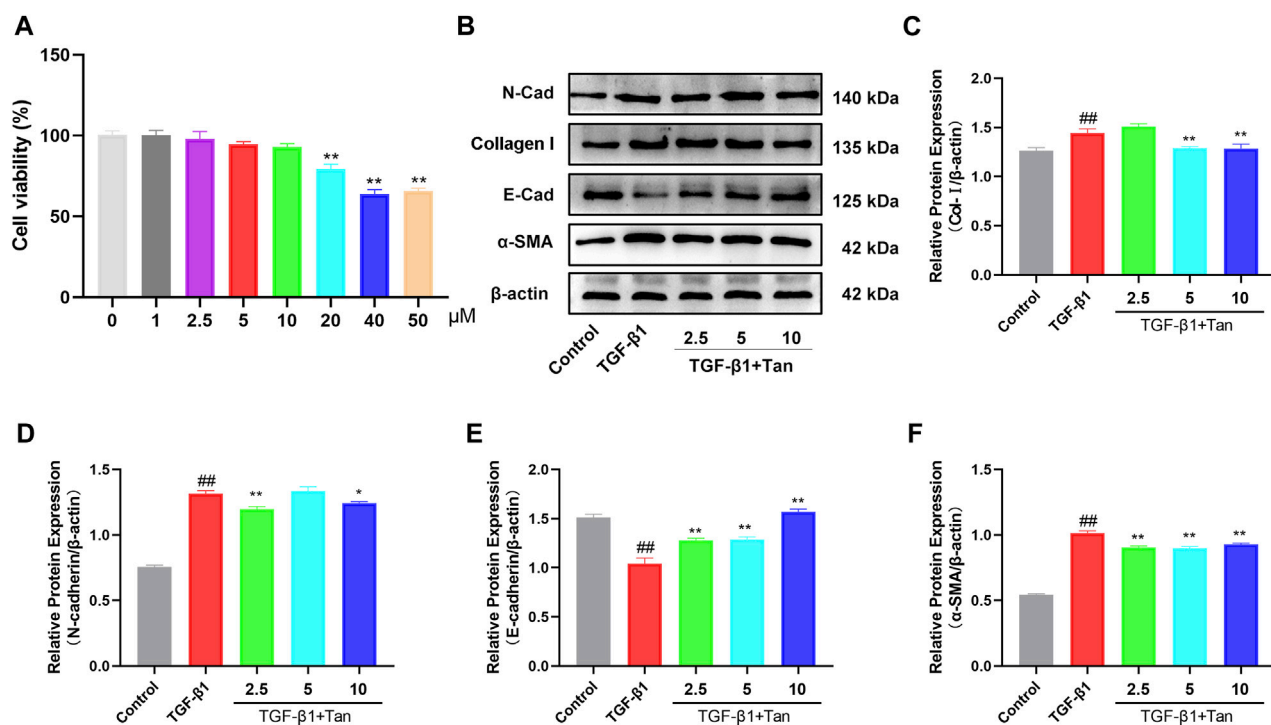
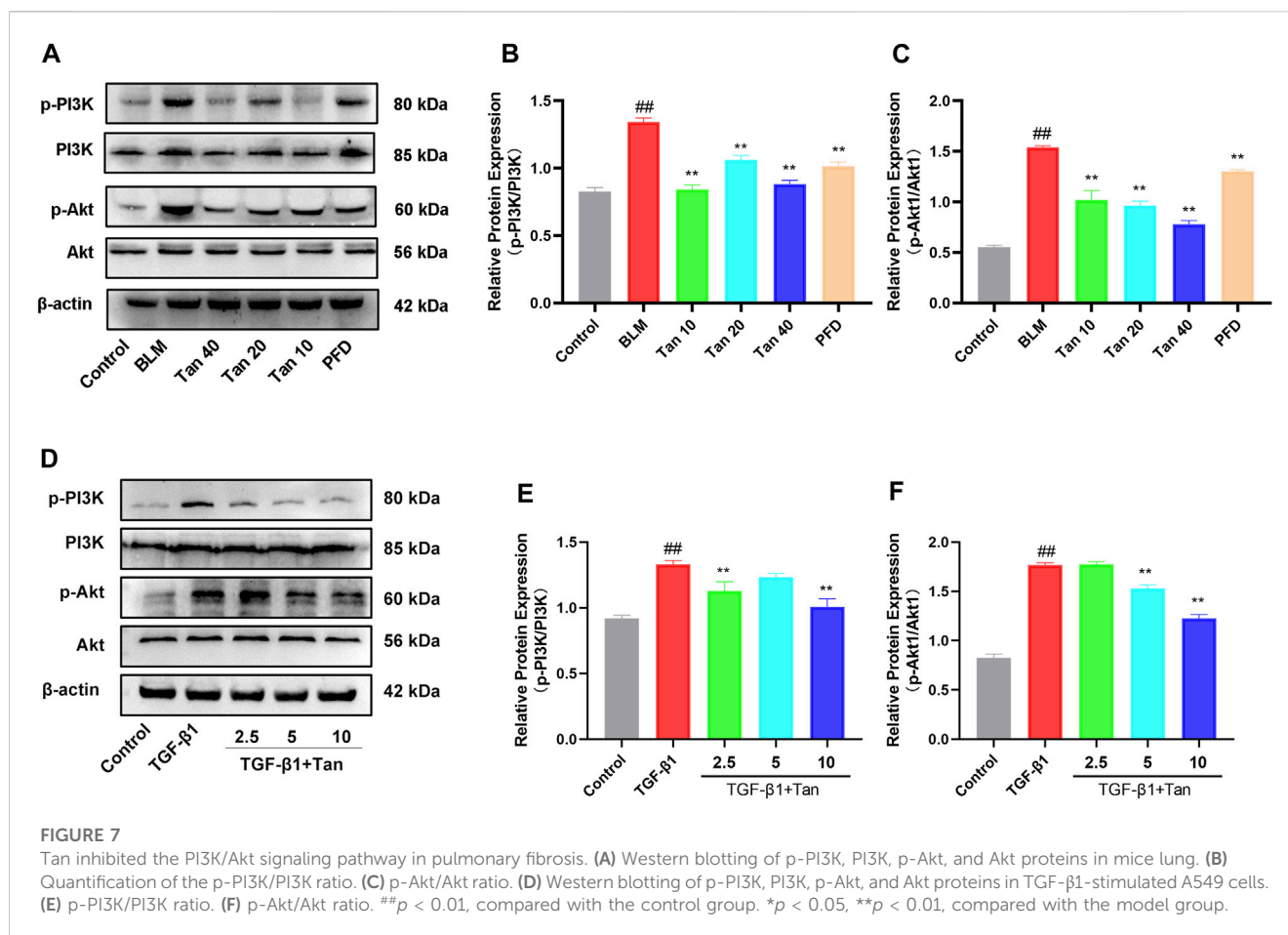


FIGURE 6
Tan alleviated the TGF- β 1-induced EMT *in vitro*. (A) The effect of Tan on the viability of A549 cells. (B) Western blotting of collagen I, E-cadherin, N-cadherin, and α -SMA protein. (C) Quantification of the collagen I/ β -actin ratio. (D) E-cadherin/ β -actin ratio. (E) N-cadherin/ β -actin ratio. (F) α -SMA/ β -actin ratio. ## p < 0.01, compared with the control group. * p < 0.05, ** p < 0.01, compared with the model group.

relationship between the ameliorative effect of Tan on pulmonary fibrosis mice and the PI3K/Akt signaling pathway, we conducted Western blotting analysis to detect relevant proteins in this pathway. The results revealed a significant increase in the expression of p-PI3K and p-Akt1 in the lung tissues of pulmonary fibrosis mice. However, Tan treatment remarkably inhibited the expression of p-PI3K and p-Akt1 (Figures 7A–C). Furthermore, Tan also exhibited a suppressive effect on the expression of p-PI3K and p-Akt1 in TGF- β 1-induced A549 cells (Figures 7D–F). These findings collectively suggest that Tan exerts its ameliorative effects on pulmonary fibrosis through the modulation of the PI3K/Akt signaling pathway.

4 Discussion

Pulmonary fibrosis represents the final stage of multiple acute and chronic lung ailments, culminating in respiratory failure and mortality. While pirfenidone and nintedanib have received FDA approval for pulmonary fibrosis treatment, they do not significantly reduce patient mortality (Trachalaki, Irfan, and Wells, 2021). Consequently, the quest for novel drugs to address pulmonary fibrosis is a pressing concern. Numerous studies have highlighted the antifibrotic advantages of the active constituents found in herbal medicines (Wang et al., 2021). Tan, an active constituent of the Chinese medicine Chen Pi, exhibits a diverse



range of pharmacological activities (Cheng et al., 2023). Research has demonstrated its potential as an antiviral agent by hindering the entry of the SARS-CoV-2 virus into cells (H. Wang et al., 2023). In this study, we elucidated the protective mechanism of Tan against pulmonary fibrosis. Transcriptome analysis of lung tissue samples from mice with pulmonary fibrosis identified several relevant DEGs. The findings suggest that Tan's amelioration of pulmonary fibrosis is associated with the PI3K/Akt signaling pathway. Further experimental validation showed that Tan inhibited TGF-β1-induced EMT in epithelial cells by suppressing PI3K/Akt signaling, which effectively attenuated pulmonary fibrosis.

BLM, an anti-tumor drug, has been utilized in animal experiments to induce pulmonary fibrosis due to its significant lung toxicity (Mouratis and Vassilis, 2011). After tracheal instillation of BLM, the lung epithelial cells undergo damage, resulting in a severe inflammatory response in the lungs. This response produces high levels of pro-inflammatory cytokines such as TNF-α, IL-1β, and IL-6, which in turn promote the recruitment of macrophages and lymphocytes, as well as the activation of fibroblasts (Xin et al., 2019; Lv et al., 2023). Our study found that the stimulation of BLM led to a significant increase in the secretion and expression of pro-inflammatory cytokines in lung tissue. However, the administration of Tan resulted in a significant reduction in the levels of these inflammatory factors. In addition, Tan was observed to alleviate the weight loss and elevated lung index caused by BLM in mice. Interestingly, the improvement observed with Tan treatment was more significant than that observed with pirfenidone

treatment. The progression of pulmonary fibrosis is dependent on the proliferation and differentiation of fibroblasts. Myofibroblasts, which overexpress α-SMA, play a crucial role in this process by secreting Collagen I and Collagen III. This leads to an increase in extracellular matrix (ECM) deposition in the interstitial lung matrix, resulting in changes in matrix composition and increased lung tissue stiffness (X. Liu et al., 2018). The enzyme MMP9 is responsible for breaking down the extracellular matrix (ECM) and changing the balance between ECM and interstitial collagen, which can lead to the formation of fibrosis (G. Li et al., 2019a). The pathological histology analysis revealed severe damage to lung tissue, along with increased collagen deposition and higher hydroxyproline content in the mice with pulmonary fibrosis, which aligns with previous findings (Saito et al., 2017). However, Tan's intervention showed a significant improvement in lung histopathological damage and collagen deposition in the mice. Additionally, the study found that Tan reduced the expression of Collagen I, MMP9, and TGF-β1 in BLM-treated mice, which are all indicators of pulmonary fibrosis.

The role of oxidative stress in the development of pulmonary fibrosis is well established (Park et al., 2021). Studies have shown that exposure to BLM can lead to DNA damage, generation of reactive oxygen species, and a decrease in serum T-SOD, CAT, and GSH activities, while increasing MDA expression (Mouratis and Vassilis, 2011). Inhibition of oxidative stress has been shown to improve the pulmonary fibrosis process in mice. Our study found that compared to the control group, mice with pulmonary fibrosis treated with BLM had

significantly higher MDA levels and lower SOD and CAT activity in lung tissue. However, treatment with Tan significantly inhibited BLM-induced oxidative stress in the lung tissue of mice.

In addition to resident lung fibroblasts, EMT is believed to be the primary source of myofibroblasts in pulmonary fibrosis (P. Wang, Yan, et al., 2022). Studies have shown that about one-third of fibroblasts in pulmonary fibrosis originate from epithelial cells (Tanjore et al., 2009). These cells undergo structural and functional changes to become mesenchymal cells when exposed to oxidative stress or TGF- β 1, leading to the development of EMT (Rout-Pitt et al., 2018). As a result, we examined the impact of Tan on EMT in our study. The study found that Tan increased the levels of protein and gene of E-cadherin and decreased the levels of protein and gene of N-cadherin and α -SMA. A549 cells were used to induce the phenotypic transformation caused by TGF- β 1 and Western blotting was employed to analyze the effect of Tan on the epithelial-mesenchymal transition (EMT) phenotype. The results indicated that consistent with previous studies, E-cadherin levels decreased and collagen I, N-cadherin, and α -SMA expression increased after TGF- β 1 treatment, but improved after treatment with Tan (Q. Chen et al., 2023). Therefore, the research demonstrated that Tan can suppress EMT and inhibit pulmonary fibrosis.

The process of TGF- β 1-induced EMT involves the activation of non-Smad-dependent signaling pathways such as PI3K/Akt, MAPK, RhoA, and NF- κ B (Y.E. Zhang, 2017). PI3K/Akt signaling pathway has been identified as a crucial regulator of pulmonary fibrosis (J. Wang, et al., 2022). Studies have shown that inhibition of PI3K/Akt disrupts EMT and the use of Akt inhibitors can partially reverse EMT (Lin et al., 2014). TGF- β 1 activates PI3K through the TGF- β receptor or EGF receptor. As a secondary messenger, PI3K activation causes the p110 subunit to bind with the p85 subunit, leading to the phosphorylation of the substrate PIP2. This conversion results in the formation of PIP3, which then binds to the PH structural domain of Akt, leading to its activation through phosphorylation (Hers et al., 2011; Saito et al., 2017). Activation of Akt can induce the expression of EMT-inducible transcription factors and phosphorylate Snail1 by inhibiting GSK-3 β or activating NF- κ B to promote EMT in squamous cell carcinoma cells (L. Zhang et al., 2013; Kaufhold and Bonavida, 2014). Moreover, sustained PI3K activation can aggravate BLM-induced pulmonary fibrosis by promoting the release of pro-inflammatory and pro-fibrotic factors (Kral et al., 2016). In conjunction with KEGG pathway enrichment analysis, we evaluated the expression of the PI3K/Akt pathway using Western blotting. The data show that Tan inhibits PI3K and Akt phosphorylation both *in vivo* and *in vitro*. Tan, a selective PI3K inhibitor, shows potential as a drug for treating upper respiratory tract infections (S. Chen et al., 2022). Furthermore, the inclusion of Tan in the diet can enhance the production of short-chain fatty acids. These fatty acids play a role in inhibiting the epithelial-mesenchymal transition (EMT) process by suppressing the PI3K/Akt/mTOR signaling cascade (B. Chen et al., 2021; D; Chen et al., 2020). Therefore, Tan may directly or indirectly act on PI3K, inhibiting the activation of the PI3K/Akt signaling pathway, and subsequently inhibiting the epithelial-mesenchymal transition (EMT) process in pulmonary fibrosis.

5 Conclusion

To conclude, this study provides evidence that Tan can improve pulmonary fibrosis both *in vivo* and *in vitro* by inhibiting EMT through the PI3K/Akt signaling pathway. The findings suggest that Tan could be a viable drug candidate for the treatment of pulmonary fibrosis.

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: Sequence Read Archive (SRA)/PRJNA987041.

Ethics statement

The animal study was approved by the Jilin University Animal Testing Ethics Committee. The study was conducted in accordance with the local legislation and institutional requirements.

Author contributions

JL, QW, and PY designed and conceived the experiments., KS, YW, and YY conducted experiments., ML, JY, and GS performed the statistical analysis. JL wrote the manuscript. LP, BF, and PY revised the manuscript. All authors contributed to the article and approved the submitted version.

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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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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fphar.2023.1247800/full#supplementary-material>

SUPPLEMENTARY FIGURE S1

Tan improved lung tissue scores and reduced mRNA expression of pulmonary fibrosis markers in mice with pulmonary fibrosis. (A) Ashcroft score. The mRNA expression of collagen I (B), MMP9 (C) and

TGF- β 1 (D) was detected by qPCR in the lung tissue in each group of mice. Data represent the mean \pm SD. * P < 0.05, ** P < 0.01, compared with the control group. * P < 0.05, ** P < 0.01, compared with the model group.

SUPPLEMENTARY FIGURE S2

Tan treatment resulted in a decrease in the expression of the TGF- β 1 receptor, TGFBR2. (A) Representative western blotting images showing the expression of TGFBR2. (B) Quantification of TGFBR2/ β -actin ratio. ** P < 0.01, compared with the control group. ** P < 0.01, compared with the model group.

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Progression of the PI3K/Akt signaling pathway in chronic obstructive pulmonary disease

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Chronic Obstructive Pulmonary Disease (COPD) is a chronic respiratory disease characterized by a slow progression and caused by the inhalation of harmful particulate matter. Cigarette smoke and air pollutants are the primary contributing factors. Currently, the pathogenesis of COPD remains incompletely understood. The PI3K/Akt signaling pathway has recently emerged as a critical regulator of inflammation and oxidative stress response in COPD, playing a pivotal role in the disease's progression and treatment. This paper reviews the association between the PI3K/Akt pathway and COPD, examines effective PI3K/Akt inhibitors and novel anti-COPD agents, aiming to identify new therapeutic targets for clinical intervention in this disease.

KEYWORDS

chronic obstructive pulmonary disease, PI3K/Akt signalling pathway, inhibitor, inflammation, oxidative stress

1 Introduction

COPD is a heterogeneous lung disease characterized by a variety of chronic respiratory symptoms, such as difficulty breathing, coughing, sputum production, and acute exacerbation. These symptoms arise from abnormal airways (bronchitis) and/or alveolar abnormalities (emphysema), resulting in persistent and frequently progressive airflow obstruction (Venkatesan, 2023). COPD ranks as the third leading cause of death globally, following ischemic heart disease and stroke (Obeidat et al., 2018). COPD arises from the complex interplay of multiple factors. Smoking stands as a significant risk factor for COPD, while environmental exposure and genetic variation can contribute to the development or exacerbation of the disease (Lareau et al., 2019). Presently, COPD is treated with a combination of medication and non-medication strategies, smoking cessation is the primary treatment, bronchodilators and glucocorticoids are the most commonly used drugs (Sandelowsky et al., 2021). Nevertheless, COPD commonly exhibits a progressive nature, and the conventional medications used to manage it entail notable side effects. These challenges emphasize the urgent need for exploring alternative treatment modalities for COPD.

The phosphatidylinositol 3-kinase (PI3K)/protein kinase B (PKB/Akt) signaling pathway is a critical cellular pathway that regulates multiple functions such as cell survival, growth, proliferation, metastasis, and metabolism (Engelman et al., 2006; Abeyrathna and Su, 2015). The abnormal activation of the PI3K/AKT pathway is associated with various human cancers (Noorolyai et al., 2019; Glaviano et al., 2023). Additionally, it is also involved in many chronic diseases such as diabetes (Savova et al.,

2023), cardiovascular diseases (Qin et al., 2021), neurological disorders (Wang Q. et al., 2022), autoimmune diseases (Cheng et al., 2022), inflammatory diseases (Xu et al., 2022), and liver diseases (Ye et al., 2023) et al. The PI3K/AKT pathway plays a crucial role in the onset and progression of numerous diseases. Recently, studies have demonstrated that inhibiting the PI3K/Akt signaling pathway reduces inflammation, apoptosis, and oxidative stress in cells, thereby playing a crucial role in COPD treatment (Sun et al., 2019).

This review comprehensively examines the structure and transduction of the PI3K/Akt signaling pathway. Additionally, it highlights the crucial role of PI3K/Akt signaling in COPD and presents a summary of potential drugs that target this pathway. The aim is to expand the therapeutic possibilities for COPD and offer innovative and effective targets for clinical intervention.

2 The PI3K/Akt signaling pathway

The PI3K/Akt signaling pathway plays a crucial role in various cellular regulatory processes such as cell growth, proliferation, migration, metabolism, and secretion. Furthermore, dysregulation of the PI3K/Akt signaling pathway is implicated in a diverse spectrum of human diseases, including cancer (Noorolyai et al., 2019), neurodegenerative disease (Rai et al., 2019), diabetes (Huang et al., 2018), and osteoarthritis (Sun et al., 2020).

2.1 The composition of PI3K

PI3Ks are a class of evolutionarily conserved intracellular lipid kinases called intracellular lipid kinases, classified into classes I, II, and III based on substrate specificity and sequence homology (Cantley, 2002). Type I PI3K can be divided into two subfamilies based on its coupling receptors. Type IA PI3K is a heterogeneous dimer composed of a p85-regulated subgroup and a p110 catalytic subgroup. It is activated by the growth factor receptor tyrosine kinase (RTK) (Katso et al., 2001). Type IB PI3K is a heterogeneous dimer composed of p101 regulatory subunits and p110- γ catalytic subunits. It is activated by G-protein-coupled receptors (GPCRs) (Voigt et al., 2006). Classes II and III PI3K are monomer types. Class II PI3K consists of a catalytic subunit similar to p110, while class III PI3K consists of a single member, Vps34 (Jean and Kiger, 2014). It is generally accepted that class I PI3K is the most widely studied, and class II and III PI3Ks have less knowledge about their specific functions. Here, we will focus on the role of Type I PI3K in COPD.

2.2 The composition of Akt

Akt, a serine/threonine kinase also known as PKB, belongs to the AGC protein kinase family. Three subtypes of Akt exist: Akt1 (PKBa), Akt2 (PKBb), and Akt3 (PKBc) (Risso et al., 2015). The three subtypes of Akt, closely related in mammals, possess three conserved domains: an amino terminal pleckstrin homology (PH) domain, a central kinase domain (excitation domain) highly similar

to other AGC protein kinases like PKA and PKC (Peterson and Schreiber, 1999), and a carboxyl terminal regulatory domain that includes HM phosphorylation sites. The three Akt isomers exhibit high sequence similarity and structural resemblance, with Akt1 and Akt2 showing broader expression in mammals (He et al., 2021).

2.3 Mechanisms of PI3K/Akt pathway activation

Common mechanisms of PI3K activation involve the activation of receptor tyrosine kinase under physiological conditions. This leads to the phosphorylation of tyrosine residues and their subsequent binding to one or both SH2 domains of the PI3K splice subunit, resulting in allosteric activation of the PI3K catalytic subunit (Fruman et al., 2017). Additionally, activation of GPCR leads to allosteric activation of PI3K (Rathinaswamy et al., 2021). PI3K activation causes the transformation of PIP2 into PIP3 inside the plasma membrane, which binds specifically to the pleckstrin homology (PH) domain of two proteins, PDK-1 and Akt/PKB, to mediate PI3K signaling (Carnero et al., 2008).

The PI3K-dependent activation mechanism of Akt involves the interaction of Akt with PIP3, leading to its translocation to the medial membrane where its Thr308 and Ser473 sites become exposed. PDK1 phosphorylates Akt's Thr308 site, serving as the initial step in Akt activation. Subsequently, PDK2 phosphorylates the Ser473 sites, located at the hydrophobic carboxyl group's end, to achieve maximal Akt activation (Cole et al., 2019). Once fully activated, Akt phosphorylates downstream target proteins, thereby regulating various cellular functions such as angiogenesis, metabolism, growth, proliferation, protein synthesis, transcription, and apoptosis (Hemmings and Restuccia, 2015).

2.4 Regulation of the PI3K/Akt pathway

The PI3K/Akt signaling pathway is regulated by various factors, particularly a group of phosphatases that exert negative regulatory effects. These phosphatases include phosphatase and tensin homologues (PTEN), protein phosphatase 2 (PP2A), and protein phosphatase in the PH domain rich in repeated sequences of leucine (PHLPP1/2). PTEN plays a crucial role as an upstream component of the PI3K/Akt signaling pathway. It catalyzes the specific dephosphorylation of PIP3 to produce PIP2, thereby exerting a negative regulatory effect on Akt activation (Viennet et al., 2023). Additionally, Inositol polyphosphate 4-phosphatase type II (INPP4B) inhibits Akt signaling by dephosphorylating PIP2 into PIP (Gewinner et al., 2009). PP2A, a trimeric protein, combats Akt signaling by selectively inhibiting phosphorylation of Akt's Thr308 site (Zhang Y. et al., 2022) and dephosphorylation of Akt's Ser473 site (Hwang et al., 2013). PHLPP1/2 primarily dephosphorylates Akt at Ser473 sites. Activation of the PI3K pathway leads to stable levels of PHLPP1 and a surge of PHLPP2, both of which attenuate Akt signaling (Chen et al., 2011). Therefore, in the absence of PTEN, PHLPP2 replaces its role in attenuating the output of the PI3K/Akt pathway (Figure 1) (Chen et al., 2014).

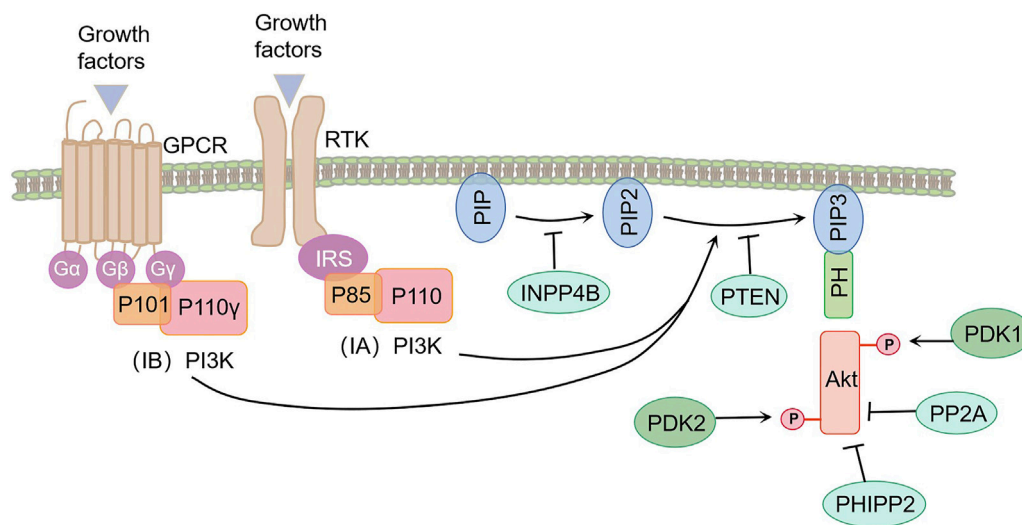


FIGURE 1

Transduction and regulatory pathways of PI3K/Akt pathway. Activation of growth factor receptor tyrosine kinase (RTK) and G-protein-coupled receptors (GPCRs) led to the activation of the PI3K catalytic subunit. Activated PI3K promotes the conversion of PIP2 to PIP3 in the medial membrane, a function that can be reversed by phosphatase and tensin homologues (PTEN). PIP3 activates Akt signaling by specifically binding to the pleckstrin homology (PH) domain of both PDK-1 and Akt proteins. Protein phosphatase 2 (PP2A) and the PH domain are rich in leucine repeats of the protein phosphatase (PHLPP1/2), negatively regulating the PI3K/Akt pathway.

3 The PI3K/Akt signaling pathway and its role in the pathogenesis of COPD

3.1 The interplay between inflammation and oxidative stress in the pathogenesis of COPD

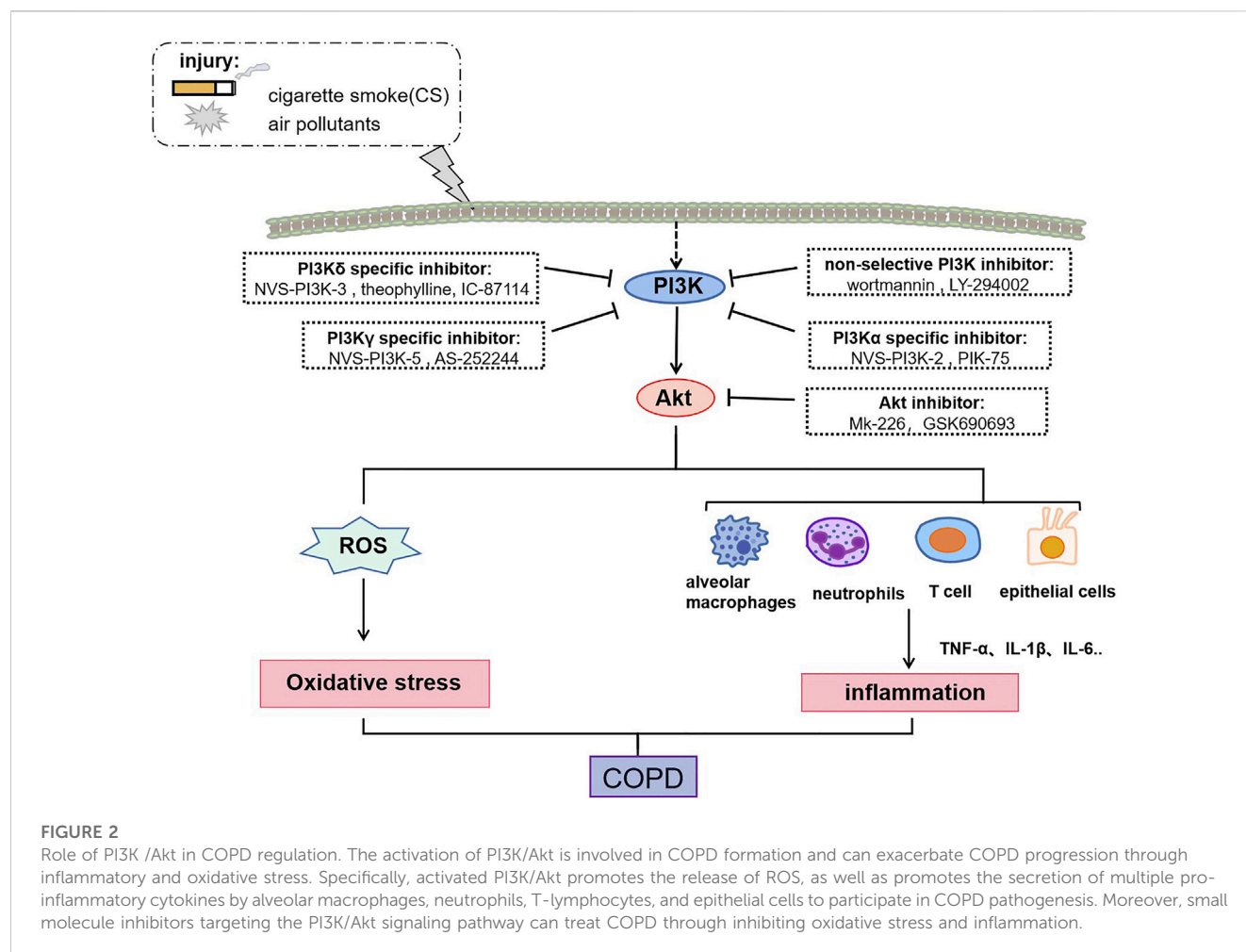
Increasing evidence suggests that inflammation and oxidative stress are interconnected pathophysiological processes (Biswas, 2016). In COPD, activated inflammatory cells in the lungs release numerous inflammatory factors that trigger the production of oxygen free radicals, leading to oxidative stress (Guo et al., 2022). Moreover, oxidative stress can amplify lung inflammation by activating multiple signaling pathways within the cells (Barnes, 2022). This closely intertwined process frequently coexists across various chronic diseases, in addition to COPD (Neves et al., 2021), there are inflammatory bowel disease (Tian et al., 2017), alcoholic liver disease (Yang et al., 2022), diabetes (Grabež et al., 2022), neuroinflammatory disease (Xue et al., 2019) and other chronic inflammatory diseases.

3.2 The PI3K/Akt pathway and inflammation in COPD

COPD is a progressive inflammatory lung condition caused by the inhalation of cigarette smoke and other toxic external particulate matter, such as air pollution and biomass fuels. Chronic inflammation of the small airways, known as bronchiolitis, serves as the primary catalyst for COPD development (Brightling and Greening, 2019). Various cytokines secreted by alveolar macrophages, neutrophils, T lymphocytes, B lymphocytes, and structural cells like epithelial, endothelial, and fibroblasts contribute to this inflammatory response (Barnes, 2016). Recent

research indicates that smoking acts as an initial trigger for activating innate immune system cells, with tobacco smoke stimulating the PI3K/Akt pathway and exacerbating the inflammatory response in monocytes. Furthermore, elevated PI3K signaling has been linked to sustained inflammation in individuals with COPD, just as shown in Figure 2 (Lee et al., 2018). Furthermore, inflammation underlies significant complications in COPD, including heart and lung diseases, respiratory failure, and cancer (Byrne et al., 2015).

Zhang et al. (2017) discovered that PI3K signaling was activated in alveolar macrophages of COPD mice, leading to a significant increase in pro-inflammatory cytokines such as TNF- α , IL-1 β , and IL-6, thereby enhancing inflammatory responses. Subsequent studies demonstrated that activation of the PI3K/Akt signaling pathway promoted polarization of macrophages in COPD from M1 to M2 phenotypes. The ratio of M1 to M2 macrophages following monocyte polarization has been linked to various inflammatory diseases (Zhang et al., 2023), and an elevated ratio of M2 macrophages has been implicated in lung inflammation (Lu et al., 2017). Neutrophil infiltration in the submucous membrane of the airway is the main driver of airway inflammation in COPD and is regulated by helper T cells 17 (Th17) and macrophages. Macrophages secrete inflammatory mediators that act as chemical inducers, increasing neutrophil infiltration in the airways and promoting lung injury and inflammatory responses in COPD patients (Holl et al., 2013). It is now evident that inflamed airways are exposed to hypoxia, triggering neutrophil degranulation and enhancing their potential for tissue damage. Hoenderdos et al. (2016) discovered that inhibiting the PI3K signaling pathway contributes to the suppression of neutrophil degranulation, suggesting that PI3K plays a crucial role in this process. Additionally, inhibiting Akt phosphorylation had no impact on degranulation regulation, implying that heightened



neutrophil reactivity is a result of early PI3K/Akt signaling. Yanagisawa et al. (2017) demonstrated that PI3K signaling is more active in bronchial epithelial cells of COPD patients. In contrast, the negative regulator of PI3K, PTEN, is frequently mutated or absent in the airway epithelial cells of smokers. Knockdown of PTEN leads to significant Akt phosphorylation and increased secretion of pro-inflammatory cytokines (e.g., IL-6, IL-8-induced CXCL8, etc.). Hence, activating PTEN could be an effective approach to impede the progression of COPD.

3.3 The role of the PI3K/Akt pathway in COPD oxidative stress

Oxidative stress arises from an imbalance between free radicals and antioxidants, playing a significant role in inflammatory diseases (Dandekar et al., 2015). Free radicals can originate from activated inflammatory cells, structural cells, cigarette smoke, indoor and outdoor air pollution, among other sources (Valavanidis et al., 2013). COPD is a progressive respiratory disease where inflammatory and structural cells in the lungs release reactive oxygen species (ROS) and reactive nitrogen species (RNS), inducing endogenous oxidative stress during the early stages of the disease. The imbalance between free radicals and antioxidants

further exacerbates ROS release (Boukhenouna et al., 2018). Thus, the elevation of oxidative stress persists even after COPD patients stop smoking. This oxidative damage results in endogenous tissue and cellular damage, ultimately leading to chronic inflammation and aging (Barnes et al., 2019). A growing body of research has demonstrated the involvement of the PI3K/Akt/mTOR signaling pathway in promoting lung cell senescence and oxidative stress (Xiaofe et al., 2022). This suggests that blocking the PI3K/Akt pathway as a means to inhibit oxidative stress could hold promise as a therapeutic strategy for COPD patients.

Recent studies have reported a significant reduction of SIRT1 and SIRT6, which are anti-aging molecules, in the lungs of COPD patients (Zhang XY. et al., 2022). Oxidative stress serves as the primary regulator of these proteins' expression (Lakhdar et al., 2018). Inhibition of the PI3K signaling pathway, as demonstrated by Baker et al. (2016), significantly enhances the expression of SIRT1 and SIRT6 while reversing oxidative stress. Additionally, the knockout of PTEN, which inhibits PI3K signaling, resulted in reduced levels of SIRT1 and SIRT6. Studies by Xie S et al. (Xie and Wang, 2022) have shown that cigarette smoke extract downregulates the expression of CRYAB, a recognized anti-apoptotic protein, in the alveoli of COPD mice. Furthermore, overexpression of CRYAB inhibits oxidative stress, delays the activation of the PI3K/Akt signaling pathway, and reduces apoptosis. Oxidative stress also

affects histone deacetylase (HDAC) activity. HDAC, a glucocorticoid functional protein, is frequently associated with glucocorticoid resistance in COPD patients (Rossios et al., 2012). Marwick et al. (2009) found reduced HDAC activity in COPD mice, and knockout of PI3K restored the activity of this enzyme. Consequently, inhibiting the PI3K pathway reinstates histone activity in the presence of oxidative stress-induced glucocorticoid resistance. This restoration, in turn, revives the anti-inflammatory properties of glucocorticoids, leading to a positive inhibition of COPD progression.

4 Potential drug targeting PI3K/Akt for COPD

The pathogenesis of COPD is unclear and is commonly linked to inflammation, oxidative stress and reduced immune function. Current treatments include medication, oxygen therapy and rehabilitation therapy to improve symptoms of airflow restriction caused by reduced lung function (Wang et al., 2020). However, these methods have done little to prevent the progression of COPD disease. Common COPD drugs include beta 2 receptor agonists, anticholinergic drugs, and glucocorticoids. However, chronic inhalation of beta 2 receptor agonists may have adverse cardiovascular and metabolic effects (Vanfleteren et al., 2018). There are a number of side effects associated with anticholinergic drugs, including the dry mouth, blurred vision, and postural hypotension. Glucocorticoids negatively affect the hypothalamic-pituitary-adrenal axis and most COPD patients are insensitive to glucocorticoids. Therefore, there is an urgent need to find novel molecular targeted therapeutics for COPD.

4.1 Application of PI3K inhibitors in COPD treatment

PI3K is a signaling cascade component downstream of multiple cell receptors. Among the three subtypes of PI3K (α , γ and δ), PI3K α is critical for airway inflammation and angiogenesis (Chen et al., 2021), while PI3K γ is pro-inflammatory and involved in inflammatory cell recruitment (Heit et al., 2008) and PI3K δ contributes to corticosteroid resistance (To et al., 2010).

Wortmannin, a PI3K inhibitor with low substrate specificity. Significantly reduced the activity of neutrophils elastase (NE) and matrix metalloproteinase-9 (MMP-9) released by airway neutrophils in COPD mice and decreased neutrophils inflammation (Vlahos et al., 2012). In addition, Wortmannin induced differentiation of alveolar epithelial stem cells in COPD mice to repair the alveoli and restore respiratory function (Horiguchi et al., 2015). LY 294002 (a non-selective PI3K inhibitor) significantly restored sensitivity to corticosteroids in PBMC cells from COPD patients, but had no effect on the production of the inflammatory factor IL-8. In addition, LY-294002 inhibits the expression of intercellular adhesion molecule -1(ICAM-1) in COPD patients, mediating monocyte/macrophage adhesion and infiltrating inflammatory sites (Liu et al., 2018).

Bewley et al. (2016) found that NVS-PI3K-2 (PI3K α specific inhibitor), NVS-PI3K-3 (PI3K δ specific inhibitor) and NVS-PI3K-5 (PI3K γ specific inhibitor) suppressed lung inflammation and bacterial colonization in COPD patients. Alveolar macrophages play a significant role in clearing bacteria and small apoptotic bodies. However, these inhibitors do not alter the phagocytosis of alveolar macrophages, i.e., do not negatively affect innate immunity of COPD macrophages. Similarly, lower concentrations of theophylline (PI3K δ specific inhibitors) can target PI3K to reverse oxidative stress-induced corticosteroid resistance and suppress lung inflammation in COPD mice exposed to cigarette smoke (To et al., 2010). In addition, IC-87114, a PI3K δ specific inhibitor, inhibits neutrophils recruitment and restores corticosteroid sensitivity impaired under oxidative stress by inhibiting PI3K signaling (Rossios et al., 2012). Wang et al. (2019) and others demonstrated that IL-1 α and IL-1 β expression in human bronchial epithelial cells (HBEC) were significantly upregulated in mucin protein Muc-5ac associated with high mucin secretion, and PIK-75 (PI3K α specific inhibitor) significantly inhibited PM-induced inflammation and mucin hypersecretion in HBEC, while AS-252244 (PI3K γ specific inhibitor) and IC-87114 did not. Small molecule inhibitors targeting the PI3K/Akt signaling pathway treat COPD through inhibiting oxidative stress and inflammation, as shown in Figure 2.

4.2 Application of Akt inhibitors in COPD treatment

It is thought that Akt is a central regulator of the molecular pathways involved in smoking-related diseases, particularly COPD. MK-2206 (Akt variant non-ATP competitive inhibitor), an anticancer agent that inhibits all Akt subtypes, is commonly used to synergistically enhance the anti-tumor efficacy of certain molecular targeted drugs (Yap et al., 2011). Jiang et al. (2018) found that MK-2206 reversed changes in markers involved with epithelial mesenchymal transition (EMT) in the lung epithelium of smoking mice. EMT is positively associated with an invasive or metastatic phenotype of COPD (Zhang et al., 2016), so MK-2206 inhibits COPD. In addition, MK-2206 pretreatment inhibited IL-1 α and IL-1 β and Muc-5ac expression (Wang J. et al., 2019), and also protected the diaphragm in COPD mice induced by hypoxia pretreatment (Chuang et al., 2018). In addition, GSK690693 (ATP-competitive pan-Akt inhibitor) significantly inhibited IL-8 induced apoptosis in inflammatory diaphragm cells (Wang L. et al., 2019). Akt inhibitors are currently understudied and underused in COPD diseases, and more recently, Akt-negative dominant mutant (Akt-DN) transfected cells from Lin CH et al. (Lin et al., 2020) have been shown to inhibit the Akt pathway and IL-8 secretion in human lung epithelial cells.

4.3 Others

In addition to some of these molecular targeted drugs, natural compounds, traditional Chinese medicine formulations, and some anti-inflammatory agents also inhibit the progression of COPD by inhibiting the PI3K/Akt pathway. It has been shown recently that

puerarin can relieve over-oxidation in cells (Zhang P. et al., 2022). Wang L. et al. (2022) found that puerarin reverses apoptosis in HBEC stimulated by cigarette smoke extract (CSE) via the PI3K/Akt signaling pathway. Icarin is one of the active components of Bufe Yishen formula, which can inhibit the mucus hypersecretion in COPD rats (Li J. et al., 2020). Icarin in combination with Nobilitin has a positive therapeutic effect on COPD by improving lung inflammation and emphysema and reducing lung pathological damage in COPD rats via the PI3K/Akt pathway (Lu et al., 2022). At the same time, Scutellaria has a reverse effect on lung pathologic injury induced by smoking in COPD rats (Xu et al., 2018). Crocin, the active ingredient in crocus, significantly inhibits the number of neutrophils and macrophages and the concentration of pro-inflammatory cytokines in COPD mice by modulating the PI3K/Akt-mediated inflammatory pathway (Xie et al., 2019).

As a vital component of complementary alternative medicine, TCM is considered to play its pharmacological role via its multi-component, multi-target, and multi-pathway properties (Ren et al., 2019). Notably, Bu-Shen-Fang-Fang-Chuan formula (BSFCF), a commonly used formula for treating COPD in China, attenuates the inflammatory response to COPD by inhibiting PI3K/Akt-Nrf2 and PI3K/Akt-NF- κ B (Li Q. et al., 2020). Xuefu Zhuyu Decoction (XFZYD) is also widely used in the treatment of COPD, and (Hu et al., 2022) and others have found that XFZYD is effective in the treatment of COPD by interfering with the PI3K/Akt signaling pathway, improving oxidative stress and inflammatory responses, and relieving airway remodeling and ventilation disorders through web-based pharmacology and molecular docking experiments. In addition, Tiaobu Feishen (TBFS) was observed to reverse lung inflammation and airway remodeling (Li et al., 2012), Zhou et al. (2023) observed that TBFS has more effective in glucocorticoid-resistant COPD patients by modulating PI3K/Akt signaling to improve glucocorticoid resistance.

Anti-inflammatory agents that interfere with the PI3K/Akt pathway also have significant potential to improve COPD steroid resistance. Macrolides may reduce lung inflammation in COPD by modulating the PI3K/Akt pathway, such as erythromycin, which enhances corticosteroid sensitivity by inhibiting the activity of the PI3K/Akt pathway (Miao et al., 2015; Sun et al., 2015). Solithromycin (SOL, CEM-101), a macrolide/fluoronolactone that inhibits airway neutrophils in steroid-insensitive mice, is an effective anti-inflammatory agent for COPD treatment (Kobayashi et al., 2013). The statin simvastatin improves lung remodeling by reversing epithelial mesenchymal transition in alveolar epithelial cells. This effect is mediated by inhibition of the PI3K/Akt pathway (Milara et al., 2015). In addition, the tricyclic antidepressant nortriptyline can also increase corticosteroid sensitivity. Mercado et al. (2011) found that nortriptyline pretreatment inhibited Akt phosphorylation and PI3K activity, restoring oxidative stress-

induced corticosteroid sensitivity as a potential treatment for respiratory diseases such as COPD that are corticosteroid insensitive.

5 Conclusion

The morbidity and mortality rates associated with COPD remain substantial, posing numerous challenges for healthcare professionals involved in COPD interventions. There is a growing body of evidence indicating the therapeutic potential of the PI3K/Akt signaling pathway, particularly different PI3K isoforms, in the treatment of COPD. Several non-specific PI3K inhibitors have demonstrated anti-inflammatory and antioxidant effects in COPD models. However, most broad-spectrum PI3K inhibitors exhibit greater genotoxicity, whereas PI3K subtype-specific inhibitors offer the desired therapeutic properties with reduced side effects. This may provide guidance for subsequent drug development targeting PI3K/Akt. In conclusion, there is an urgent need for further insights into the key regulatory mechanisms of the PI3K/Akt pathway in COPD development, as well as the exploration of safer and more effective therapeutic strategies derived from this approach.

Author contributions

YL designed and wrote this manuscript, HK wrote this manuscript, HeC designed this manuscript, GC checked this manuscript, HuC checked this manuscript, WR checked this manuscript. All authors contributed to the article and approved the submitted version.

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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Role and mechanisms of SGLT-2 inhibitors in the treatment of diabetic kidney disease

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Diabetic kidney disease (DKD) is a chronic inflammatory condition that affects approximately 20-40% of individuals with diabetes. Sodium-glucose co-transporter 2 (SGLT-2) inhibitors, emerging as novel hypoglycemic agents, have demonstrated significant cardiorenal protective effects in patients with DKD. Initially, it was believed that the efficacy of SGLT-2 inhibitors declined as the estimated glomerular filtration rate (eGFR) decreased, which led to their preferential use in DKD patients at G1-G3 stages. However, recent findings from the DAPA-CKD and EMPA-KIDNEY studies have revealed equally beneficial cardiorenal effects of SGLT-2 inhibitors in individuals at stage G4 DKD, although the underlying mechanism behind this phenomenon remains unclear. In this comprehensive analysis, we provide a systematic review of the mechanisms and functioning of SGLT-2 inhibitors, potential renal protection mechanisms, and the therapeutic efficacy and safety of SGLT-2 inhibitors in kidney diseases, with a particular focus on stage G4 DKD. Gaining a deeper understanding of the renal protective effect of SGLT-2 inhibitors and their underlying mechanisms is highly significance for the successful utilization of these inhibitors in the treatment of diverse kidney disorders.

KEYWORDS

SGLT-2 inhibitor, diabetic kidney disease, renal protection mechanism, efficacy, safety

Abbreviations: ABCG2, ATP-binding cassette subfamily G member 2; AGEs, Advanced glycosylation end products; AKI, Acute kidney injury; ATP, Adenosine triphosphate; CKD, Chronic kidney disease; DKD, Diabetic kidney disease; eGFR, Estimated glomerular filtration rate; EPO, Erythropoietin; ESRD, End-stage renal disease; GLUT9, Proteins glucose transporter protein 9; KDIGO, Kidney Disease: Improving Global Outcomes; NHE3, Na⁺-H⁺ exchanger 3; NO, Nitric oxide; RAAS, Renin-angiotensin-aldosterone system; RAGE, Receptors for advanced glycosylation end products; RAS, Renin-angiotensin system; SGLT-1, Sodium-glucose co-transporter protein 1; SGLT-2, Sodium-glucose co-transporter protein 2; SNS, Sympathetic nervous system; TGF, Tubuloglomerular feedback; TGF-1, Transforming growth factor 1; CANVAS, Canagliflozin and Cardiovascular and Renal Events in Type 2 Diabetes; CREDENCE, Canagliflozin and Renal Outcomes in Type 2 Diabetes and Nephropathy; DAPA-CKD, Dapagliflozin in Patients with Chronic Kidney Disease; DECLARE-TIMI 58, Dapagliflozin and Cardiovascular Outcomes in Type 2 Diabetes; EMPA-KIDNEY, Empagliflozin in Patients with Chronic Kidney Disease; EMPA-REG OUTCOME, Empagliflozin, Cardiovascular Outcomes, and Mortality in Type 2 Diabetes; SCORED, Sotagliflozin in Patients with Diabetes and Chronic Kidney Disease.

1 Introduction

Diabetes, a prevalent illness worldwide, poses a significant threat to human health. As of 2019, approximately 463 million individuals were affected by diabetes, and this number is projected to reach 700 million by 2045 (1). Diabetic kidney disease (DKD), a common microvascular complication associated with diabetes, affects around 20–40% of diabetic patients and can progress to end-stage renal disease (ESRD) in some cases (2–4). While controlling blood glucose levels is crucial in slowing DKD progression, it becomes challenging to lower glycated hemoglobin in patients with advanced DKD, leading to difficulties in halting disease advancement due to patient or pharmaceutical factors (5). Consequently, the pursuit of effective therapeutic approaches that can safeguard kidney function and delay the onset of DKD has emerged as a prominent research area in DKD studies.

Currently, renin-angiotensin system inhibitors are recommended as the primary drugs per the guidelines for treating DKD. However, they are not entirely adequate for DKD treatment due to their potential increased risk of ESRD and acute renal failure (6, 7). The effectiveness and safety of SGLT-2 inhibitors, a novel hypoglycemic agent, have been validated for stage G1–G3 DKD therapy, resulting in the 2020 KDIGO guidelines recommending their use for DKD patients with an estimated glomerular filtration rate (eGFR) ≥ 30 mL/min/1.73 m² (8). Further research is still necessary to ascertain their efficacy and safety for individuals with stage G4–G5 DKD.

Recent findings from the DAPA-CKD and EMPA-KIDNEY trials have revealed that SGLT-2 inhibitors offer significant benefits in improving cardiovascular and renal function, as well as delaying the progression of renal disease in stage G4 DKD patients, irrespective of their diabetes status (9, 10). As a result, the 2022 KDIGO guidelines have also recommended a revision of the eGFR threshold to 20 mL/min/1.73 m² for DKD patients (11). Therefore, this paper aims to comprehensively review the research progress surrounding the mechanisms of action of SGLT-2 inhibitors, their potential renal protective effects, and their efficacy and safety in patients with stage G4 DKD.

2 The function of SGLT-2 inhibitors

2.1 SGLT-2 inhibitors and mechanism of action

SGLT-2 inhibitors are a relatively new class of antidiabetic medications that have gained attention in recent years. The use of non-selective SGLT inhibitors, extracted from apple tree root bark glycosides, was first reported in the 1830s and since then, SGLT-2 inhibitors have become a popular focus of research due to their unique mechanism of action, which does not rely on insulin (12). SGLT-1 and SGLT-2 are crucial molecules involved in glucose reabsorption in the kidney and are primarily located in the renal tubular epithelium. In normal physiological conditions, glucose

filtered from the glomerulus enters the tubules and is reabsorbed by SGLT-1 and SGLT-2. Among these transporters, SGLT-2 is predominant in the S1 and S2 segments of the renal proximal tubule and functions as a high-capacity glucose transporter, responsible for approximately 90% of glucose reabsorption in the renal tubules. On the other hand, SGLT-1 functions as a low-capacity glucose transporter and is found not only in the kidneys but also in the gastrointestinal tract, where it plays a role in reabsorbing a smaller amount of glucose in the renal tubules (13) (Figure 1).

SGLT-2 inhibitors are a class of hypoglycemic agents that have gained popularity in recent years. They work by competing with the SGLT-2 protein for glucose binding in the renal tubules. This competition prevents SGLT-2 from binding to glucose, leading to reduced glucose reabsorption by the renal tubules (Figure 1). As a result, there is an increased excretion of glucose, sodium, and water in the urine. This leads to lower blood glucose and reduced volume load (14). Importantly, the mechanism of action of SGLT-2 inhibitors is independent of insulin regulation. It does not rely on the regulation of insulin secretion by pancreatic β -cells or insulin resistance in the body. Currently, there are several selective SGLT-2 inhibitors available on the market, such as empagliflozin, dapagliflozin, and luseogliflozin. These medications specifically inhibit SGLT-2. However, there are also SGLT-1 and SGLT-2 inhibitors, such as sotagliflozin and canagliflozin, which can inhibit both transporters (15). Overall, the discovery and development of SGLT-2 inhibitors have provided a novel approach for managing blood glucose levels in individuals with diabetes.

2.2 Hypoglycemic effects

The hypoglycemic effect of SGLT-2 inhibitors relies on renal tubular reabsorption, and thus the amount of glucose excretion in the urine is directly related to the glomerular filtration rate (16, 17). In individuals with advanced DKD, specifically those with stage G4–G5 DKD, the options for hypoglycemic medications are limited, and dosage is often restricted. Therefore, it is crucial to assess the effectiveness of treating patients with relatively advanced DKD using SGLT-2 inhibitors. Several clinical studies have focused on the glycemic efficacy of SGLT-2 inhibitors in individuals with type 2 diabetes and stage 3 chronic kidney disease (CKD). Their findings indicate that the glucose-lowering effect is attenuated compared to patients with normal renal function (18–20). In a study involving dapagliflozin treatment for patients with type 2 diabetes and stage 3b–4 CKD, glycated hemoglobin levels did not decrease over the 102-week treatment period (21). Similarly, another study focusing on DKD patients treated with luseogliflozin found that the increase in urinary glucose excretion was lower in those with stage G4 DKD compared to patients with stage G1–G3 DKD (22). These findings suggest that the hypoglycemic efficacy of SGLT-2 inhibitors is reduced in patients with stage G4 DKD when compared to those with stage G1–G3 DKD.

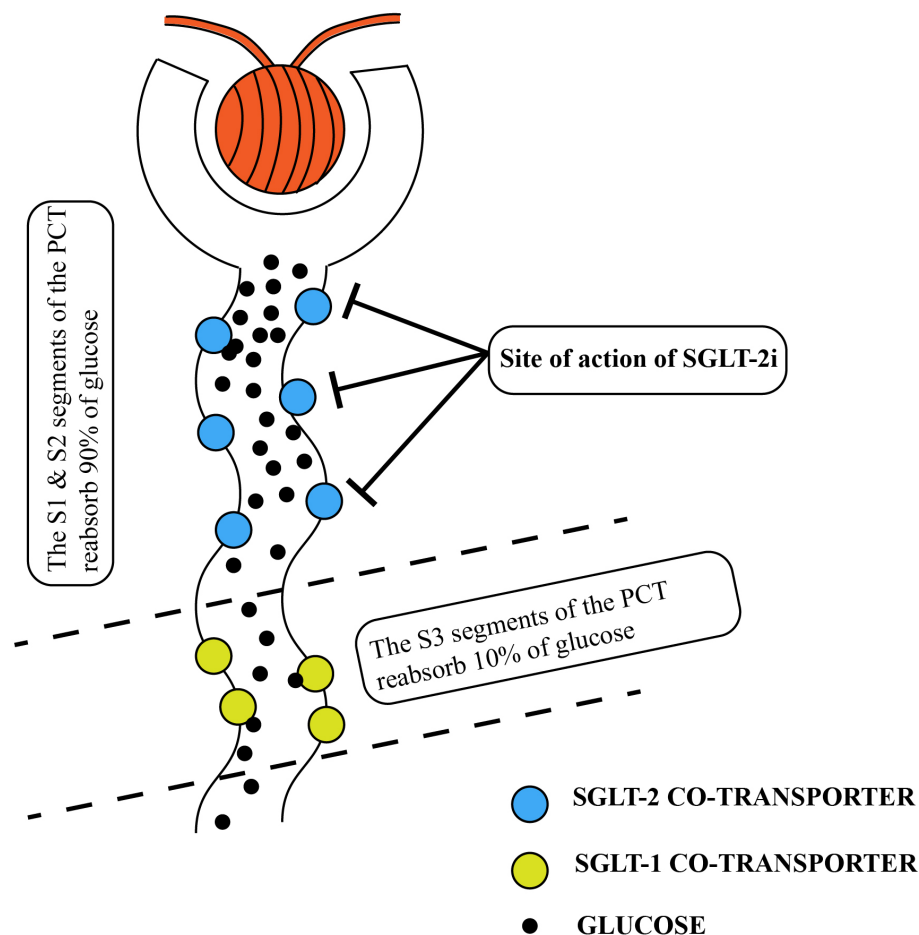


FIGURE 1

Normal renal tubular resorption of glucose. The location of the SGLT2-inhibitor's action is also shown in the diagram. PCT, proximal convoluted tubules; SGLT, sodium-glucose co-transporter.

2.3 Nephroprotective effects

2.3.1 Reduction of glomerular hyperfiltration

On one hand, SGLT-2 receptors are primarily found in the proximal tubule and are responsible for the reabsorption of glucose and sodium ions. Consequently, the decreased sodium concentration sensed at the macula densa location triggers a tubuloglomerular feedback (TGF) mechanism, which stimulates contraction of the efferent arteries and dilation of the afferent arteries. This results in increased blood flow into the glomerulus, raising the glomerular pressure and leading to glomerular hyperfiltration and subsequent damage (23). In contrast, SGLT-2 inhibitors can reduce Na^+ reabsorption in the renal tubules by competitively binding glucose. This restoration of the TGF mechanism promotes relaxation of the small arterial outflow, reducing intraglomerular pressure and alleviating glomerular hyperfiltration. These effects are crucial in preserving renal function and slowing the progression of nephropathy (24).

However, another important player in Na^+ reabsorption in the proximal tubule is the Na^+ - H^+ exchanger 3 (NHE3), responsible for

about 70% of Na^+ reabsorption through direct or indirect mechanisms (25). Activation of the TGF system leads to increased intraglomerular pressure and subsequent glomerular hyperfiltration. Recent research has demonstrated that NHE3 works synergistically with SGLT-2 in Na^+ reabsorption, with SGLT-2 tightly regulating NHE3 activity. Therefore, NHE3 is sensitive to the modulation by SGLT-2 inhibitors (26, 27). A study conducted on diabetic mice revealed that SGLT-2 inhibitors have the ability to inhibit NHE3 function by promoting NHE3 phosphorylation. This phosphorylation enhances Na^+ excretion, effectively reducing sodium levels within the body (28). This finding demonstrates the potential of SGLT-2 inhibitors as therapeutic agents in regulating NHE3 activity and mitigating glomerular hyperfiltration.

Hence, the underlying mechanism behind the natriuretic effect of SGLT-2 inhibitors is to combat sodium-water retention and repair TGF system, thereby alleviating the condition of glomerular hyperfiltration for renal protection. This effect could be attributed to the competitive inhibition of SGLT receptors and the subsequent inhibition of NHE3. Notably, NHE3 seems to play a pivotal role in the overall natriuretic effect of SGLT-2 inhibitors.

2.3.2 Regulation of the renin-angiotensin-aldosterone system (RAAS)

The activation of RAAS, particularly the increased secretion of angiotensin II (Ang II) and aldosterone, has been established as a crucial factor in the progression of DKD (29–31). In response to elevated blood glucose levels, SGLT-2 in the proximal renal tubule enhances Na^+ and glucose reabsorption. This leads to reduced sensing of Na^+ by the macula densa, resulting in decreased adenosine production, which further activates the RAAS and causes constriction of the small afferent arteries. Moreover, the enhanced production of Ang II, stimulated by RAAS activation, also triggers the release of aldosterone. The resulting oxidative stress, inflammation, and renal fibrosis contribute to the accelerated progression of DKD (32). With the usage of SGLT2 inhibitors, the macula densa becomes more sensitive to changes in Na^+ concentration. This results in increased adenosine production and suppression of RAAS activation. Consequently, there is vasoconstriction in the afferent arteries, while the inhibition of RAAS also reduces the release of aldosterone release. These combined effects help to alleviate oxidative stress, inflammation, and fibrosis in the kidney, thereby mitigating the progression of DKD (33).

In the past few decades, RAAS inhibitors have been widely used as the primary approach to treat DKD (34). However, the distinction between SGLT-2 inhibitors and RAAS inhibitors lies in their differential effects on the small afferent and efferent glomerular arteries. RAAS inhibitors dilate both the afferent and efferent arterioles, but the efferent arterioles are dilated to a greater extent, resulting in continued glomerular ultrafiltration and subsequent damage to kidney units and podocytes (35). Consequently, RAAS inhibitors alone may not effectively halt the progression of early-stage DKD or provide optimal treatment for individuals with advanced DKD (29, 36). However, SGLT-2 inhibition provides a greater degree of renal protection compared to RAAS inhibition as it not only relieves glomerular hyperfiltration but also reduces intra-glomerular pressure by dilating small outgoing glomerular arteries and constricting small incoming glomerular arteries. This unique mechanism of action suggests

that SGLT-2 inhibitors may offer enhanced efficacy in delaying the progression of DKD.

3 Potential renal protection mechanisms

Although the exact mechanisms by which SGLT-2 inhibitors protect the kidneys are not fully understood, recent research has shown that these medications have numerous potential renoprotective effects in addition to their traditional hypoglycemic effects. These effects include reducing glomerular hyperfiltration and volume load, inhibiting inflammation and fibrosis, improving oxidative stress, enhancing erythropoietin (EPO) production, enhancing mitochondrial energy supply, inhibiting the sympathetic nervous system, protecting vascular endothelial cells, and reducing blood uric acid levels, among others (37–42) (Figure 2).

3.1 Anti-inflammatory, anti-oxidative stress and anti-fibrotic effects

Mild systemic inflammation is commonly observed in patients with DKD. Prolonged hyperglycemia leads to the production of advanced glycosylation end products (AGEs) through the glycosylation of non-enzymatic proteins. These AGEs promote the formation of receptors for advanced glycosylation end products (RAGE), resulting in oxidative stress and increased levels of reactive oxygen species. This oxidative stress contributes to the progression of kidney fibrosis and further decline in renal function, marking a crucial phase in the development of DKD (43, 44). One of the key pro-fibrotic factors involved in this process is transforming growth factor 1 (TGF-1). TGF-1, along with other pro-fibrotic factors, intensifies inflammation and exerts strong pro-fibrotic effects. It promotes the proliferation of mesangial cells and the deposition of extra-mesenchymal matrix, leading to glomerulosclerosis and interstitial fibrosis (45).

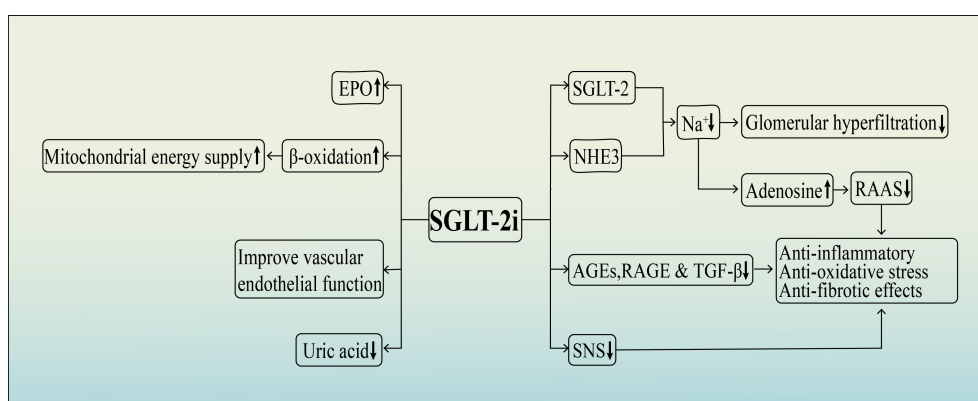


FIGURE 2

The diagram shows the renal protection mechanism of SGLT-2 inhibitors.

In a study by Ojima et al., diabetic rats were used to investigate the effects of empagliflozin on renal tissues. After 4 weeks of empagliflozin treatment, there was a significant reduction in the expression of AGEs, RAGE, and other proteins in renal tissues. This resulted in the inhibition of the AGE-RAGE oxidative stress axis, demonstrating empagliflozin's potential as an anti-inflammatory, anti-fibrotic, and tubular protective agent (46). Further experiments revealed that empagliflozin effectively mitigated oxidative stress and attenuated damage to the renal tissues. It is believed that this protective effect may be attributed to empagliflozin's ability to downregulate the TGF- β -Smad pathway and upregulate the Nrf2/ARE pathway (47). Consequently, SGLT-2 inhibitors such as empagliflozin have the potential to safeguard kidney health by suppressing the expression of AGEs, RAGE, and TGF- β 1, thereby exerting anti-inflammatory, anti-oxidative stress, and anti-fibrotic effects.

3.2 Promotion of EPO production

Renal anemia is a prevalent complication in advanced DKD, and its management has been shown to slow down the progression of renal failure (48, 49). In diabetic patients, increased glucose reabsorption through SGLT-2 by proximal tubular epithelial cells results in excessive consumption of adenosine triphosphate (ATP) produced by the Na⁺/K⁺ pump. This leads to heightened oxygen consumption by tubular epithelial cells and subsequently reduced oxygen partial pressure in the kidney's cortical tissue. The hypoxic microenvironment of renal tubular epithelial cells triggers the transformation of EPO-producing fibroblasts into myofibroblasts, consequently reducing EPO production (50, 51). By diminishing glucose reabsorption and lowering the demand on the Na⁺/K⁺ pump ATP, SGLT-2 inhibitors alleviate metabolic stress on proximal tubules, thereby improving the microenvironment within renal tubules.

This leads to the transformation of myofibroblasts to fibroblasts, which partially increases EPO production and contributes to the correction of anemia (52). The EMPA-HEART CardioLink-6 trial demonstrated that empagliflozin-induced early elevation of EPO and subsequent increments in hematocrit correlated with reductions in ferritin and hemoglobin levels (53). An analysis of data from the EMPA-REG outcome trial suggests that approximately 50% of the mortality benefits associated with increased hematocrit in SGLT-2 inhibitor-treated patients may be attributed to enhanced erythropoietin production. This gain might be due to the protective effects of EPO as a circulating pleiotropic cytokine, including promoting angiogenesis, improving mitochondrial function, and suppressing inflammation. Moreover, the elevated hematocrit resulting from EPO also directly enhances the oxygen-carrying capacity of systemic tissues (54). Hence, by stimulating the production of EPO, SGLT-2 inhibitors have the potential to safeguard renal function and slow down the advancement of renal failure.

3.3 Improved mitochondrial energy supply

The renal tubule's epithelial cells contain abundant mitochondria, which play a crucial role in supplying energy for

the reabsorption of metabolic substances like glucose and Na⁺ in the renal tubules. ATP, produced by mitochondria, is essential for glucose uptake by tubular epithelial cells. Glucose and fatty acids are the primary sources of substrates for ATP production, with β -oxidation of fatty acids generating significantly more ATP than aerobic fermentation of glucose (55, 56). In a hyperglycemic environment, there is an increase in glycolysis, tricarboxylic acid cycle, and β -oxidation, along with an elevation in oxygen free radical production, leading to tubulointerstitial fibrosis and hastening the progression of renal failure (57, 58). Research indicates that impaired fatty acid oxidation occurs in parallel with the advancement of DKD (59, 60). Hence, enhancing mitochondrial fatty acid oxidation to ensure a more efficient energy supply could potentially delay the progression of DKD.

SGLT-2 inhibitors have been found to increase urinary glucose excretion, leading to a decrease in glucose levels in the body. This causes a shift in energy utilization, where fatty acid β -oxidation is employed as the main source of energy. This shift in energy supply is primarily responsible for the weight loss observed with SGLT-2 inhibitors (61). Furthermore, increased β -oxidation results in the production of excess acetyl coenzyme A, which generates ketone bodies (β -hydroxybutyrate, acetoacetate, and acetone). These ketone bodies serve as a fuel source for ATP production in the mitochondria, thus improving mitochondrial energy supply (62, 63). Moreover, SGLT-2 inhibitors can enhance mitochondrial energy supply through various mechanisms. They promote EPO production, enhance renal tissue oxygenation, and facilitate the conversion of synthetic ATP fuel from glucose to ketone bodies (64). Numerous clinical studies have demonstrated that the application of SGLT-2 inhibitors promotes the synthesis of ketone body and decreases the insulin-to-glucagon ratio (65–67). Hence, it is believed that SGLT-2 inhibitors have the potential to enhance kidney function by augmenting ketone body production through β -oxidation, thereby improving the mitochondrial energy supply to the renal tubular epithelial cells.

3.4 Inhibition of the sympathetic nervous system (SNS)

Persistent activation of the SNS has been strongly linked to the onset of type 2 diabetes (68). Moreover, its excessive activation is associated with a negative prognosis in patients suffering from advanced DKD (69). SNS hyperactivity has been correlated with glomerulosclerosis, protein loss, and microalbuminuria. Additionally, it promotes the development of renal fibrosis by triggering pro-inflammatory and pro-fibrotic markers such as tumor necrosis factor- β , it also hastens the development of renal fibrosis. This, in turn, leads to a decline in glomerular filtration rate and further exacerbates SNS activation, creating a harmful cycle that accelerates the progression of DKD (70, 71). Sano has proposed that the kidneys play a central role in sympathetic overactivation and has suggested that SGLT-2 inhibitors could potentially provide cardiovascular and renal benefits by reducing afferent renal nerve activity and inhibiting reflex mechanisms within the central nervous system that activate the systemic sympathetic nerves (72).

Herat et al. proposed that the neurotransmitter norepinephrine, released by the sympathetic nervous system, may enhance the expression of SGLT-2. This, in turn, leads to an increase in the reabsorption of glucose and sodium in the renal tubules, as well as elevated levels of blood sugar and blood pressure (73). It has also been demonstrated that dapagliflozin can reduce the expression of tyrosine hydroxylase and norepinephrine in hypertensive mice. These findings suggest that the effect of SGLT-2 inhibitors in protecting renal function could be attributed to a decrease in renal sympathetic nerve activity.

3.5 Improve vascular endothelial function

DKD is a complication of diabetes mellitus characterized by damage to the small blood vessels. The dysfunction of the vascular endothelium is considered the initial factor contributing to the development of diabetic microangiopathy. Impaired function of endothelial cell often results in reduced production of nitric oxide (NO) (74, 75). However, extended administration of SGLT-2 inhibitors has been shown to effectively improve vascular endothelial dysfunction in diabetic rats by enhancing NO diastolic function, reducing oxidative stress, and alleviating glucose toxicity in the aortic rings (76, 77). In a study investigating endothelial dysfunction in diabetes, dapagliflozin was found to potentially facilitate the repair of vascular endothelial by decreasing the expression of vascular adhesion molecules, phosphorylated I κ B expression, and infiltration of inflammatory macrophages *in vivo* (41).

3.6 Reduce uric acid

Chronic hyperuricemia has been consistently identified as a risk factor for the progression of CKD, particularly in individuals with coexisting type 2 diabetes (78). The kidneys play a crucial role in eliminating uric acid from the body, primarily through the renal tubules (79). Within the renal tubules, specific proteins, namely glucose transporter protein 9 (GLUT9) and ATP-binding cassette subfamily G member 2 (ABCG2), are responsible for the reabsorption and excretion of urate, respectively. Of these proteins, GLUT9 plays a central role in the handling of urate (78). The hypouric acid effect of SGLT-2 inhibitors has been linked to the excretion of sugar in the urine (80). These inhibitors work by blocking SGLT receptors, leading to increased glucose excretion in the urine. The excess urinary glucose then competes with GLUT9, reducing the reabsorption of urate and increasing the excretion of uric acid (78). Research has demonstrated that the ability of empagliflozin to lower uric acid levels is associated with the upregulation of ABCG2 expression, which is mediated by the AMPK/Akt/CREB signaling pathway (81).

4 Efficacy and safety of SGLT-2 inhibitors in stage G4 DKD

In recent years, the effectiveness and safety of SGLT-2 inhibitors in treating patients with type 2 diabetes and mild to moderate renal insufficiency (eGFR \geq 30 mL/min/1.73 m²) have been confirmed

through large clinical trials such as EMPA-REG OUTCOMES (82), DECLARE-TIME 58 (83), CANVAS-R (84), and CREDENCE (85). However, the efficacy and safety of SGLT-2 inhibitors in patients with stage G4 and even G5 DKD have remained unclear until the release of the results from DAPA-CKD (9) and EMPA-KIDNEY (10). These studies have provided a significant basis for establishing the effectiveness and safety of SGLT-2 inhibitors in patients with stage G4 DKD.

4.1 Effect on cardiac and renal outcomes

The DAPA-CKD clinical trial enrolled patients with CKD and an eGFR ranging from 25 to 75 mL/min/1.73 m², with up to 67.5% of them having DKD. During the study, which had a median follow-up duration of 2.4 years, the results demonstrated a significant reduction in the risk of the primary endpoint event, which included sustained reduction in eGFR exceeding 50%, ESRD, and a composite endpoint of death resulting from renal or cardiovascular causes in the dapagliflozin treatment group (9). In the subgroup analysis of patients with stage 4 CKD, the use of dapagliflozin group demonstrated significant benefits. The dapagliflozin group exhibited a 27% reduction in the risk of experiencing the main composite endpoint event, which included sustained decline in eGFR exceeding 50%, ESRD, and death from kidney disease. Additionally, there was a 29% decrease in the risk of experiencing sustained decline in eGFR > 50%, ESRD, and death from kidney disease. The risk of hospitalization for heart failure or cardiovascular death was lowered by 17%, and the risk of all-cause mortality decreased by 32%. Furthermore, dapagliflozin treatment also resulted in a slower rate of decline in eGFR and significantly reduced proteinuria. Remarkably, there were no significant differences in therapeutic benefits and safety observed between stage 2-3 CKD and stage 4 CKD groups (86).

The EMPA-KIDNEY trial, with a median follow-up of 2 years, included 46% of patients with DKD and 34.5% of patients with stage 4 CKD and an eGFR of 20–30 mL/min/1.73 m². The primary endpoint events were cardiovascular death or progression of kidney disease. Progression of kidney disease was defined as a > 40% reduction in eGFR from baseline values, a sustained decrease in eGFR to < 10 mL/min/1.73 m², ESRD, or death due to kidney disease causes. The results of the trial showed that the group receiving empagliflozin had a 28% lower risk of cardiac and kidney endpoints compared to the placebo group. Furthermore, there was a 14% lower risk of hospitalization for any reason in the empagliflozin group. Additionally, empagliflozin treatment delayed the decline in eGFR and reduced albuminuria, particularly in patients with a higher urine protein to creatinine ratio at baseline. These beneficial outcomes were consistent across subgroups defined by different eGFR ranges (10). Overall, the EMPA-KIDNEY trial demonstrates that empagliflozin is effective in reducing the risk of cardiovascular and kidney events, hospitalization, and progression of kidney disease in patients with DKD and CKD stage 4. These findings highlight the potential benefits of empagliflozin in managing kidney disease in these patient populations.

In the CREDENCE trial, which focused on patients with DKD, the primary endpoint was defined as doubling of blood creatinine levels, development of ESRD, or death from cardiovascular or renal causes. After 2.6 years of follow-up, the results indicated that canagliflozin reduced the risk of the primary outcome by 30% and the risk of progressing to ESRD by 32% (85). Interestingly, in the subgroup of patients with stage G4 DKD, canagliflozin did not significantly improve glycated hemoglobin levels. However, it did lead to a significant 33% reduction in urinary albumin levels and a slower decline in eGFR compared to the placebo group. These findings were consistent with the DAPA-CKD and EMPA-KIDNEY trials, where the risk of major outcomes in the stage G4 DKD subgroup was similar to that of other subgroups defined by eGFR (87). Overall, these results highlight the efficacy of canagliflozin in reducing the risk of renal and cardiovascular events, as well as slowing the progression of kidney disease in patients with DKD, including those with stage G4 DKD.

The SCORED trial aimed to evaluate the effects of sotagliflozin in patients with DKD, specifically those with an eGFR of 25–65 mL/min/1.73 m². The trial had a median follow-up period of 16 months. The primary endpoint was the incidence of serious cardiovascular adverse events. Additionally, the advancement of renal disease was assessed as a secondary endpoint, which included a decline in eGFR of more than 50% from baseline, ESRD, dialysis, or renal transplantation. However, the results of the trial did not demonstrate statistically significant differences in either all-cause mortality or the renal composite endpoint outcomes between the sotagliflozin group and the control group (88). Surprisingly, the subgroup analysis focusing on patients with stage G4 DKD did not show substantial reductions in the primary endpoints of cardiovascular death and heart failure (89).

A separate study investigating the effects of sotagliflozin over a 52-week period showed that it did not significantly improve glycated hemoglobin levels after 26 weeks. Furthermore, its cardiorenal outcomes were consistent with the findings from the SCORED trial (90). Notably, sotagliflozin did not demonstrate a

significant reduction in the risk of cardio-renal outcomes specifically in patients with stage G4 DKD, which is in contrast to the positive results observed in other trials such as DAPA-CKD, EMPA-KIDNEY, and CREDENCE studies. To summarize, SGLT-2 inhibitors have been found to offer significant cardiac and renal benefits to patients with stage G4 DKD, which were comparable to those observed in patients with stage G1–G3 DKD. It is widely acknowledged that as the eGFR decreases, patients experience a decline in glomerular filtration function and a reduced ability to reabsorb glucose and Na⁺ in the renal tubules.

Therefore, their ability to lower blood sugar, improve glomerular hyperfiltration, and reduce volume load is diminished. However, even in the presence of a significant decrease in eGFR, SGLT-2 inhibitors still provide notable cardiorenal benefits. These benefits may be attributed to potential renoprotective effects, such as reducing inflammation and fibrosis, improving oxidative stress, enhancing mitochondrial energy supply, inhibiting the SNS, promoting EPO production, and improving vascular endothelial function. Additionally, considering that sotagliflozin is less effective in improving cardiovascular and renal outcomes in patients with more advanced DKD, dapagliflozin, empagliflozin, and canagliflozin are recommended for the treatment of patients with relatively advanced DKD (Table 1).

4.2 Adverse reactions

When evaluating the safety of SGLT-2 inhibitors in patients with stage G4 DKD, it is crucial to consider both their positive impact on the heart and kidneys, as well as any potential negative side effects they may cause. Various types of SGLT-2 inhibitors exhibit different adverse events, particularly hypoglycemia, genitourinary infection, ketoacidosis, acute kidney injury (AKI), fractures or amputations, and other adverse events. Therefore, when utilizing SGLT-2 inhibitors, a thorough assessment of the patient's condition should be conducted.

TABLE 1 Effect of SGLT-2 inhibitors on cardiac and renal outcomes.

Drug	DAPA-CKD	EMPA-KIDNEY	CREDENCE	SCORED
	Dapagliflozin	Empagliflozin	Canagliflozin	Sotagliflozin
Median follow-up(years)	2.4	2.0	2.6	1.3
eGFR(mL/min/1.73m ²)	25–75	20–90	30–90	25–60
Stage 4 CKD rate	14%(n=624)	34.2%(n=1131)	4%(n=174)	7.7%(n=813)
Renal outcomes Hazard Ratio(95%CI) P Value	0.56(0.45–0.68) p<0.001	0.72(0.64–0.82) P<0.001	0.66(0.53–0.81) P<0.001	0.71(0.46–1.08) p>0.05
Cardiovascular outcomes Hazard Ratio(95%CI) P Value	0.71(0.55–0.92) P=0.009	0.84 (0.64–0.82) P=0.15	0.69(0.57–0.83) P<0.001	0.74(0.63–0.88) P<0.001
Deaths from any cause Hazard Ratio(95%CI) P Value	0.69(0.53–0.88) P=0.004	0.87(0.70–1.08) P=0.21	0.83(0.68–1.02) p>0.05	0.99(0.83–1.18) p>0.05

4.2.1 Hypoglycemia

Since the primary mechanism of SGLT-2 inhibitors involves inhibiting renal glucose excretion, which is independent of insulin secretion, the risk of hypoglycemia is low (91). Clinical trials such as DAPA-CKD, EMPA-KIDNEY, SOCRD, and CREDENCE have demonstrated no increased risk of hypoglycemia in patients with stage G4 DKD (9, 10, 85, 88). Additionally, a study involving type 2 diabetic patients with CKD stages 3b-4 also found no severe hypoglycemic events in the dapagliflozin group, while three (4.3%) severe hypoglycemic events occurred in the placebo group (21). Therefore, SGLT-2 inhibitors have not been shown to raise the incidence of hypoglycemia in patients with advanced DKD.

4.2.2 Ketoacidosis

Ketoacidosis, which is often characterized by gastrointestinal symptoms such as nausea, vomiting, and diarrhea, is a serious adverse effect of SGLT-2 inhibitors (92). The occurrence of ketoacidosis may have a multifaceted mechanism. On one hand, the reduction in blood glucose induced by SGLT-2 inhibitor inhibits insulin secretion. On the other hand, the mechanisms associated with SGLT-2 inhibitors also lead to an increase in glucagon secretion, resulting in a high glucagon/insulin ratio. This elevated ratio plays a significant role in promoting hepatic fatty acid oxidation and ketone bodies production (93). Additionally, the loss of glucose in the kidneys promotes the secondary reabsorption of ketone bodies, further contributing to ketoacidosis (94).

In a recent multicenter study, the risk ratios for ketoacidosis were found to be 3.58, 2.52, and 1.86 for canagliflozin, empagliflozin, and dapagliflozin respectively. The high incidence of ketoacidosis with canagliflozin is primarily attributed to its greater selectivity for SGLT-1 over SGLT-2. Inhibition of SGLT-1 contributes to the development of diarrhea and volume deficit, which can serve as important trigger for ketoacidosis (95). In both the EMPA-KIDNEY and SOCRD trials, ketoacidosis occurred more frequently in the empagliflozin and sotagliflozin groups. Adverse events of diarrhea were also more common in the sotagliflozin group, further increasing the risk of ketoacidosis (10, 88). Therefore, individuals taking SGLT-2 inhibitors should be vigilant for potential ketoacidosis if they experience gastrointestinal symptoms.

4.2.3 Genitourinary system infections

SGLT-2 inhibitors, by promoting the excretion of high amounts of sugar in urine through the kidneys, can increase the risk of urinary tract infections, particularly *Candida* infections. These infections are more common in females than males and can typically be alleviated with conventional drug therapy (96). Findings from the SCORED trial indicate a higher incidence of genital fungal infections in the sotagliflozin group compared to the placebo group, and this difference was statistically significant (88). Furthermore, other related studies have also suggested a higher likelihood of genital fungal infections in patients with type 2 diabetic CKD stages 3b-4 who use dapagliflozin (21).

4.2.4 Acute kidney injury

Previous explanations for SGLT-2 inhibitor-induced AKI have often focused on the diuretic effect of these inhibitors, which can lead to a decrease in eGFR due to constriction of the small incoming glomerular arteries through tubular feedback (97). However, as research progressed, a more plausible mechanism for the development of AKI was proposed. SGLT-2 inhibitors cause uric aciduria by enhancing the excretion of uric acid via GLUT9 in the renal proximal tubules. This, in turn, triggers an immune response through the activation of inflammatory vesicles and localized inflammatory reactions, ultimately resulting in AKI (98). Additionally, when SGLT-2 inhibitors inhibit glucose reabsorption in the S1 and S2 segments of the renal tubules, there is an increased influx of glucose into the S3 segment. Conversely, the uninhibited SGLT1 receptors also facilitate greater glucose uptake, which may activate aldose reductase and lead to the conversion of glucose in the S3 segment into fructose and sorbitol.

The conversion of glucose in the S3 segment into fructose through fructose kinase activity contributes to the local production of uric acid, oxidative stress, and the release of chemokines, which promote AKI (99). Moreover, the accumulation of sorbitol and fructose due to decreased inositol levels in hyperglycemia may also predispose individuals to the development of AKI (100). Although some studies suggest a potential risk of AKI with SGLT-2 inhibitors, a larger body of research, including studies involving patients with advanced diabetic nephropathy, has failed to demonstrate an increased risk of AKI. The DAPA-CKD trial has indicated that the decrease in serious adverse events related to AKI may reflect the potential protective effect of dapagliflozin beyond the initial decline in eGFR (9). Similarly, the application of empagliflozin, sotagliflozin, and canagliflozin in patients with relatively advanced CKD has also shown no elevated risk of AKI (10, 85, 88). Hence, further studies are needed to confirm whether SGLT-2 inhibitors actually increase the incidence of AKI.

4.2.5 Fracture and amputation

According to the findings from the CANVAS clinical study, the group treated with canagliflozin exhibited a significantly higher incidence of fracture and amputation compared to the placebo group, with incidences that were 97% and 26% higher, respectively. However, the exact mechanism by which SGLT-2 inhibitors contribute to fractures and amputations remains unclear. There have been suggestions that hypovolemia caused by osmotic diuresis and altered bone metabolism due to increased phosphate uptake may be the primary factors responsible for fractures (101, 102). Similarly, hypovolemia and reduced blood flow to the lower extremities resulting from diuresis are thought to be the main causes of amputation (103). In contrast, no increased risk of fracture or amputation was observed in the CREDENCE trial involving canagliflozin (85). Likewise, the DAPA-CKD, EMPA-KIDNEY, and SOCRD trials also found no elevated risk of fracture or amputation (9, 10, 88). After evaluating the potential risks of amputation linked to the use of SGLT-2 inhibitors, the panel reached the conclusion that canagliflozin was the only specific medication associated with

an increased risk. They found no evidence suggesting that other SGLT-2 inhibitors posed a similar risk of amputation (104).

Following a comprehensive assessment of the extended effectiveness and adverse events of four SGLT-2 inhibitors in patients with stage G4 DKD, over a follow-up period ranging from 1.3 to 2.6 years, it has been observed that these medications exhibit reduced efficacy in lowering blood glucose levels in such individuals. Additionally, they are associated with adverse events, including urinary tract infections, as well as potential serious risks such as ketoacidosis, fractures, and amputations. However, instances of hypoglycemia and AKI are infrequent. Moreover, most SGLT-2 inhibitors significantly decrease the likelihood of cardiovascular and renal complications in both diabetic and non-diabetic patients with kidney disease over long-term treatment. Consequently, SGLT-2 inhibitors represent a valuable drug option for managing stage G4 DKD in the long run. Furthermore, findings from a 4-year study focusing on patients with diabetes indicate that dapagliflozin demonstrates favorable safety and tolerability profile when used over an extended duration (105). In general, the long-term safety and tolerability of SGLT-2 inhibitors in patients with G4 DKD were found to be relatively favorable. However, it is important to note that the four primary clinical study populations may not fully represent patients with DKD, particularly those in stages G4-5. Therefore, further studies are required to evaluate the effectiveness and safety of SGLT-2 inhibitors specifically in this patient population.

4.3 Advantages and disadvantages of individual SGLT-2 inhibitors

4.3.1 Dapagliflozin

Dapagliflozin, the first SGLT-2 inhibitor approved for the treatment of type 2 diabetes (106), continues to demonstrate significant benefits in reducing renal and cardiovascular outcomes, as well as the risk of mortality in patients with stage G4 DKD. Furthermore, its long-term use does not appear to increase the incidence of adverse events, even when patients have an eGFR as low as 15 mL/min/1.73 m². Regarding adverse events, the incidence of serious adverse events was found to be 34.5%. However, the dapagliflozin group did not show an increased risk of adverse events such as hypoglycemia, ketoacidosis, AKI, fracture, and amputation compared to the DKD dapagliflozin group in stages G2-3 or the placebo group in stage G4 DKD. It is worth noting, however, that the incidence of renal-related adverse events was higher in patients with stage G4 DKD.

4.3.2 Empagliflozin

In the EMPA-KIDNEY trial, it was observed that empagliflozin had a beneficial effect in reducing the risk of renal outcomes. However, it did not show a significant reduction in the risk of cardiovascular outcomes or death. Regarding adverse events, the incidence of serious adverse events was found to be 35.2%. It is worth noting that while there is a potential risk of genitourinary infection and ketoacidosis, there was no increased risk of fracture or amputation.

4.3.3 Canagliflozin

In the CREDENCE trial, canagliflozin demonstrated a reduction in the risk of both renal outcomes and cardiovascular outcomes. However, it did not show a significant reduction in the risk of all-cause mortality. With regard to adverse events, the incidence of serious adverse events was found to be 33.5%. The most common serious adverse events were urinary tract infections (13.4%) and ketoacidosis (0.5%). Importantly, there was no increased risk of fracture or amputation associated with canagliflozin usage.

4.3.4 Sotagliflozin

In the SOCRD trial, sotagliflozin showed a reduction in cardiovascular outcomes risk. However, it did not demonstrate a reduction in renal or cardiovascular risk specifically in the stage G4 DKD subgroup. In terms of adverse events, the incidence of serious adverse events was 23.4%. Diarrhea (8.5%), ketoacidosis (0.6%), and urinary tract infections (11.5%) were more frequently reported with sotagliflozin compared to placebo. Importantly, there was no increased risk of fracture or amputation observed.

In summary, all four SGLT-2 inhibitors have shown the ability to reduce renal, cardiovascular, and mortality risks in patients with stage G4 DKD, with generally favorable safety profiles. Among them, dapagliflozin stands out as it effectively reduces renal, cardiovascular, and mortality risks without the occurrence of ketoacidosis, and it also lowers the incidence of AKI. However, sotagliflozin appears to be less effective in improving cardiac and renal outcomes in advanced DKD patients and should be used with caution in this population. In terms of adverse events, sotagliflozin has the lowest incidence of serious adverse events, but is more associated with diarrhea and urinary tract infections. It is worth noting that, except for dapagliflozin, the other three SGLT-2 inhibitors carry a potential risk of ketoacidosis. Therefore, dapagliflozin is recommended as a preferable option for patients with advanced DKD.

5 Conclusion and Prospect

Delaying the progression of diabetic nephropathy, a leading cause of ESRD, is of utmost importance. SGLT-2 inhibitors, a novel class of glucose-lowering drugs, have shown substantial cardiovascular and renal protective effects in patients with stage 1-4 CKD, regardless of the presence of diabetes. However, as eGFR declines, the hypoglycemic effects, improvement of glomerular hyperfiltration, and suppression of the RAAS by SGLT-2 inhibitors become less effective. Despite this, SGLT-2 inhibitors continue to demonstrate significant cardiorenal benefits in advanced DKD, potentially due to their ability to suppress inflammation and fibrosis, improve oxidative stress, enhance EPO production, optimize mitochondrial energy supply, inhibit the SNS, and protect vascular endothelial cells. These mechanisms likely contribute to the observed renal protective effects of SGLT-2 inhibitors in advanced DKD.

Further investigation and clarification are needed to fully understand the linked mechanisms and the renal protective effects of SGLT-2 inhibitors from multiple perspectives. Currently, the efficacy and safety of SGLT-2 inhibitors in treating patients with advanced DKD have been increasingly supported. The threshold for using SGLT-2 inhibitor has been lowered to an eGFR of 20 mL/min/1.73 m², and they can be continued until the initiation of dialysis or renal transplantation, as long as they are well-tolerated by the patient. It is exciting to anticipate whether future advancements will relax the restrictions on the use of SGLT-2 inhibitors for patients with all stages of CKD.

Author contributions

J-XT and C-WY formulated and conceived of this study. Z-CD, J-XC, RZ, X-BL, J-XT, and C-WY wrote the manuscript. All authors contributed to the article and approved the submitted version.

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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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Research progress of NF- κ B signaling pathway and thrombosis

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Venous thromboembolism is a very common and costly health problem. Deep-vein thrombosis (DVT) can cause permanent damage to the venous system and lead to swelling, ulceration, gangrene, and other symptoms in the affected limb. In addition, more than half of the embolus of pulmonary embolism comes from venous thrombosis, which is the most serious cause of death, second only to ischemic heart disease and stroke patients. It can be seen that deep-vein thrombosis has become a serious disease affecting human health. In recent years, with the deepening of research, inflammatory response is considered to be an important pathway to trigger venous thromboembolism, in which the transcription factor NF- κ B is the central medium of inflammation, and the NF- κ B signaling pathway can regulate the pro-inflammatory and coagulation response. Thus, to explore the mechanism and make use of it may provide new solutions for the prevention and treatment of thrombosis.

KEYWORDS

thrombosis, NF- κ B signal pathway, inflammation, miRNA, TCM, natural compounds, drugs

1 Introduction

Deep-vein thrombosis (DVT) is a serious disease threatening human life. The incidence of DVT is 10-40% after general surgery and 40-60% after major orthopedic surgery, and in the absence of preventive measures, DVT can lead to further diseases such as pulmonary hypertension, recurrent thrombosis, post-thrombotic syndrome, and even fatal pulmonary embolism (1, 2). Therefore, patients with acute DVT face a high risk of death. The treatment of DVT in modern medicine can be roughly divided into anticoagulation therapy and thrombectomy (3). Anticoagulation therapy and surgery have made great progress in the treatment of DVT and are widely used. If more methods can continue to be found to treat thrombosis, then the recovery probability of related patients will be increased. Therefore, research on the prevention and treatment of thrombosis has never stopped.

Blood flow retardation, blood hypercoagulability, and endothelial cell injury are the three major factors of venous thrombosis (4, 5). They play different roles in the mechanism of venous thrombosis but are related to each other. Vascular endothelial cells divide blood from subendothelial tissue, store and secrete factors that affect platelet function, prevent platelet adhesion, and allow blood to flow normally. However, when the endothelium is disturbed by physical or chemical factors, the endothelial cells will undergo programmed biochemical changes, transform into the front surface of the thrombus, express TF, and accelerate the activation of factor X and factor IX, thereby activating the coagulation system (6). Changes in hemodynamics promote changes in the state of the vascular endothelium, and the flow of blood through the vasculature generates wall shear stress, resulting in structural and functional changes in the vessel wall (7). Shear stress also strongly affects endothelial cell gene expression (8, 9). There are “shear-stress response elements” in the promoters of related genes (10, 11), various “mechanical transducers” and downstream signal pathways, which associate external mechanical stimuli with intracellular and nuclear events (12–14). The hypercoagulable state is one of the important factors of venous thrombosis (15). When too many clotting proteins are produced in the blood, abnormal clotting proteins are produced to resist decomposition, and too few proteins that prevent thrombosis are produced, which will cause the blood to become hypercoagulable (16). The combination of the hypercoagulable state and acquired risk factors (surgery, braking, or hormone therapy) increases the risk of thrombosis (17, 18). Proper thrombus prevention can prevent the risk of thrombosis from exceeding this critical threshold, but thrombosis occurs when internal and external forces exceed the critical threshold (19).

In recent years, studies have found that inflammation is closely related to the formation and development of deep venous thrombosis. Inflammation mediates vascular endothelial cell injury (20, 21), releases vascular cell adhesion molecules (VCAM) and intercellular adhesion molecules (ICAM), stagnates blood flow, and accelerates venous thrombosis (22–25). The formation of blood clots exacerbates the inflammatory response, and the two affect each other. Therefore, study of the occurrence of venous thrombosis and the discovery of related proteins regulating inflammatory factors are of great significance for delaying and alleviating the formation of venous thrombosis and judging the prognosis.

2 Overview of the NF- κ B signaling pathway

The NF- κ B family consists of a group of structurally related and evolutionarily conserved transcription factors that play a key role in inflammatory response, immune function, cell survival, and prevention of apoptosis (26). There are currently five members of the mammalian NF- κ B family, known as RelA (also known as p65), RelB, c-Rel, NF- κ B1 (p50 and its precursor p105), and NF- κ B2 (p52 and its precursor p100) (27).

Despite the expanding complexity of NF- κ B signaling, the two most recognized pathways in mammalian cells are the so-called

classical and atypical pathways (28–30), both of which are important in inflammatory response and immune regulation, despite their differences in signaling composition and biological function. The classical NF- κ B pathway is induced by pro-inflammatory cytokines and depends on the induced degradation of I κ B, specifically I κ B α , to activate the NF- κ B1 p50, RelA, or c-Rel complex (28). The non-classical NF- κ B pathway is triggered by certain members of the TNF family of cytokines rather than by TNF- α itself and depends on the induction process of p100 rather than the degradation of I κ B α , leading to the activation of the NF- κ B2 P52 or RelB complex (31–33). Activated NF- κ B is transferred from the cytoplasm to the nucleus, where it causes the expression of target genes associated with inflammation. The NF- κ B family has been shown to activate more than 500 inflammation-related genes (34, 35) and can initiate the expression of cytokines necessary for inflammation. Some of these cytokines, such as IL-1 and TNF- α , activate NF- κ B itself, leading to the formation of a positive feedback loop that has the potential to produce chronic and excessive inflammation when NF- κ B becomes abnormally or persistently active.

3 Relationship between NF- κ B, inflammation, and thrombosis

3.1 The inflammatory response promotes thrombosis

In general, DVT can be caused by a variety of risk factors, including genetics, dietary habits, obesity, aging, trauma, and cancer (2). In recent years, with the deepening of research, inflammation is considered to be an important way for various risk factors to trigger the formation of VTE (36–39). In our recent case, the novel coronavirus infection (COVID-19) is caused by the novel coronavirus SARS-CoV-2, which is characterized by an excessive inflammatory response. It has been reported that about half of the hospitalized patients with COVID-19 have serious symptoms, such as deep-vein thrombosis and coagulation dysfunction in the lower extremities, and some patients may die (40–44). It has also been reported that the injection of the COVID-19 vaccine can cause an immune inflammatory response, thus promoting thrombosis and thrombocytopenia (45–50). When studying the changes of inflammatory factors in the plasma of DVT patients, it was found that the expression level of IL-17A was up-regulated, and the level of platelet aggregation was increased, which promoted platelet activation and aggregation, thus playing a role in promoting the formation of DVT (51). In addition, pro-inflammatory factors represented by interleukin-1 (IL-1), IL-6, IL-1 β , IL-18, cox-2, TNF- α (52–55), and other inflammatory factors can induce inflammatory response, accelerate tissue injury, and stimulate the release of inflammatory mediators, leading to vascular endothelial injury and apoptosis (20, 21). This indicates that inflammation has become a factor that cannot be ignored in the mechanism of thrombosis.

3.2 NF- κ B induces an inflammatory response

Transcription factor NF- κ B is the central mediator of inflammatory response, mainly in the form of p65 and p50 binding and in the form of dimer; when stimulated, NF- κ B p65/p50 dissociates with I κ B α and enters the nucleus to activate the corresponding gene transcription (56). The NF- κ B signaling pathway is the central link of various inflammatory responses, which can up-regulate the expression of pro-inflammatory factors in the activated state, and inflammatory response can release inflammatory factor IL-1 β through the NF- κ B pathway, resulting in increased expression of monocyte chemotactic protein-1 (MCP-1) and activation of endothelial cells (57, 58). Releasing intercellular adhesion molecule-1 (ICAM-1), platelet endothelial cell adhesion molecule-1 (PECAM-1), and vascular cell adhesion molecule-1 (VCAM-1), etc. (59, 60), further activates NF- κ B, amplifies inflammatory response, and releases more inflammatory factors. Increased platelet reactivity, activation of the plasma coagulation cascade, and impaired function of physiological anticoagulants result in the hypercoagulability of blood (61, 62).

3.3 NF- κ B is involved in thrombosis

NF- κ B signaling plays an important role in the vascular system and in the cell types involved in thromboinflammatory processes. By mediating the interaction between endothelial cells, platelets, and inflammatory response, NF- κ B disrupts the coagulation-fibrinolysis balance and induces thrombosis (63).

3.3.1 Platelets

Platelets are not only involved in primary hemostasis but also in the formation of thrombus induced by inflammation. Platelet activators include not only thrombin and ADP but also molecules involved in inflammation (64). Platelets as non-nucleated cells also contain members of the NF- κ B family and their corresponding signaling molecules, which are involved in platelet activation and secondary feedback loops (56). Activated platelets express or secrete pro-inflammatory and pro-coagulant substances on their surfaces, such as adhesion molecules, growth factors, cytokines, and the fibrinolytic inhibitor PAI-1, inducing surface aggregation of coagulation factors (65).

3.3.2 Endothelial cell

The injury of the vein wall or vein endothelial cells caused by various factors is one of the factors that cause DVT. Studies have confirmed that NF- κ B signaling molecules exist in endothelial cells (63). When injured, endothelial cells are activated, which can inhibit the expression of thrombomodulin (TM) and activate the expression of endothelial tissue factor (TF), resulting in the activation of adhesion molecules such as P-selectin and clotting factor vWF (66), and the endothelial cells change from anticoagulant, anti-inflammatory, and vasodilator functions to proinflammatory and pre-thrombotic states.

3.3.3 NETs

Inflammatory cells represented by neutrophils and monocytes were able to rapidly aggregate and adhere to the venous endothelium (67). Among them, neutrophils can activate coagulation factors XII, initiate endogenous coagulation, and also form neutrophil extracellular traps (NETs) after apoptosis. NETs, as part of the body's innate immunity, are an extracellular network of fibers made up of disaggregated chromatin (DNA fibers and histones) released by neutrophils and more than 30 granule proteins with antimicrobial properties (68, 69), providing a supporting basis for thrombosis through their fiber network structure (70). They interact with platelets to further stimulate platelet aggregation, activate thrombin, and accelerate the DVT process (71, 72) (Figure 1).

4 Interference with NF- κ B signaling pathway and deep-vein thrombosis

The NF- κ B signaling pathway is closely related to thrombosis. Activation of the NF- κ B signaling pathway can significantly increase the levels of thromboxane B2 (TXB2), interleukin6 (IL-6), tumor necrosis factor- α (TNF- α), and PAI and significantly decrease the levels of 6-keto-PGF1 α and t-PA, exacerbating inflammation and thrombosis (73). Therefore, we may think that thrombosis can be prevented and that it can be reduced by inhibiting the NF- κ B signaling pathway.

4.1 microRNA regulates NF- κ B signaling pathway to interfere with deep-vein thrombosis

MiRNAs are key regulators of many biological processes (cell differentiation, proliferation, apoptosis, and metabolism), and abnormal expression of miRNAs is known to be associated with a variety of human diseases. Hugo's (2016) study demonstrated the abnormal expression of miRNA in venous thrombosis and suggested that miRNA may be related to the molecular mechanism of DVT. There is evidence that miRNA plays an important role in hemostasis (74), and some foreign scholars (75) have confirmed that miR-181a-5p can inhibit the expression of F11 mRNA and coagulation factor XI. Some members of the miRNA family (miR-126 and miR-145) can promote the dissolution and recanalization of thrombus (76, 77), suggesting that miRNA may be involved in the formation of DVT.

4.1.1 miRNA-181b

DVT group and miR-181b overexpression and inhibition of rat models were constructed by producing a deep-vein thrombosis model and injecting normal saline, miR-181b mimics, and inhibitors into the tail vein. The changes of NF- κ B (P65) in the venous endothelium of rats in each group were analyzed, and the expression level of NF- κ B (P65) in the venous endothelium of rats in the Normal group was used as a reference. The results showed

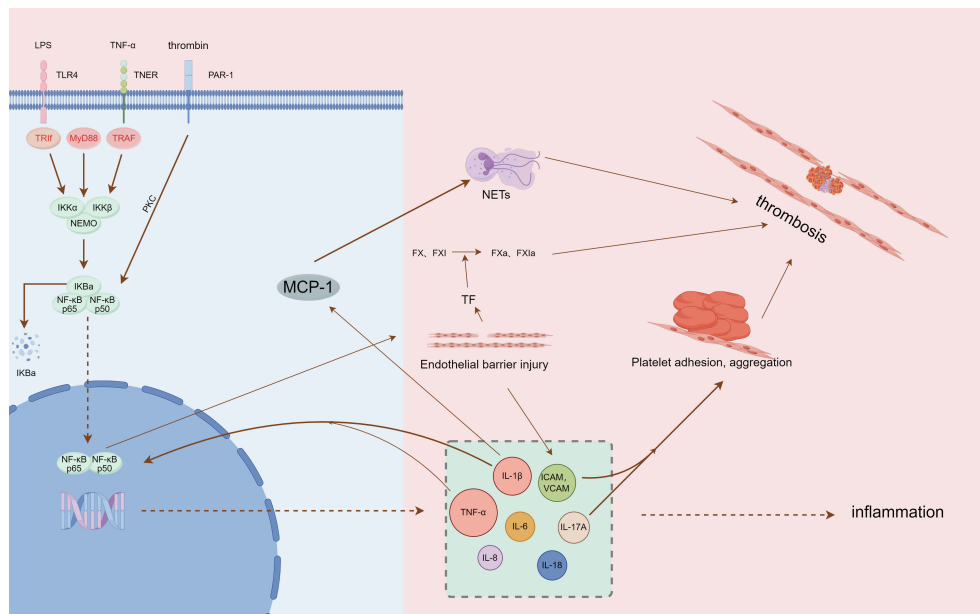


FIGURE 1

Summary of NF-κB pathway mediating inflammation and thrombosis (by Figdraw, authorization ID: PIWYI6b557).

that the expression of NF-κB (P65) in the venous endothelium of rats in the 181b-i group was the highest, followed by the DVT group, and the 181b-m group was lower than the DVT group but higher than the Normal group; moreover, the difference was statistically significant ($P < 0.05$). These results indicate that the expression of NF-κB (P65) is increased in the rat vena cava DVT model, and miR-181b can inhibit the expression of NF-κB (P65). By comparing the length and wet weight of the thrombus in each model group, no thrombus formation was observed in the Normal group. Overexpression of miR-181b can shorten the length of the thrombus and lighten the wet weight after thrombus formation in rats; inhibition of miR-181b expression can lengthen the length of thrombus and increase the wet weight after thrombus formation. These results suggest that miR-181b can reduce the formation of DVT by inhibiting the NF-κB signaling pathway to a certain extent (78).

4.1.2 miRNA-150

Up-regulating the expression of miR-150 inhibited thrombosis in DVT rats. The effect of miR-150 on inflammation was studied *in vivo* and *in vitro*. The rats were injected with LV-NC, and it was found that the administration of LV-miR-150 inhibited the platelet aggregation inhibition rate and TXB2 content in the rat model and significantly inhibited thrombosis. Transfected into *in vivo* skin cells, PAI-1, TNF-α, IL-6, and IL-8 levels were significantly reduced, indicating that miR-150 alleviated inflammation and inhibited apoptosis of vascular endothelial cells. The expression level of NF-κB p50 in vascular endothelial cells transfected with miR-150 mimics was significantly decreased, while the expression level of NF-κB p50 was significantly increased by miR-150 inhibitors. These results suggest that miR-150 may have a negative regulatory effect on NF-κB p50. Therefore,

overexpression of miR-150 can be used as a potential therapeutic target for future DVT (79).

4.1.3 miRNA-141

This study found that by overexpression of miRNA-141, the expression of TLR4 and its signaling pathway-related proteins NF-κB, Rac1, and IL-1β in vascular tissues of thrombotic rats was significantly down-regulated, and by restoring the expression of TLR4 and NF-κB, the expression of Rac1 and IL-1β was restored at the same time, and multiple related indexes of miRNA-141 on thrombus were significantly reversed (80). Activated TLR4 induces late activation of NF-κB, which significantly increases TNF-α expression and causes widespread inflammation (53). Furthermore, TNF-α stimulates the TNF receptor (TNFR) and induces phosphorylation of IκB kinase (IKK), which in turn enhances NF-κB activity (81). NF-κB is the end point of the TLR4/NF-κB pathway and the regulatory hub of an inflammatory response, and its activation can enhance the inflammatory response and promote the formation of a thrombus. This may be a key mechanism by which miRNA-141 inhibits thrombus formation by regulating the TLR4/NF-κB signaling pathway (Table 1).

4.2 TCM preparations alleviate thrombosis by modulating NF-κB signaling

4.2.1 Qihong Tongluo prescription

Qihong Tongluo prescription is mainly composed of Astragalus and safflower. Astragalus has a variety of biological functions, including potent immunomodulatory, antioxidant, anti-inflammatory, and antitumor activities (82). Isoflavones, saponins,

TABLE 1 The effect of miRNA on NF- κ B-mediated inflammatory response.

MiRNA	Anti-inflammatory effect	Action target	reference
miRNA-181b	e-selectin, VCAM-1, ICAM-1	NF- κ B p65	(78)
	Thrombus length and wet weight		
miRNA-150	PAI-1, TNF α , IL-8, IL-6	NF- κ B p50	(79)
	Reduce the degree of vascular obstruction; Endothelial cell proliferation was enhanced		
miRNA-141	Rac1, IL-1 β	TLR4, NF- κ B	(80)
	Inhibit thrombosis and platelet aggregation		

and polysaccharides are three types of beneficial compounds for their pharmacological activity and therapeutic efficacy (82–84). Astragalus polysaccharides decreased the expression of IL-1 β , IL-6, TNF- α , and INF- γ by regulating the toll-like receptor 4 (TLR4)/NF- κ B signaling pathway (85, 86). In addition, safflower can inhibit platelet activation, adhesion, and aggregation (87, 88). In summary, we believe that Qihong Tongluo prescription's inhibition of thrombosis is the result of the joint action of its active components.

4.2.2 Gegen Qinlian pills

The high incidence of thrombotic events is one of the clinical features of coronavirus disease (COVID-19) due to the high inflammatory response caused by the virus. Gegen Qinlian pill (GQP) is a traditional Chinese medicine, which can inhibit toll-like receptor 4 (TLR4)/nuclear factor κ B (NF- κ B) signaling (89–91), has good anti-inflammatory activity, has a good effect on the treatment of COVID-19, and has shown anti-thrombotic potential. In our study, GQP treatment significantly reduced the expression of TNF- α , NLRP3, and NF- κ B, reduced lung, liver, and tail thrombosis, and increased tail blood flow in mice (92). This at least partially supports the hypothesis that GQP can inhibit inflammation-induced thrombosis by inhibiting NF- κ B/NLRP3 signaling.

4.2.3 Huanglianjiedu Decoction

HLJJD is a famous prescription in China, and its main compounds have been studied as baicalin and berberine (93). Baicalin, a flavonoid compound extracted from the root of *Scutellaria baicalensis*, has significant anti-inflammatory and antibacterial effects, scavenging oxygen free radicals and anti-allergic reactions (94, 95). Baicalin can inhibit the NF- κ B signaling pathway, reduce the expression level of the p-NF- κ B p65 protein, and reduce inflammatory response (96, 97). Berberine is an isoquinoline alkaloid isolated from *Coptis chinensis*, a Chinese medicinal plant, and has significant anti-inflammatory effects (98, 99). For the infection-induced tissue injury model, the gene and protein expression levels of TNF- α , TLRs, and NF- κ B p65 were significantly reduced in the berberine treatment group (100–102). TLR4 is a pattern recognition receptor, and activated TLR4 induces late activation of NF- κ B, which significantly increases TNF- α expression and causes widespread inflammation (53). TNF- α stimulates the phosphorylation of I κ B kinase (IKK), which in turn enhances the activity of NF- κ B (81). As

the endpoint of the TLR4/NF- κ B pathway and the regulatory hub of the inflammatory response, the activation of NF- κ B can enhance the inflammatory response and promote the formation of thrombosis.

Through intravenous injection of the effective components of Huanglian Jidutang into the thrombus model, the results showed that the contents of IL-1 β , IL-6, and TNF- α and the expression levels of TLR4, NF- κ B, NLRP3, and Caspase-1 were decreased (103), and they also showed significantly reduced thrombus dry weight, Block platelet aggregation, and adhesion induced by collagen (104). In conclusion, the inhibitory effect of the active components of Huanglian Jiedu Decoction on the NF- κ B pathway is the cause of alleviating inflammation and reducing thrombosis.

4.2.4 Liu Shen Wan

LSW is a classic proprietary Chinese medicine with anti-inflammatory and analgesic effects (105). Its main components are cow gallstone, musk secretion, toad secretion, pearl shell, realgar, and borneol (106). In PR8-infected cells, LSW significantly down-regulated the expression levels of IL-1 β , TNF- α , IL-6, and IFN- γ . In mice infected with PR8, LSW reduced the secretion of TNF- α , IL-1 β , IL-6, and IFN- γ in lung tissue, significantly improving survival. In addition, LSW significantly reduced the expression levels of TLR4, phosphor-NF- κ B p65, and phosphor-I κ B α (107). It is suggested that LSW exerts anti-inflammatory effects by regulating the TLR4/NF- κ B signaling pathway.

4.2.5 Rhein

Rhein is widely found in a variety of Chinese herbs, including *Rhubarb palmatum*, *aloe curacao*, *cassia stenophyllum*, and *polygonum multiflorum*. It has antioxidant, antiviral, anti-inflammatory, anti-tumor, and immunomodulatory activities (108). In mice infected with PR8, rhein significantly improved survival and reduced the lung index and lung expression levels of IL-1 β , IL-6, IL-8, and TNF- α . In addition, rhein significantly reduced the protein levels of TLR2, TLR3, and TLR4 and the phosphorylation of NF- κ B p65 in PR8-infected cells. The addition of TLR4 and NF- κ B activators can antagonize the inhibitory effect of rhein on viral replication (109), so the anti-inflammatory effect of rhein may be related to inhibiting the activation of the TLRs/NF- κ B signaling pathway.

4.2.6 Flavonoids

H. cordatum Thunb. is an important plant medicine with antiviral, antibacterial, anti-inflammatory, and antioxidant activities (110–112). Flavonoids, one of the effective components of this phytomedicine, can reduce lung and intestinal damage in mice, inhibit the over-release of tumor necrosis factor- α , IL-1, IL-8, and MCP-1 in the lung tissue of infected mice, and inhibit the up-regulated expression of TLR and NF- κ B p65 proteins (113). HCP may play an anti-inflammatory role by inhibiting the activation of the TLR/NF- κ B signaling pathway (Table 2).

There are studies that Xiaoshuantongmai decoction can mediate microRNA-181b intervention in deep-vein thrombosis. According to the equivalent dose ratio of kg body weight of human and animal, the drug dose was converted, and based on the deep-vein thrombosis model, normal saline and Xiaoshuantongmai decoction were administered. The results showed that the expression level of miR-181b in the venous endothelium of the Xiaoshuantongmai Tang group was the highest, followed by the blank control group and the sham operation group, and the lowest was in the model control group, with a statistical difference. It was proved that Xiaoshuantongmai decoction can up-regulate the expression of miR-181b in the venous endothelium of DVT model rats (78).

4.3 Anticoagulant and antiplatelet agents inhibit thrombosis by regulating the NF- κ B signaling pathway

4.3.1 Aspirin and salicylate

Acute pulmonary thromboembolism (APE) is a disorder of pulmonary circulation caused by a blockage of the pulmonary

artery. Extensive inflammatory responses have been demonstrated in the lung tissue of APE rats, accompanied by significantly elevated levels of tumor necrosis factor- α , interleukin-1- β , and IL-8 (114, 115). High levels of NF- κ B were also observed in rats after APE induction (116, 117). Aspirin and salicylate have been reported to inhibit NF- κ B equally (118, 119). Healthy SD rats were randomly divided into a control group, sham operation group, APE model group, and aspirin low-dose, medium-dose, and high-dose groups. After APE induction for 6, 24, and 72 h, rats in the low-, medium-, and high-dose aspirin groups were given daily doses of aspirin at 150, 300, and 600 mg/kg, respectively, for 3 consecutive days. The other groups were given the same amount of normal saline. In the APE model group, thrombus formation, alveolar wall injury, pulmonary hemorrhage, and inflammatory cell infiltration occurred at all time points. After aspirin treatment, pathological changes such as pulmonary hemorrhage and inflammatory cell infiltration were reduced. Compared with the APE model group, the expression of the NF- κ B protein measured by Western blotting was significantly decreased in other groups at each time point ($P < 0.05$, $P < 0.001$). The highest expression of the NF- κ B protein was observed in the APE model group, and NF- κ B protein expression decreased gradually in a dose-dependent manner in rats receiving aspirin (120). In summary, aspirin can significantly inhibit the NF- κ B pathway in a dose-dependent manner to reduce inflammation and alleviate lung injury after APE.

4.3.2 Platelet P2Y₁₂ receptor antagonist

Clinically, ticagrelor and clopidogrel (antiplatelet coagulants) are often combined with PCI for acute coronary syndromes (ACS) (121). They cure ACS12 adenosine diphosphate (ADP) receptors by targeting the platelet P2Y to inhibit platelet aggregation and reduce

TABLE 2 The effect of traditional Chinese medicine on NF- κ B-mediated inflammatory response.

TCM	Single active component	Anti-inflammatory effect	Molecular target	reference
Qihong Tongluo prescription	Astragalus polysaccharide	IL-1 β , IL-6, TNF- α , INF- γ , MCP-1	TLR4, NF- κ B p65	(85), (86)
	Safflower flower	Inhibited platelet aggregation		(87), (88)
Gegen Qinlian Pills (GQP)	---	TNF- α , IL-6, IL-1 β , IL-4	HMGB1, TLR4, NF κ B, NLRP3	(89), (92)
		Reduced lung, liver, and tail thrombus formation in mice; increased tail blood flow. The adhesion of platelet to HUVEC was decreased		
Huanglianjiedu Decoction(HLJJD)	baicalin	IL-1 β , TNF- α , PEG2	TLR4,NF- κ B p65, CD14,p- $\text{IKB}\alpha$ /IKB α	(94), (96)
	berberine	TNF - α ,ICAM - 1,MCP - 1,IL-1 β ,IL-6,NLRP3	AMPK,MyD88,NF- κ B-p65,TLR4	(98), (100), (103)
Liu Shen Wan (LSW)	---	TNF- α ,IL-1 β ,IL-6,INF- γ	TLR4,p-NF- κ B p65, NF- κ B p65,p - κ B α	(107)
		The infiltration of inflammatory cells in the lung was reduced		
---	Rhein	It improved the survival rate of mice and reduced lung inflammation	TLR4,Akt,p38,JNK, MAPK,NF- κ B	(109)
---	Flavonoids	MCP-1,IL-8,TNF- α ,MDA	TLR3/4/7,NF- κ B p65	(113)
Xiao shuan jing mai decoction		The expression of miR-181b in venous endothelium of DVT model rats was significantly up-regulated	miRNA-181	(78)

thrombosis (122). In this study, human umbilical vein endothelial cells (HUVECs) were cultured with ticagrelor or clopidogrel and given lipopolysaccharide (LPS) and CD14. Human umbilical vein endothelial cells (HUVECs) were cultured with ticagrelor or clopidogrel and given lipopolysaccharide (LPS) and CD14. Ticagrelor and clopidogrel reduce the expression of TNF- α , IL-1, IL-6, IL-8, and IL-2, inhibit p65 phosphorylation and IKB- α degradation, and significantly reduce the amount of nuclear translocation p65 (123, 124). These findings suggest that ticagrelor and clopidogrel inhibit the production of inflammatory cytokines by inhibiting the NF-KB pathway.

4.3.3 The PAR-1 antagonist

PAR-1 can be activated by thrombin to regulate platelet aggregation and endothelial permeability, so it is clinically used as a target for anti-platelet drugs to prevent thrombosis (125–127). Vorapaxar is a representative drug (128). IR induction was performed in rat lung models by perfusion *in vitro*. Male rats were treated with the specific PAR-1 antagonist vorapaxar or the control agent with 40 min of ischemia and 60 min of reperfusion. *In vitro*, mouse lung epithelial cells (MLE-12) were treated with vorapaxar and subjected to hypoxic reoxidation (HR). We found that vorapaxar reduced the production of thrombin, inflammatory factors, cytokine-induced neutrophil chemokine-1, interleukin-6, and tumor necrosis factor- α , pulmonary edema and neutrophil infiltration, and it alleviated lung cell apoptosis and down-regulated the nuclear factor- κ B (NF- κ B) pathway. It also blocked HR-induced NF- κ B activation and the production of inflammatory chemokines in MLE12 cells. The results suggest that vorapaxar acts by blocking PAR-1 expression and modulating the NF- κ B pathway (129) (Table 3).

5 Limitations in inhibiting NF- κ B signaling pathways

At present, the targeted inhibition of the NF- κ B signaling pathway for the treatment of thrombus has not reached the most perfect degree. On the one hand, these drugs/compounds can

inhibit the inflammatory response and inhibit the expression of NF- κ B, but there is no clear evidence of a targeted relationship, and studies have shown that combination drugs work better (130) and are a more clinically promising therapeutic strategy.

On the other hand, inhibition of the NF- κ B pathway is a double-edged sword due to its broad effects. NF- κ B mediates cell survival, cell differentiation, and cell proliferation (131), and inhibition of NF- κ B has also been shown to play an important role in cancer treatment (132–135). However, long-term use of NF- κ B inhibitors can cause side effects such as immune deficiency (136, 137) and intestinal homeostasis imbalance (138), and NF- κ B inhibitors should be treated with for a short period. An ideal NF- κ B inhibitor would only target the NF- κ B pathway without affecting other signaling pathways. However, NF- κ B inhibitors interfere with the NF- κ B pathway by interfering with other pathways, such as PI3K/Akt and MAPK signaling (87, 115, 117).

6 Conclusion

In conclusion, the NF- κ B signaling pathway plays an important role in inflammation and deep-vein thrombosis, and the regulation of the NF- κ B pathway may bring new strategies for the treatment of thrombosis. Although the role of NF- κ B signaling in venous thrombosis has been extensively studied in recent years, the application of NF- κ B inhibitors in the treatment of thrombosis has a long way to go, regulating miRNAs or using drugs to interfere with the NF- κ B signaling pathway. It may be a potential therapeutic option to improve thrombosis, but the dose and side effects of medication and whether regulating miRNAs will improve other downstream pathways of NF- κ B signaling remain to be explored. Given the relationship between inflammation and blood clots, preventing inflammation is a better way to reduce blood clots. Therefore, in-depth study of the mechanism of the NF- κ B signaling pathway inducing inflammation will help to elucidate the pathogenesis of venous thrombosis and will also have a far-reaching impact on the development of safer and more effective drugs and the prevention and treatment of thrombosis.

TABLE 3 The effect of common antithrombotic drugs on NF- κ B-mediated inflammatory response.

Drugs	Representative drug	Anti-inflammatory effect	Action target	reference
anticoagulant	Aspirin and salicylate	Inhibited inflammation and relieved lung injury after APE	NF- κ B	(120)
Platelet P2Y ₁₂ receptor antagonist	Ticagrelor and clopidogrel	TNF α , IL-1, IL-8, IL-6, IL-2, IL-7, TNF- α , CRP Alleviated LPS-induced cell viability, cell migration and angiogenesis, cell cycle changes, and apoptosis and reduced myocardial ischemia-reperfusion injury (IRI) in ischemic myocardium	NF- κ B	(123), (124)
The PAR-1 antagonist	Vorapaxar	CINC-1, IL-6, TNF- α , PAR-1, MPO Improved pulmonary edema, pulmonary histopathological changes.	PI3K, NF- κ B, MAPK, IKB- α	(129)

Author contributions

ZW: Writing – original draft, Writing – review & editing. CF: Investigation, Writing – review & editing. MY: Conceptualization, Investigation, Writing – review & editing. DW: Supervision, Writing – review & editing. MC: Supervision, Writing – review & editing. TG: Supervision, Writing – review & editing, Investigation. JM: Investigation, Supervision, Validation, Writing – review & editing.

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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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Whether MTHFD2 plays a new role: from anticancer targets to anti-inflammatory disease

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KEYWORDS

methylenetetrahydrofolate dehydrogenase 2, T cells, inflammatory disease, therapeutic target, one-carbon metabolism enzyme

1 Introduction

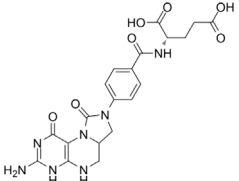
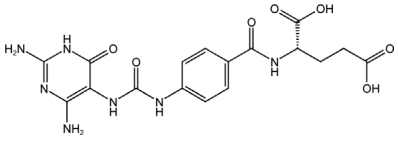
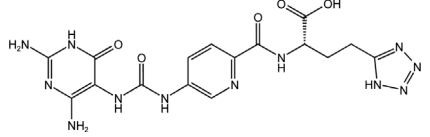
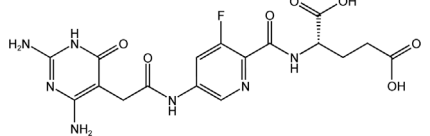
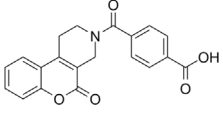
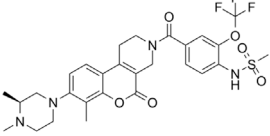
Methylenetetrahydrofolate dehydrogenase 2 (MTHFD2) is a mitochondrial one-carbon (1C) metabolism enzyme that is overexpressed in cancer cells and barely expressed in most healthy adult tissues (Nilsson et al., 2014; Jha et al., 2023). The overexpression of MTHFD2 could provide the basis for biosynthesis of pyrimidine and purine during rapid proliferation of cancer cells which is widely needed for the growth of all tumors (Kim et al., 2016; Zhao et al., 2021; Bonagas et al., 2022; Zhao et al., 2022). Inhibition of MTHFD2 leads to imbalance of NADPH and redox homeostasis, which inhibits tumorigenic proliferation and growth, and increases cancer cell death under hypoxia (Ju et al., 2019). The knockdown of MTHFD2 leads to decreased expression of cell cycle genes suggesting interference with cell cycle progression (Yu et al., 2020). Because of the low expression of MTHFD2 in most adult tissues, targeting MTHFD2 is unlikely to produce significant side effects and MTHFD2 could be as a novel target for cancer therapy (Nishimura et al., 2019; Cuthbertson et al., 2021; Yang et al., 2021).

Recent research found that MTHFD2 was consistently overexpressed in many diseases, including ulcerative colitis, Celiac's disease, systemic lupus erythematosus (SLE), psoriatic arthritis, Sjogren's syndrome, multiple sclerosis (MS) and so on (Sugiura et al., 2022). Inhibition of MTHFD2 promotes regulatory CD4 T cell (Treg) activity, which suppresses the immune response. Does MTHFD2 play a new role from anticancer targets to anti-inflammatory disease?

2 A new role on anti-inflammatory disease and proposed mechanisms

In fact, what we are more interested in is that MTHFD2 deficiency can reduce disease degree in various inflammatory condition models. T-cell dependent Delayed Type Hypersensitivity (DTH) mouse models trials showed that MTHFD2 inhibitors did not increase inflammatory symptoms in mice, and increase animal weight, suggesting that the inhibitor has a protective effect on inflammation extending to B cell function (Sugiura et al., 2022). MS is an inflammatory demyelinating disease originating in the central nervous system. Compared to control group, Experimental Autoimmune Encephalomyelitis (EAE) model using with MTHFD2 inhibitors (MTHFD2i) resulted in significantly lower disease degree and cumulative clinical score. The infiltration of CD4st, CD4⁺ and CD8⁺ cells in the spinal cord of mice was significantly reduced after MTHFD2i treatment (Sugiura et al., 2022). In two other different inflammatory models-inflammatory bowel disease (IBD) and

TABLE 1 Novel MTHFD2 inhibitors.

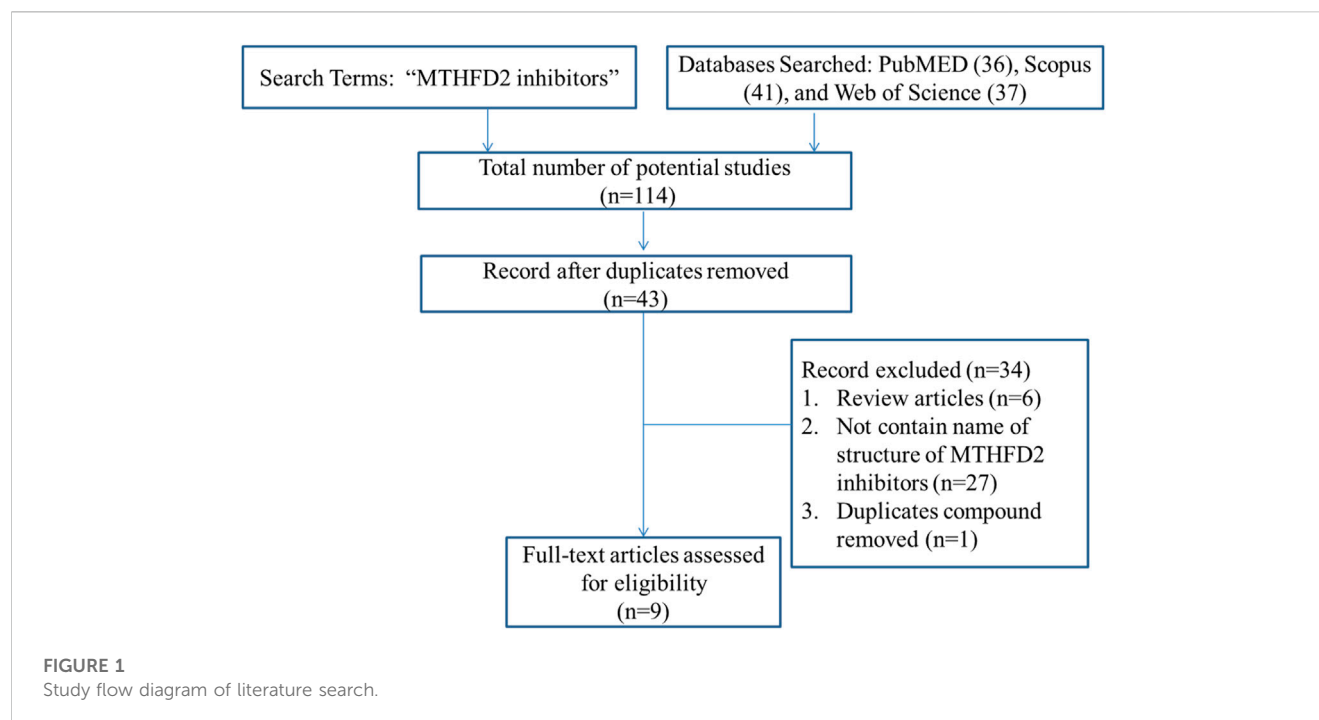
Name	Target	Structure	Pathology
LY345899	Dual MTHFD1/2 inhibitor		LY345899 treatment statistically significantly suppresses tumor growth and decreases the tumor weight in CRC patient-derived xenograft models
TH7299	Dual MTHFD1/2 inhibitor		(–)
TH9028	Dual MTHFD1/2 inhibitor		TH9028 and TH9619 showed overall strong antiproliferative efficacy in acute myeloid leukemia (AML) cells and T-ALL Jurkat cells comparable to standard-of-care compounds, with reduced effect on lymphoblastoid cell line (LCL) viability
TH9619	Dual MTHFD1/2 inhibitor		
DS44960156	MTHFD2 inhibitor		DS44960156 has > 18-fold selectivity for MTHFD2 over MTHFD1, with a low molecular weight and a good ligand efficiency
DS18561882	MTHFD2 inhibitor		DS18561882, combined with enzalutamide can significantly inhibit CRPC cell proliferation <i>in vitro</i> and tumor growth <i>in vivo</i> . DS18561882 has also been shown to reduce disease degree in variety of inflammatory disease models <i>in vivo</i>

allergic airway disease, mice receptor of CD4^{ΔMthfd2} T cells continued gaining body weight, the number and frequency of CD4^{ΔMthfd2} T cells in spleen and mesenteric lymph nodes (MLNs) were significantly reduced. Meanwhile, the neutrophil richness in the bronchioalveolar lavage fluid (BALF) of CD4^{ΔMthfd2} mice affected by Alternaria-induced allergic airway disease showed a decreasing tendency (Sugiura et al., 2022). The sensitivity of T-cell to MTHFD2i might provide an efficacious strategy of immunotherapy for CD4⁺ T-cell-driven inflammation, and produce fewer adverse reactions than presently usable therapeutics. It should be worth studying whether T cell nucleus carries MTHFD2 and whether MTHFD2 is a therapeutic target for inflammatory disease.

CD4⁺ T cells are the key mediators and adaptive immunity which play a crucial role in host defense against pathogens (Candia and Matarese, 2022). CD4⁺ T cell subpopulations need MTHFD2 to varying degrees for activation, proliferation, survival, and cytokine production (Sugiura et al., 2022). Sugiura et al. (2022) have found that MTHFD2 in patients with inflammatory disease continues to upregulate combined with cell CRISPR-based screening and genetic

test. The research showed that MTHFD2 may function as a metabolic checking point for the Th17/Treg cell axis and highlight its potential as a target for anti-inflammatory immunotherapeutic treatment. Meanwhile, MTHFD2i raised the basal and maximal oxygen consumption rate (OCR) of Th17 cells and decreased the expression of interferon-gamma (IFN-γ) and interleukin (IL)-17 in Th1 and Th17 cells, which appears to alter the counterbalance between the pathogenic and anti-inflammatory state.

MTHFD2 has been shown to regulate *de novo* purine synthesis and signal transduction in activated T cells, promoting proliferation and the production of inflammatory cytokine (Ducker et al., 2016). MTHFD2 has been reported to transport to the nucleus and is presumed regulate gene expression (Gustafsson Sheppard et al., 2015). The lack of MTHFD2 could lead to the accumulation of intermediates in the purine synthesis pathway, which activates AMP-activated protein kinase to inhibit the mechanistic target of rapamycin (mTORC)1 (Su et al., 2019). The mTORC1 pathway plays a crucial role in promoting synthetic metabolism, driving a



mass of the transcription factor ATF4 and inducing the expression of MTHFD2 (Ben-Sahra et al., 2016). Inhibition of mTORC1 signaling transduction might lead to changes in the metabolic process from glycolysis to mitochondrial respiration, and alter T cell receptor cycle metabolites (Shang et al., 2021).

3 Novel MTHFD2 inhibitors

One possible mechanism is that MTHFD2i damages T cell expansion through inadequate nucleotide production. Scientists have been working on the design and development of MTHFD2i as anticancer drugs (Table 1). Tricyclic coumarins and xanthine compounds are the only selective inhibitors of MTHFD2 reported to date (Jha et al., 2023). Comprehensive searches of English databases, including PubMed, Scopus, and Web of Science, and the time of index was from inception to 30 April 2023 for each database. Full-text searches were performed using “MTHFD2 inhibitors” in all fields (Figure 1). The dual MTHFD1/2 inhibitor LY345899 synthesized in 2017 has been demonstrated efficacy in improving disease conditions in the EAE model (Gustafsson et al., 2017; Ju et al., 2019). A simplification of the tricyclic core of LY345899 shows that TH9028, TH9619 and TH7299 are actually more active against MTHFD1 and MTHFD2L (Bonagas et al., 2022; Scaletti et al., 2022; Green et al., 2023). A novel isozyme-selective MTHFD2 inhibitor DS44960156 might provide further optimization options due to its >18-fold selectivity for MTHFD2 over MTHFD1, with a smaller molecular weight and favorable ligand efficiency (Kawai et al., 2019a). Subsequently, the same team developed an effective, selective, and oral MTHFD2i (DS18561882) which has favorable oral pharmacokinetic characteristics with the strongest cell activity and tumor growth inhibition (Kawai et al., 2019b; Lee et al., 2021). Most importantly, DS18561882 has been shown to reduce disease degree in variety of

inflammatory disease models *in vivo* (Sugiura et al., 2022), which leads us to believe that MTHFD2 may be an anti-inflammatory and autoimmune target *in vivo* in the future.

4 Conclusion

MTHFD2 is a mitochondrial one-carbon metabolism enzyme highly expressed in several human tumors, and targeting MTHFD2 has been used as the target of tumor therapy. Recent research suggests that MTHFD2 inhibitors appear to reduce inflammatory disease severity and alter the counterbalance between the pathogenic and anti-inflammatory state, which may serve as an anti-inflammatory and autoimmune target *in vivo* in the future. The research of anti-inflammatory drugs is expected to be promoted and developed.

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HT: Conceptualization, Writing–original draft. NH: Conceptualization, Writing–review and editing.

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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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β -sitosterol alleviates dextran sulfate sodium-induced experimental colitis via inhibition of NLRP3/Caspase-1/GSDMD-mediated pyroptosis

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Background: Inflammation-related NLRP3/Caspase-1/GSDMD-mediated pyroptosis is involved in the progression of ulcerative colitis (UC). β -sitosterol (SIT) was reported to have anti-inflammatory effects on experimental colitis, while the regulation of SIT on pyroptosis is unclear. Therefore, the present study aimed to define the protective and healing effects of SIT on dextran sulfate sodium (DSS)-induced experimental UC rats and human epithelial colorectal adenocarcinoma cells (Caco-2) and explore the underlying mechanisms that are responsible for its effects on NLRP3/Caspase-1/GSDMD-mediated pyroptosis in UC.

Methods: UC model rats were established by oral 4% DSS. Following colitis injury, the animals received SIT (doses of 50, 100, and 200 mg/kg) treatment for 2 weeks. For *in vitro* study, we exposed Caco-2–50 mg/mL DSS with or without SIT (concentrations of 8 and 16 μ g/mL). Disease activity index (DAI) and histopathological injury were assessed *in vivo*. Activation proteins of nuclear factor kappa B (NF- κ B) signaling axis, and tight junction-related proteins of zonula occludens-1 (ZO-1) and occludin were detected in colon tissues. TNF- α , IL-1 β , and IL-18 in serum and cell supernatant were measured by enzyme-linked immunosorbent assay (ELISA). Changes in NLRP3/Caspase-1/GSDMD-mediated pyroptosis signaling pathway activation were analyzed both in tissues and cells.

Results: Our findings suggested that SIT treatment attenuated the severity of 4% DSS-induced UC by protecting rats from weight and colon length loss, and macroscopic damage. SIT also reduced proinflammatory factors production (TNF- α , IL-1 β , and IL-18) in serum and cell supernatant. Mechanistically, SIT

Abbreviations: ASC, apoptosis-associated speck-like protein; CON, control; DAI, disease activity index; DSS, dextran sulfate sodium; ELISA, enzyme-linked immunosorbent assay; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GSDMD, gasdermin D; GSDMD-N, gasdermin D-N-terminal; HD, high-dose; HRP, horse radish peroxidase; IHC, immunohistochemistry; IL, interleukin; IBD, inflammatory bowel disease; IL, interleukin; LD, low-dose; MD, middle-dose; NF- κ B, nuclear transcription factor-kappa B; NLRP3, nucleotide-binding oligomerization domain (Nod)-like receptor thermal protein domain associated protein 3; PVDF, polyvinylidene fluoride; TNF, tumor necrosis factor; SD, standard deviation; SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel; UC, ulcerative colitis; ZO, zonula occludens.

downregulated the expression levels of pyroptosis-related proteins including Caspase-1, cleaved-Caspase-1, NLRP3, GSDMD, and GSDMD-N in colon tissues and Caco-2 cells. Further analysis indicated that SIT maintained the colonic barrier integrity by enhancing the protein expression of ZO-1 and occludin.

Conclusion: We confirmed that SIT exerts protective and therapeutic effects on DSS-induced colitis injury by suppressing NLRP3/Caspase-1/GSDMD-mediated pyroptosis and inflammation response. These findings demonstrated that SIT could be a potential medication for UC treatment.

KEYWORDS

β -sitosterol, ulcerative colitis, inflammatory factors, Caspase-1, GSDMD, pyroptosis

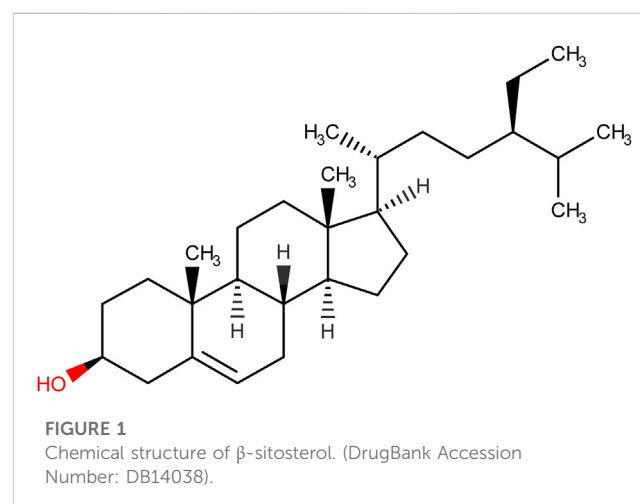
1 Introduction

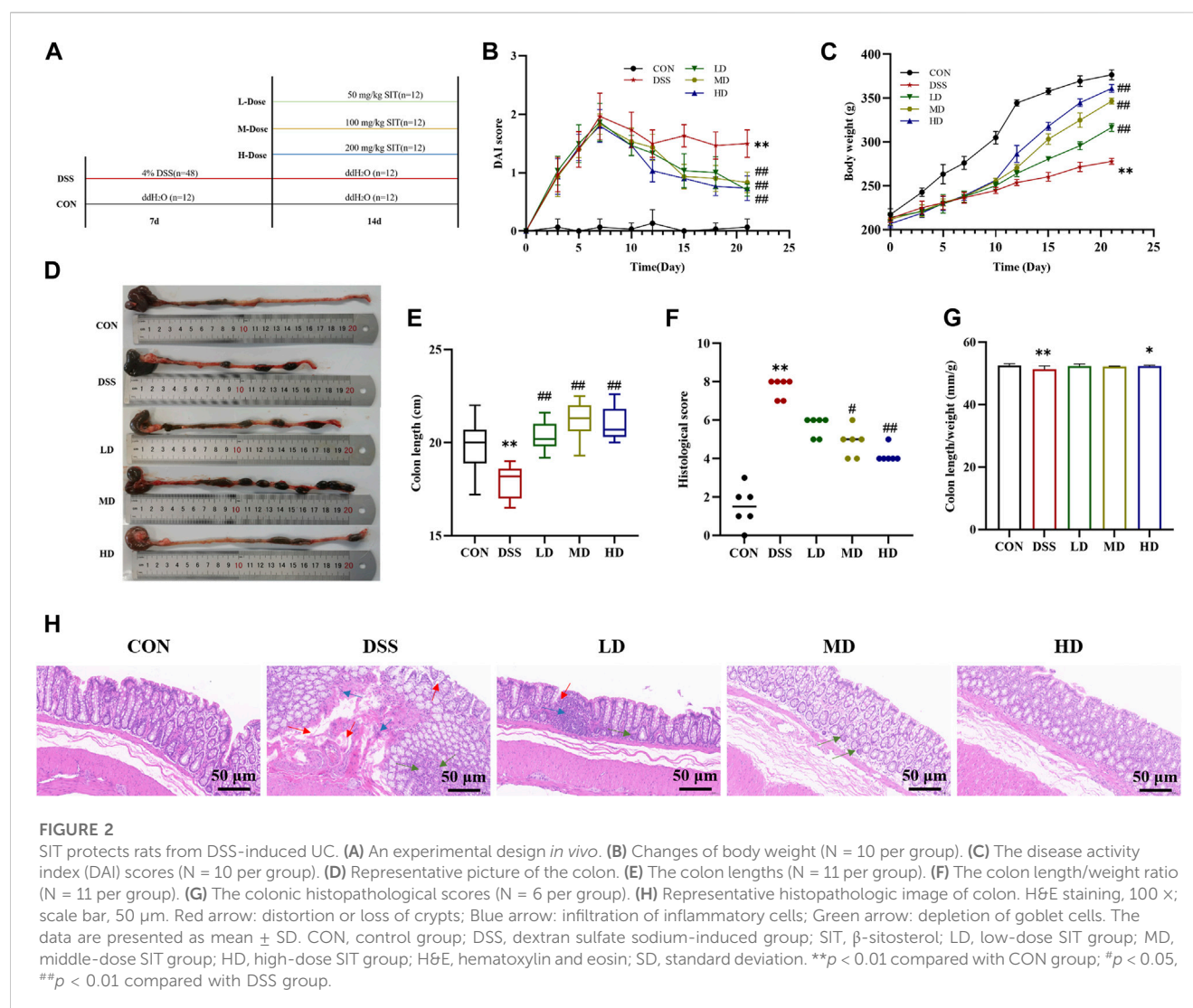
Ulcerative colitis (UC), a global public health problem, which is a chronic non-specific, non-infectious, and inflammatory intestinal disease. It is a continuous mucosal ulcer with unknown origin and usually begins in the rectum, involves the colonic mucosa and submucosa layer, and then spreads to the cecum for the longest, which is characterized by continuous and diffuse distribution. Clinical manifestations of this illness are chronic and recurrent with abdominal pain, diarrhea, fecal bleeding, weight loss, and intestinal mucosal (Ordás et al., 2012). In recent years, UC has had increasing prevalence and incidence in developing and developed countries worldwide due to the rapid economic development and westernized diet uptake (Ng et al., 2017). Additionally, the incidence among people with UC in China has nearly tripled in the past decades (Ye et al., 2013). Research shows that patients with long-term UC have a higher risk of developing colorectal cancer and colitis-associated cancer is a major cause of death in patients with UC (Rogler, 2014), thereby resulting in a high economic burden on individuals and society health systems. For the above reasons, effective intervention in the course of UC is urgent.

Though the etiology of UC remains undefined, the inflammatory response definitely exists in the pathogenesis of UC (Du and Ha, 2020). Studies have suggested the large aggregation of inflammatory molecules such as TNF- α , IL-1 β , and IL-18 could lead to colonic tissue injury and epithelial integrity disruption in the gut while inhibiting cytokine-mediated inflammation could treat or cure UC (Elmaksoud et al., 2021). NF- κ B is a key transcriptional regulator in the regulation of proinflammatory mediators and chemokines production and secretion, which leads to an inflammatory cascade (Cui et al., 2019). The abnormal activation of NF- κ B signaling was founded in colonic tissues of UC patients and experimental models (Neurath et al., 1996). Pyroptosis is a newly found form of pro-inflammatory programmed cell death unlike traditional necrosis and apoptosis (Shi et al., 2015). Pyroptosis plays an essential role in host defense and inflammatory responses, in which Caspase-1 or Caspase-11/4/5 was activated during this process (Yu P. et al., 2021). Activation of inflammatory caspases can trigger pyroptosis and release pro-inflammatory cytokines IL-1 β and IL-18, which are relevant to inflammatory diseases (Yuan et al., 2018). In addition, over-expression of pyroptosis-related proteins, including nucleotide-binding oligomerization segment-like receptor family 3 (NLRP3), apoptosis-associated speck-like protein (ASC), Caspase-1, and gasdermin D-N-terminal (GSDMD-N) in colonic tissues has been observed in experimental colitis (Chao et al., 2020; Wei et al., 2021)

and suppression of the NLRP3/Caspase-1/GSDMD-mediated pyroptosis signaling pathway can attenuate the damage of UC (Jie et al., 2021), thus therapy targeting pyroptosis could be promising and merits further investigation.

While immunosuppressants, glucocorticoids, salicylic acid, and biological agents are the frontline therapy for clinical patients with UC (Nakamura et al., 2008; Berends et al., 2019), there are many side effects associated with these pharmaceutical medications (Moreau and Mas, 2015). Therefore, more researchers have paid attention to natural plant substances, which will be safe and beneficial with less deleterious effects (Cao et al., 2019). Phytosterols are a critical class of bioorganic compounds that are abundant in a range of organisms such as plants, animals, and fungi, and exert an important role in the physiological processes of eukaryotes (Zhang et al., 2022). β -sitosterol (SIT) (Figure 1), the major compound of phytosterol, is a plant-derived natural product widely present in many countries. Its pharmacological effects and biological activities were well documented in the literature including anti-inflammation (Loizou et al., 2010; Sun et al., 2020), anti-anxiety (Panayotis et al., 2021), antiviral properties (Chen et al., 2022), anti-oxidant stress, immunomodulation (Cheng et al., 2020), anti-diabetes (Babu et al., 2020), anti-tumor (Bae et al., 2021), anti-microbes (Pierre Luhata and Usuki, 2021), hepatoprotective effects (Kim et al., 2014), cardioprotective effects (Lin et al., 2020), anti-diabetes (Ponnulakshmi et al., 2019), as well as regulation of gut microbiota (Yu Y. et al., 2021). These studies showed that SIT could be a potential measure of various diseases. Furthermore, evidence from experimental studies on SIT indicates its anti-inflammatory ability and can be used as





a safe pharmaceutical complement in the treatment of experimental colitis (Lee et al., 2012; Aldini et al., 2014; Bin Sayeed et al., 2016; Feng et al., 2017; Ding et al., 2019). Of note, SIT has been proven experimentally that it does not produce cytotoxic impacts under long-term use (Malini and Vanithakumari, 1990; Paniagua-Pérez et al., 2005; Feng et al., 2020). Despite this, further experimental studies are required to uncover the role of SIT in the recovery of experimental UC and elucidate its possible anti-pyoptosis mechanism behind this.

Thus, in this study, we established the DSS-induced experimental colitis in rats and Caco-2 cells to assess the protective and therapeutic effects of SIT on UC and further explore its underlying mechanism.

2 Materials and methods

2.1 Drug, and reagents

Dextran sulfate sodium and β-sitosterol (SIT, purity >95% and HPLC ≥98%) were purchased from Shanghai Yuanye Bio-Technology

Co., Ltd. (Shanghai, China). Carboxymethyl cellulose was purchased from Biotopped Technology Co. Ltd. (Beijing, China). Enzyme-linked immunosorbent assay (ELISA) kits of TNF-α, IL-1β, and IL-18 were obtained from Cloud-Clone Corp (Wuhan, China). Antibodies against NLRP3, occludin, β-Actin, goat-anti-rabbit IgG H&L (HRP), and goat-anti-mouse IgG H&L (HRP) were purchased from Abcam (Cambridge, United Kingdom). Antibodies against Caspase-1, GSDMD, IκBα, and ZO-1 were obtained from Proteintech (Wuhan, China). Antibodies against NF-κappaB p65, phospho-NF-κappaB p65, and phospho-IκBα were purchased from Invitrogen (Carlsbad, CA). Antibody against cleaved Caspase-1 was purchased from Cell Signalling Technology (Danvers, MA, United States). Antibody against GSDMD-N terminal was purchased from ABclonal (Wuhan, China). The Cell Counting Kit-8 (CCK-8) was purchased from Biorigin (Beijing, China).

The following reagents were obtained from GenePool Biotechnology (Beijing, China): Total RNA Extraction with DNase I Kit, mRNA cDNA Synthesis Kit, mRNA qPCR Kit, RNA Loading Buffer, BSA Blocking Buffer, SDS-PAGE Gel Ki, SDS-PAGE Loading Buffer, Tris-Glycine Running Buffer, WB Transfer Buffer, and TBST. The following reagents were

TABLE 1 Disease activity index (DAI) scoring system.

Score	Weight loss (%)	Stool consistency	Gross bleeding/rectal bleeding
0	0	Normal	None
1	1–5	Loose stool	Haemoccult positive
2	6–10	Loose stool	Haemoccult positive
3	11–20	Loose stool	Haemoccult positive
4	>20	Diarrhea	Severe bleeding

purchased from Beyotime Biotechnology (Shanghai, China): Cell lysis buffer for Western and IP, Protein Extraction Kit, BCA protein assay kit, enhanced chemiluminescence (ECL) kit, Citrate-EDTA Antigen Retrieval Solution, and Hematoxylin and Eosin Staining Kit. The following reagents were purchased from Gibco (Carlsbad, CA, United States): fetal bovine serum (FBS), minimum essential medium (MEM), Penicillin-Streptomycin antibiotics, non-essential amino acids (NEAA), and 0.25% trypsin solution with EDTA. All other chemicals were of reagent grade.

2.2 Animal experimental design and treatment

Sixty male Sprague-Dawley rats (6–8 weeks old, weighing 180–200 g) were purchased from Beijing Sibeifu Bioscience, Co., Ltd. (Beijing, China) (License NO. SCXK [Beijing] 2019-0010). All animals were raised under standard specific pathogen-free (SPF) conditions (temperature, 25°C ± 1°C; humidity, 60% ± 5%) with a 12 h light/dark cycle per day and allowed *ad libitum* eat and drink. Ethical approvals for the animal experiments were obtained from the animal ethics committee of Beijing University of Chinese Medicine (NO. BUCM-4-2022102901-4029).

This experimental design consists of two steps: a DSS-induced colitis stage and a drug treatment stage as described in Figure 2A. 60 rats were randomly assigned to five groups: 1) Control group (CON): received only double-drilled water; 2) DSS group (DSS): received 4% DSS (molecular weight: 40 000 Da; purity >98%) dissolved in double-drilled water in their daily drinking water; 3) Low-dose group (LD): received DSS and then gavaged with 50 mg/kg of SIT (purity >95%) suspended in 0.1% carboxymethyl cellulose; 4) Middle-dose group (MD): received DSS and then gavaged with 100 mg/kg SIT; 5) High-dose group (HD): received DSS and then gavaged with 200 mg/kg SIT. The intervention period of DSS was from day 1 to day 7 and the period of drug treatment was from day 8 to day 21.

Following the 14-day intervention, rats were all deeply anesthetized after 24 h fasting with 1% sodium pentobarbital (40 mg/kg). After recording the colon length and weight, blood samples were collected and centrifuged for serum. Then the colon specimens were immediately removed and then fixed in 4% paraformaldehyde for histopathological studies or stored at −80°C for molecular biology detection.

2.3 Observation of UC symptoms and signs in rats

During this experimental period, body weight, stool status, and rectal bleeding were recorded every day to calculate disease activity index (DAI) scores on a previously established scoring system (Kihara et al., 2003) and listed in Table 1. DAI score is the average of the three categories. All evaluations were performed while unaware of the conditions.

2.4 Histological examination

Hematoxylin and eosin (H&E) detection was conducted with a standard protocol. The colon tissues were fixed in 4% paraformaldehyde and embedded in paraffin. Then, the paraffin-blocked samples were cut into 5-μm sections on slides for staining with hematoxylin and eosin. Slides were scanned using a Panoramic MIDI Scan Whole Slide Scanner (3DHISTECH Ltd., Budapest, Hungary) and viewed with Panoramic Viewer 1.15.4 (3DHISTECH); in addition, histopathological scores for histopathological changes were calculated based on a previously developed scoring system (Dieleman et al., 1998) and listed in Table 2. The individual scoring was blinded to the identity of the slides.

2.5 Cell preparation and viability assay

Human epithelial colorectal adenocarcinoma (Caco-2) cell lines (originally obtained from ATCC) were purchased from IMMOCELL (Xiamen, China). The Caco-2 cells were maintained in minimum essential medium (MEM) containing 10% fetal bovine serum (FBS), 100 U/ml of penicillin, 100 μg/mL of streptomycin, and 1% non-essential amino acids supplements. Cells were maintained at 37°C with 5% CO₂ atmosphere.

Caco-2 cell viability was measured by CCK-8 assay followed by a standard protocol. After preparing single-cell suspensions, cells (5 × 10⁴ cells/well) were added to 96-well plates and continued to culture till 80% confluency. Then, 10 μL/well of CCK-8 solution was added and incubated protected from light for 2 h at 37°C. The 450 nm absorbance values were detected with a multifunctional microplate reader (Thermo, Manassas, United States) to measure the cell growth inhibition rate.

TABLE 2 Histopathological scoring system.

Score	Inflammation	Mucosal damage	Regeneration	Crypt damage	Range of lesions (%)
0	None	None	Complete regeneration or normal tissue	None	0
1	Mild	Mucous layer	Almost complete regeneration	Basal 1/3 damage	1%–25%
2	Moderate	Mucousa and submucosa	Regeneration with crypt depletion	Basal 2/3 damage	26%–50%
3	Severe	Transmural	Surface epithelium not intact	Crypt lost; surface epithelium present	51%–75%
4	-	-	No tissue repair	Crypt and surface epithelium lost	76%–100%

TABLE 3 Primers used in quantitative RT-PCR assay.

Gene		Primer sequences (5'-3')
IL-1 β	Forward	CCCAACTGGTACATCAGCACCTCTC
	Reverse	CTATGTCCCGACCATTGCTG
IL-18	Forward	CCGAACAGCCAACGAATCC
	Reverse	ACATCCTTCCATCCTTCACAGA
Caspase-1	Forward	CTGGTCTTGACTTGGAGGA
	Reverse	TCAGTGGTTGGCATCTGTAGT
NLRP3	Forward	AGACCTCCAAGACCACGACTG
	Reverse	CATCCGCAGCCAATGAACAGA
GSDMD	Forward	GCAGTGGTGAGCAGGTAGAG
	Reverse	CCAGAGCCTTAGTAGCCAGTAG
GAPDH	Forward	TGGAGTCTACTGGCGTCTT
	Reverse	TGTCATATTTCTCGTGTTCA

2.6 Caco-2 inflammation model establishment and treatment

Cells were cultured overnight with or without SIT (HPLC $\geq 98\%$) dissolved in absolute ethanol (concentrations of 8 $\mu\text{g}/\text{mL}$ as Low-dose group and 16 $\mu\text{g}/\text{mL}$ as High-dose group). Supernatants of cells were discarded and washed with PBS, and 50 mg/mL DSS was added to establish the inflammation model.

2.7 Cytokine assays

The serum of rats and supernatant of cells were collected and then calculated for TNF- α , IL-1 β , and IL-18 levels using ELISA kits according to the manufacturer's scheme.

2.8 Quantitative polymerase chain reaction

Relative levels of NLRP3, Caspase-1, GSDMD, IL-1 β , and IL-18 mRNAs in colonic tissues were analyzed by a quantitative real-time (qRT)-PCR. Total RNA of colonic tissues was isolated using the Total RNA Extraction Kit and cDNA was synthesized by using the mRNA cDNA Synthesis Kit in accordance with the manufacturer's protocols. The specific primers for NLRP3,

Caspase-1, GSDMD, IL-1 β , and IL-18 were designed and synthesized by GenePool Biotechnology (Beijing, China) and listed in Table 3. The PCR reaction parameters were predetermined: 95°C for 5 min, followed by a 35 cycle-denaturation for 30 s at 95°C, 55°C for 30 s, and extension for 1 min at 72°C. Each sample underwent three biological replications for statistical analysis to determine significant differences. GAPDH was an internal control and relative gene expression levels were calculated using the $2^{-\Delta\Delta\text{CT}}$ method.

2.9 Western blot analysis

The total proteins of tissues and cells were extracted using Western and IP lysate buffer, BCA protein assay kit was applied to determine protein concentration. After homogenization, an equal quantity of proteins was separated with SDS-PAGE and transferred to PVDF membranes (Millipore corp., Massachusetts, United States), then blocked with 5% BSA. Primary antibodies of NLRP3 (dilution 1:1 000), Caspase-1 (dilution 1:2 000), cleaved-Caspase-1 (dilution 1:1 000), GSDMD (dilution 1:2 000), GSDMD-N (dilution 1:1 000), p65 (dilution 1:1 000), p-p65 (dilution 1:1 000), I κ B α (dilution 1:1 000), p-I κ B α (dilution 1:1 000), ZO-1 (dilution 1:5 000), occludin (dilution 1:1 000), and β -Actin (dilution 1:5 000) were incubated overnight at 4°C. After being washed with TBST three times, membranes were then incubated with secondary antibodies against Goat Anti-Rabbit IgG H&L (HRP) (dilution 1:5 000) or Goat Anti-Mouse IgG H&L (HRP) (dilution 1:5 000) for 1 h at 37°C, and bands were visualized with an ECL kit captured with Tanon 5200 Chemiluminescent Imaging System (Tanon, Shanghai, China). Finally, the relative grey values of the target proteins blots normalized to β -Actin were analyzed by the ImageJ software (National Institutes of Health, United States).

2.10 Statistical analysis

Statistical analysis was performed by SPSS 26.0 system. Quantitative results were expressed as arithmetic mean plus or minus the standard deviation (SD) and analyzed using one-way analysis of variance (ANOVA) followed by least significant difference (LSD)'s multiple-comparison test, while Kruskal-Wallis test was performed for difference analysis of non-parametric data. p -value < 0.05 was considered statistically significant.

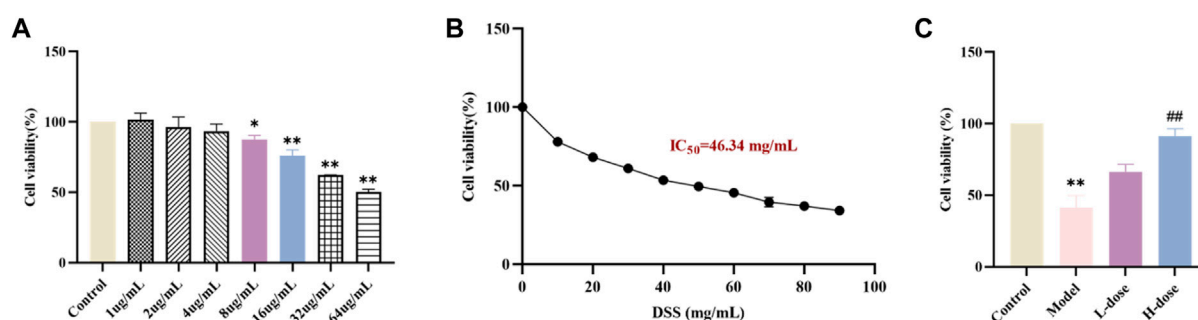


FIGURE 3

SIT protects Caco-2 cells from DSS-induced damage. (A) The viability of Caco-2 cells under the treatment with different concentrations SIT-containing medium for 24 h, and the viability was assayed by CCK-8. (B) Caco-2 cells were cultured with 10, 20, 30, 40, 50, 60, 70, 80, and 90 mg/mL DSS-containing medium for 24 h. (C) The cells were first cultured with SIT-containing medium for 24 h, incubated in 50 mg/mL DSS-containing medium for 6 h, and then replaced with fresh complete medium to culture for 18 h. $N = 6$ per group. The data are presented as mean \pm SD. DSS, dextran sulfate sodium-induced group; SIT, β -sitosterol; SD, standard deviation. * $p < 0.05$, ** $p < 0.01$ compared with Control group; ## $p < 0.01$ compared with Model group.

3 Results

3.1 SIT alleviates DSS-induced UC

In order to investigate the therapeutic effects of SIT *in vivo*, UC model rats were induced by 4% DSS for 7 consecutive days. During the experiment period, rats in the control group remained in a normal state, and body weight was rising steadily, while those in the model group represented a poor mental state with disheveled fur, decreased feeding, persistent fecal bleeding, and obvious body weight loss. Compared to the control group DAI score in the DSS-induced model group was significantly increased, which was consistent with the clinical characteristics. Notably, administration of SIT recovered the body weight and colon length gradually (Figures 2C–E) as well as decreased DAI score (Figure 2B) in DSS-induced rats, especially at the dose of 200 mg/kg.

Furthermore, colonic shortening caused by DSS was evidently mitigated after SIT intake. As can be seen from Figure 2F, DSS in the UC group led to a significant decrease in colon length/weight ratio compared with the control group. High dose of SIT agonist partly offset the decrease of colon length/weight ratio. Under microscopy, results by H&E staining showed that there were pathological lesions and superficial inflammation in the DSS-induced colonic tissues characterized by inflammatory cell infiltration, crypt architectural distortion or absence and mucosa defects or damage. Consistent with the remission of clinical signs, the pathological changes were improved to varying degrees following the administration of SIT (Figures 2F,G). Collectively, these results indicated that SIT is protective against DSS-induced colitis and the effects might be dose-dependent.

3.2 Effects of SIT on the viability of Caco-2 cells

Before the formal *in vitro* experiments, toxicity evaluation of different concentrations of SIT (1, 2, 4, 8, 16, 32, and 64 μ g/mL) on Caco-2 was carried out using the CCK-8 assay. After the

24 h-intervention, we observed that there was a significant decline in cell viability of Caco-2 following the higher concentrations of SIT (Figure 3A). Based on this, we chose the relatively safe concentrations for low-dose SIT (LD, 8 μ g/mL) and high-dose SIT (HD, 16 μ g/mL), respectively. In addition, at the concentration of 46.34 mg/mL DSS, growth of 50% cells was inhibited (Figure 3B). For convenience, we used 50 mg/mL DSS for subsequent experimental Caco-2 modeling, and found that SIT serves protectively against DSS-induced Caco-2 damage, (Figure 3C).

3.3 SIT inhibits proinflammatory mediators

To validate the suppressive effects of SIT on inflammation involved in UC, we detected the levels of inflammatory-related factors. The ELISA results showed that there was a significantly increase of TNF- α , IL-1 β , and IL-18 levels after DSS treatment compared with the control group in rats and SIT effectively decreased the expression (Figure 4A). We further noticed the protective effects of SIT on Caco-2 from inflammation after being exposed to DSS (Figure 4B).

3.4 SIT regulates the NF- κ B inflammatory pathway

NF- κ B signaling participates in the regulation of inflammatory response. We wondered whether the anti-inflammatory role of SIT was associated with the signaling. The expression levels of the major proteins p-p65, p65, p-I κ Ba, and I κ Ba in the NF- κ B signaling pathways were consequently measured by Western blot. The experimental results showed that the levels of p-p65 and p-I κ Ba in DSS-induced colonic tissues were abnormally higher compared to the control group. In comparison with the DSS group, the protein expression ratio of p-p65/p65 and p-I κ Ba/I κ Ba were attenuated after stimulation with SIT (Figures 4C,D) while none were statistically significant. These results indicate that NF- κ B

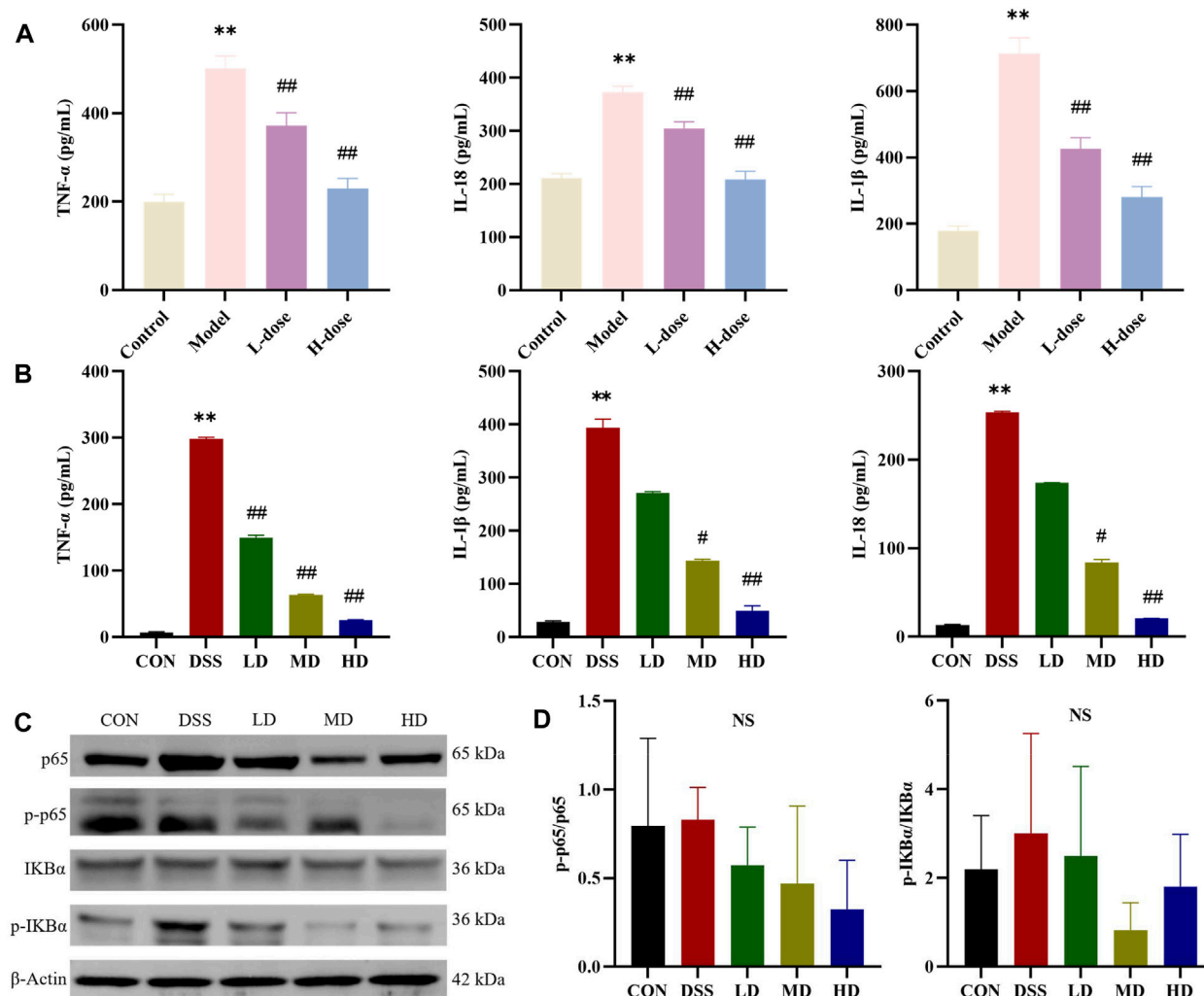


FIGURE 4

SIT regulates the pro-inflammatory cytokines and NF- κ B pathway. The expression levels of TNF- α , IL-1 β , and IL-18 in serum (A) and Caco-2 cells (B) were analyzed by ELISA (N = 6 per group). (C) Gel electrophoresis images of p-p65, p65, p-I κ B α , and I κ B α were analyzed by Western blot. (D) Analysis of protein expression levels (N = 3 per group). The data are presented as mean \pm SD. NF- κ B, nuclear transcription factor-kappa B; CON, control group; DSS, dextran sulfate sodium-induced group; SIT, β -sitosterol; LD, low-dose SIT group; MD, middle-dose SIT group; HD, high-dose SIT group; TNF, tumor necrosis factor; IL, interleukin; ELISA, enzyme-linked immunosorbent assay; SD, standard deviation. ** p < 0.01 compared with CON or Control group; # p < 0.05, ## p < 0.01 compared with DSS or Model group; NS, not statistically significant.

signaling might be involved in the reduction of DSS-induced UC inflammation by SIT administration.

3.5 SIT suppresses critical indicators activity of pyroptosis

Pyroptosis is a type of programmed cell death (PCD) and participates in inflammatory disease processes involved in UC. For this reason, we further measured the expression of critical indicators of NLRP3/Caspase-1/GSDMD-mediated pyroptosis to explicit the anti-inflammatory effects of SIT. RT-qPCR analysis was carried out to assess the gene expression of Caspase-1, NLRP3, GSDMD, IL-1 β , and IL-18 in colonic tissues. When compared to the control group, the mRNA expression levels of

the above genes were upregulated in the DSS group while significantly downregulated with SIT administration (Figure 5A).

As expected, Western blot analysis showed that protein expression levels of Caspase-1, Cleaved-Caspase-1, NLRP3, GSDMD, and GSDMD-N distinctly increased after DSS treatment in colonic tissues and Caco-2 cells and significantly counteracted following the intervention with SIT (Figures 5B–E). Meanwhile, ELISA indicated that SIT treatment significantly inhibited DSS-induced increased levels of IL-1 β and IL-18 in serum and cell supernatant; it has been shown that secretion of cytokines IL-1 β and IL-18 were associated with the NLRP3 inflammasome and induced an inflammatory cell death mode termed as pyroptosis (He et al., 2015). Comprehensively, the above results suggest that SIT plays a possible therapeutic role in UC via regulating Caspase-1-mediated pyroptosis.

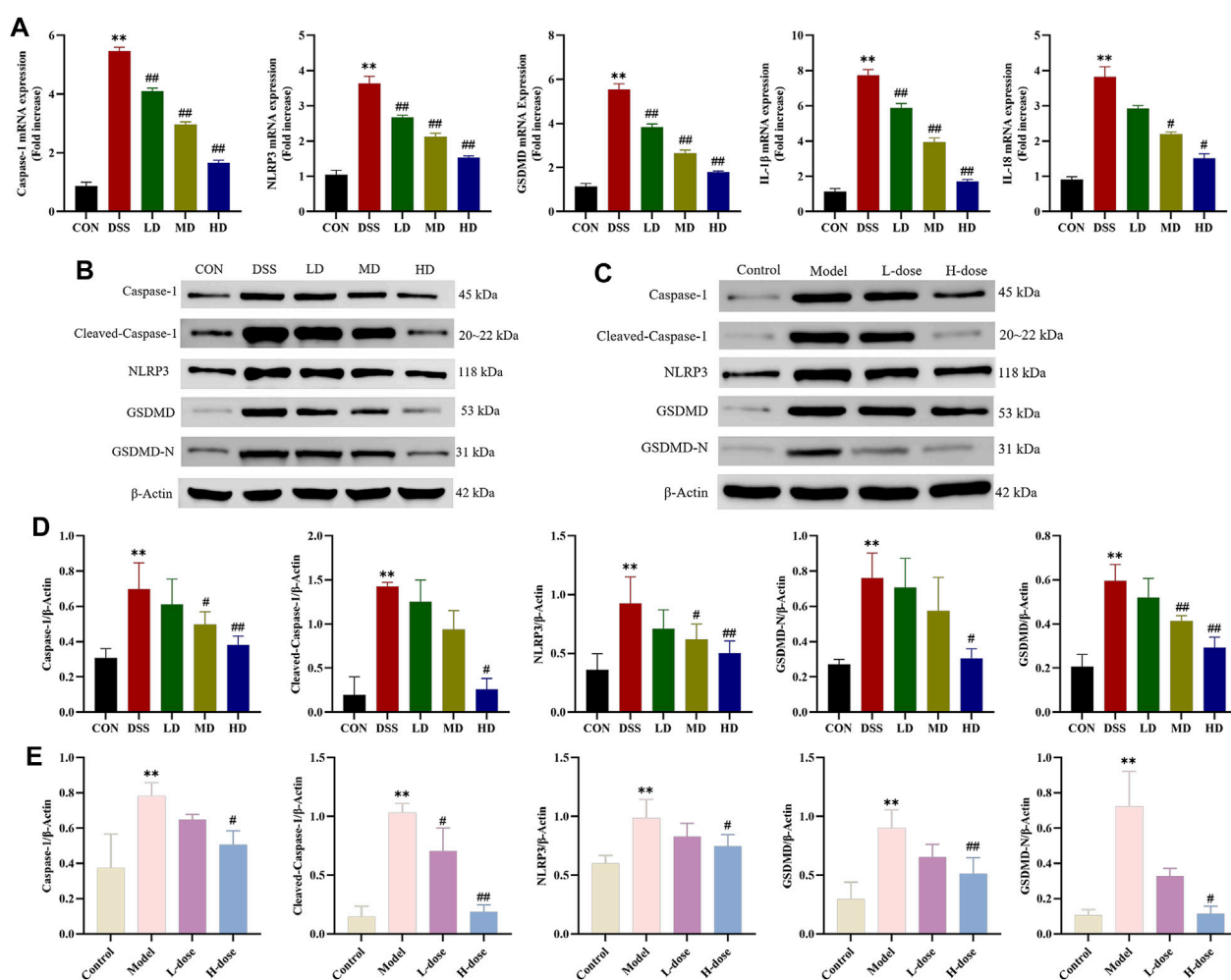


FIGURE 5

SIT inhibits DSS-induced Caspase-1 mediated pyroptosis pathway activation. (A) The mRNA levels of Caspase-1, NLRP3, GSDMD, IL-1 β , and IL-18 in colon tissues. Gel electrophoresis images of Caspase-1, Cleaved-Caspase-1, NLRP3, GSDMD, and GSDMD-N in colon tissues (B) and Caco-2 cells (D) were analyzed by Western blot. Analysis of protein expression levels was analyzed and shown in (C) and (E). N = 3 per group. The data are presented as mean \pm SD. CON, control group; DSS, dextran sulfate sodium-induced group; SIT, β -sitosterol; LD, low-dose SIT group; MD, middle-dose SIT group; HD, high-dose SIT group; NLRP3, nucleotide-binding oligomerization domain (Nod)-like receptor thermal protein domain associated protein 3; GSDMD, gasdermin D; GSDMD-N, gasdermin D-N terminal; IL, interleukin; SD, standard deviation. ** p < 0.01 compared with CON or Control group; # p < 0.05, ## p < 0.01 compared with DSS or Model group.

3.6 SIT attenuates colonic mucosal barrier

Tight junction proteins are the essential parts for the maintenance of the gut mucosal barrier integrity, which could against the invasion of luminal detrimental substances and lower the risk of microbe-induced inflammation (Parikh et al., 2019). Therefore, we further verified whether the protective mechanism of SIT on the colon is related to the restoration of intestinal barrier function. ZO-1 and occludin, are important two tight junction-associated proteins (Ji et al., 2016), which were measured by Western blot. The expression levels of ZO-1 and occludin were decreased compared with the control group, which were significantly reversed by SIT as provided in Figure 6, suggesting that SIT could alleviate colitis through enhancing mucosal barrier integrity.

4 Discussion

UC is a main subtype of chronic relapsing inflammatory bowel disease and is highly prevalent worldwide. The nature of UC is complex and the pathogenesis of UC has not been well elucidated yet. Current therapeutic agents are not entirely desirable in terms of potency with many side effects, erratic efficacy, and recurrence or failure after reduction or termination of administration as well as a heavy financial burden (Bressler et al., 2015; Berends et al., 2019). Hence new alternative therapeutic medication from natural products is of high interest in research. SIT is a well-known bioactive phytosterol naturally plentiful in dietary and non-dietary plant cell membranes, accounting for about 65% of human herbal nutrition forming (Weihrach and Gardner, 1978). They are not only highly found in lipid-rich plant foods such as nuts,

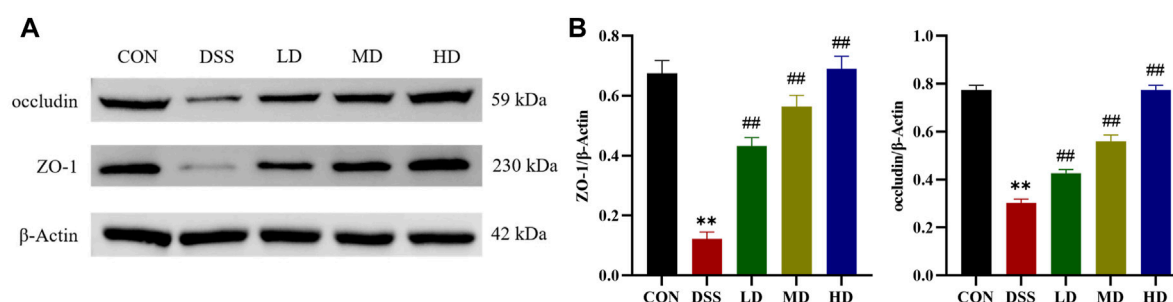


FIGURE 6

SIT alleviates colitis from barrier damage. (A) Gel electrophoresis images of occludin and ZO-1 in colon tissues were analyzed by Western blot. (B) Analysis of protein expression levels (N = 3 per group). The data are presented as mean \pm SD. CON, control group; DSS, dextran sulfate sodium-induced group; SIT, β -sitosterol; LD, low-dose SIT group; MD, middle-dose SIT group; HD, high-dose SIT group; ZO, zonula occludens; SD, standard deviation. ** p < 0.01 compared with CON group; ## p < 0.01 compared with DSS group.

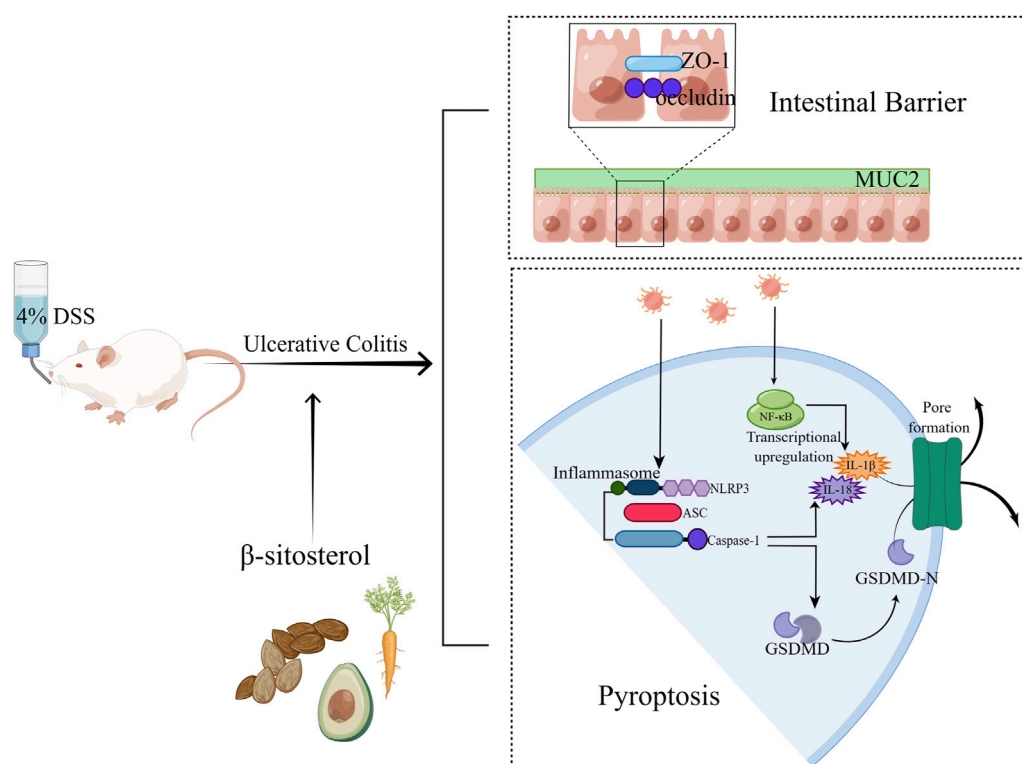


FIGURE 7

Overview of the effects of SIT on DSS-induced UC (By FigDraw, ID: SSITU8168e).

seeds, and legumes but also in vegetables and fruits (Khan et al., 2022). Over the past few decades, research on SIT was at an ever-accelerating pace and has suggested it may exert preventable and therapeutic effects on UC (Lee et al., 2012; Ding et al., 2019) with much less research on its role in pyroptosis.

DSS-induced experimental colitis is a reliable and mature animal model, which resembles clinically pathological symptoms and histological features in chronic UC (Tessner et al., 1998). In our current study, we demonstrated that SIT did significantly relieve the body weight loss in rats with 4% DSS-induced UC, with an increased DAI score, a main indicator in the assessment of the severity of UC.

In addition, colonic shortening, another indirect indicator in the evaluation of the severity of UC, was attenuated by SIT treatment, indicating that SIT has therapeutic potential in UC rats. For colon pathological injury, we detected histological analysis and found that administration of SIT could improve cryptal glands and submucosa and reduce inflammatory cells infiltrating. Also, with the increase of SIT dosages, the therapeutic effects improve correspondingly, suggesting that SIT may be a potential drug of choice for UC treatment.

Self-limiting acute inflammation is crucial for the body to eliminate the danger and restore homeostasis, while unresolved

inflammation contributes to the pathogenesis of autoimmune diseases including UC (Afonina et al., 2017). An increasing body of evidence has shown that aberrant inflammatory responses are the key contributors to the progression and exacerbation of UC. Pyroptosis, a novel type of programmed cell death, is mainly elicited by either classical Caspase-1-mediated or non-classical Caspase-11/4/5/11-mediated pathways in inflammation (Fang et al., 2020). Research has indicated that both Caspase-1-mediated and Caspase-11-mediated pyroptosis are closely linked to the development of UC (Chao et al., 2020), in which NLRP3 inflammasome plays a key role (Chen et al., 2019; Zhen and Zhang, 2019). NLRP3 first interacts with ASC and combines with Caspase-1 to assemble the inflammasome complex (Lu et al., 2014). Cleaved Caspase-1 then cleaves GSDMD to the N-terminal fragment (GSDMD-N). After that, the activated N-terminal domain of GSDMD translocates and forms cell membrane pores, thus resulting in the occurrence of pyroptosis and triggering the damage of the epithelial cells in the gut, and releasing pro-inflammatory cytokines (Yuan et al., 2018). The secretion of IL-1 β and IL-18 can further amplify and perpetuate the inflammatory reaction (He et al., 2015; Shi et al., 2015). Of note, as the co-substrate of multiple inflammasomes and two main pathways of pyroptosis, GSDMD performs the primary function of pyroptosis executioner (Kayagaki et al., 2015; Shi et al., 2015).

Inflammatory cytokines IL-1 β and IL-18 are the main markers for pyroptosis and their overproduction was found in various regions of the colon in UC active patients (Thinwa et al., 2014). Recent findings suggested that both Caspase-1 and Caspase-11 activation possess the function to induce the release of IL-1 β and IL-18, but only Caspase-1 could directly cleave them (Man and Kanneganti, 2015); in addition, epithelium IL-18 secretion was independent on NLRP3 but dependent on Caspase-1 (Song-Zhao et al., 2014). Numerous experimental studies on animals have demonstrated inhibiting Caspase-1-dependent pyroptosis could protect against DSS-induced colitis (Tian et al., 2020; Cui et al., 2022; Xue et al., 2022). In view of this, we observed the regulation effect of SIT on inflammatory mediators in our present study. The results showed that SIT alleviated DSS-induced inflammation both in UC rats and Caco-2 cells with downregulation of pro-inflammatory cytokines including TNF- α , IL-1 β , and IL-18. Furthermore, we explored the canonical Caspase-1 dependent pathway which underlies UC and we found that SIT treatment downregulated the protein levels of Caspase-1, cleaved-Caspase-1, NLRP3, GSDMD, and GSDMD-N in tissues and cells as expected. Taken together, SIT did ameliorate experimental colitis by inhibiting the NLRP3/Caspase-1/GSDMD-dependent pyroptosis pathway.

Furthermore, NF- κ B pathway played an important role in the inflammatory responses of UC (Tong et al., 2021). In mammals, NF- κ B family can form homo- or heterodimers of which the most common form is a dimer of p50 and p65. Normally, NF- κ B remains inactive with the combination of members of IKB family (Lawrence, 2009). Clinical studies also have demonstrated excessive inflammation activated by NF- κ B exists in UC (Zhou et al., 2018). Activation of NF- κ B signaling cascade response was reported to participate in the regulation of NLRP3 inflammasome transcription and Caspase-1 has been proven as an active activator of NF- κ B (Danelishvili et al., 2011; Hu et al., 2019; Zhen and Zhang, 2019). Previous studies have demonstrated that SIT could reduce the secretion of inflammatory mediators such as TNF- α and IL-1 β ; in addition, SIT has the ability to suppress the initiation of

NLRP3 and the activation of Caspase-1 as well as partial inhibition of NF- κ B *in vitro* (Liao et al., 2018). In this study, we also assessed the major proteins of NF- κ B pathway. We observed the over-expressed phosphorylation levels of p65 subunit and I κ B α , the protein content in colon tissues was suppressed under the SIT treatment. However, it cannot be stated with certainty that SIT-mediated inflammation alleviation is associated with NF- κ B pathway in UC in light of our present results.

The mechanical barrier is the most important barrier among the intestinal mucosal barrier, with the structural basis consisting of intact intestinal epithelial cells and tight junction (TJ) proteins between the cells (Odenwald and Turner, 2017). Once the intestinal barrier was disrupted, the bacteria and toxins from the gut would translocate to the mucosa and activate deleterious intestinal inflammation (Liao et al., 2018; Zhang et al., 2018). Previous literature has demonstrated that the dysfunction of intestinal barrier integrity is responsible for the exacerbation of inflammatory bowel disease including UC (Zhao et al., 2020). Therefore, restoring the intestinal barrier integrity can act in preventing or treating UC. To gain further insight into the actions of SIT on the colonic barrier function, we detected the expression levels of the TJ-associated proteins ZO-1 and occludin. Western blot results suggested that the protein expression of ZO-1 and occludin were markedly weakened by DSS treatment while increasing in response to SIT administration. These results suggest that SIT could protect the gut against the occurrence of intestinal inflammation by maintaining mucosal barrier integrity, and therefore halt UC progression.

5 Conclusion

In summary, SIT not only inhibits the production of pro-inflammatory mediators and suppresses pyroptosis via suppression the NLRP3/Caspase-1/GSDMD-dependent pathway, but also enhances the function of the intestinal mucosal barrier through regulation of epithelial tight junction proteins expression (Figure 7). These findings indicate that SIT is an effective drug candidate and may be potential in clinical applications of UC treatment in the future.

As far as we know, it is the first evidence to show that SIT is effective in regulating pyroptosis in experimental UC. Although many studies have shown that SIT has good safety profiles, its poor stability, low water solubility, and short half-life also confine its broader application, and await to be addressed.

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

Ethical approval was not required for the studies on humans in accordance with the local legislation and institutional requirements because only commercially available established cell lines were used. The animal study was approved by the animal ethics committee of

Beijing University of Chinese Medicine. The study was conducted in accordance with the local legislation and institutional requirements.

Author contributions

The contribution of the authors in this work is as follows, D-MZ and MC conceived and designed the research, and provided financial support. DZ performed the experiments, carried out the data processing, and drafted the original manuscript. JJ and FG assisted in the investigation and conducting experiments. Y-JL and F-RZ assisted in the manuscript revision. S-JZ and S-YW provided the test medicine and technical support. D-MZ and MC supervised the research and reviewed the manuscript. All authors contributed to the article and approved the submitted version.

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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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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fphar.2023.1218477/full#supplementary-material>

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Progress in studying the impact of hyperlipidemia and statins on rotator cuff injury and repair

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This review delves into the intersection of two prevalent conditions, hyperlipidemia and rotator cuff injuries, both of which bear substantial healthcare burdens. Our investigation begins with an exploration of rotator cuff injuries, common musculoskeletal disorders that severely impair shoulder functionality and quality of life. These injuries are notably pervasive among sports enthusiasts and the older adult, with an incidence rate estimated at 5–10% in the general population. Despite their widespread occurrence and the diverse, multifactorial etiological factors, effective treatment strategies remain elusive. We then examine hyperlipidemia, a metabolic disorder affecting approximately 40% of the global adult population. Characterized by elevated levels of cholesterol and triglycerides, hyperlipidemia can precipitate severe cardiovascular complications and presents a significant socioeconomic burden. Although current management strategies encompass lifestyle modifications and pharmacological interventions, the condition remains a formidable health challenge. Central to this review is the exploration of a potential association between hyperlipidemia and rotator cuff injuries. We aim to synthesize the current understanding of hyperlipidemia's role in the pathophysiology of rotator cuff injuries, thereby offering fresh insights into their common etiological underpinnings, potential therapeutic targets, and drugs, such as Statins. The influence of other lipid-lowering therapeutics on tendon health is also considered, and further research into the molecular pathways and potential therapeutic benefits of these drugs is required. This pursuit aligns with broader efforts to enhance patient outcomes, minimize healthcare burdens, and contribute to the global understanding of these prevalent conditions.

KEYWORDS

rotator cuff injury, hyperlipidemia, statin, mechanism, treatment, inflammation

Introduction

The rotator cuff, a sophisticated orchestration of muscles and tendons that envelope the shoulder joint, serves an indispensable role in bestowing stability and enabling a diverse array of shoulder movements (1–3). Afflictions to this vital assembly, which span the spectrum from benign inflammation or tendonitis to partial or even full-throttle tendon ruptures, predominantly impact the shoulder's soft tissues (4, 5). These injuries frequently culminate in acute pain, muscular weakness, and restricted mobility, thereby epitomizing a pervasive musculoskeletal disorder (6). Rotator cuff injuries manifest with particular frequency among sports aficionados and the geriatric population, often inducing substantial debilitation in shoulder functionality and a significant deterioration in the quality of life (3). The annual incidence rate of rotator cuff

injuries hovers around 5–10% within the general populace, with a conspicuous surge in prevalence commensurate with advancing age (asymptomatic tears were found in more than 20% of individuals over the age of 60) (7). A rough estimate of the economic burden for a single patient undergoing surgery for a rotator cuff injury can be in the range of \$10,000–\$30,000 or even more, including both direct and indirect costs. Thus, this condition represents a substantial quota of visits to orthopedic clinics, exerting a hefty strain on healthcare resources, and thereby emerging as a noteworthy public health quandary.

The precise etiology of rotator cuff injuries remains nebulous, likely being multifactorial in nature. The onslaught of years is a well-entrenched risk factor, with degenerative alterations in the rotator cuff tendons becoming increasingly commonplace as individuals age (8). Furthermore, lifestyle determinants such as smoking have been implicated, with empirical evidence indicating that smokers are at an escalated risk of succumbing to rotator cuff injuries in contrast to their non-smoking counterparts (9). Medical conditions such as diabetes and hypertension have also been correlated with an augmented risk of these injuries, thereby suggesting a role for systemic health in the integrity of the rotator cuff (10, 11). The stewardship of rotator cuff injuries is multifarious, with therapeutic options customized to the individual patient's needs, factoring in the severity of the injury, the patient's overarching health status, and their functional exigencies. Conservative management approaches, encompassing physical therapy, pain mitigation with non-steroidal anti-inflammatory drugs (NSAIDs), and corticosteroid injections, typically constitute the initial line of treatment (12). However, in cases of severe injuries or when conservative management proves ineffective, surgical intervention may be necessitated (8). Despite these treatment modalities, a significant number of patients persist in experiencing pain and functional limitations, thereby highlighting the need for further research into innovative therapeutic strategies (11, 13).

Hyperlipidemia, a pervasive metabolic aberration, is characterized by escalated levels of total cholesterol (TC), triglycerides (TG), and low-density lipoprotein cholesterol (LDL-C), coupled with a reduction in high-density lipoprotein cholesterol (HDL-C) (1, 14, 15). This condition often manifests covertly, with no symptoms in its incipient stages. However, unaddressed hyperlipidemia can precipitate atherosclerosis, engendering grave cardiovascular ramifications such as heart disease, cerebrovascular accident, and peripheral artery disease (10, 16, 17). As a substantial global health quandary, the World Health Organization posits that approximately 40% of the global adult populace grapples with elevated total cholesterol levels, a key indicator of hyperlipidemia. This widespread disorder imposes a significant socioeconomic encumbrance, accounting for a considerable proportion of healthcare expenditure. Therapeutic stratagems encompass lifestyle modifications, including dietary adjustments and consistent physical exertion, along with pharmacological interventions like statins, fibrates, and niacin (16, 18, 19). Despite these measures, hyperlipidemia persists as a formidable health challenge, underscoring the exigency for continued exploration into innovative therapeutic approaches and prophylactic strategies. The potential correlation between hyperlipidemia and rotator cuff injuries further accentuates the necessity for a comprehensive understanding and efficacious management of this disorder (16).

Given the substantial prevalence and socio-economic burden of hyperlipidemia (20, 21), and its potential association with rotator

cuff injuries, a comprehensive understanding of the interplay between these two conditions is essential. Therefore, this review aims to amalgamate the current understanding of the role of hyperlipidemia in the pathophysiology of rotator cuff injuries. Our objective is to elucidate this connection, thereby providing novel insights for etiological research and clinical management. By probing into the underlying mechanisms, we expect to shed light on potential therapeutic targets and preventive strategies, thereby contributing to the global efforts in addressing these prevalent conditions.

Hyperlipidemia as a risk factor for rotator cuff injuries

The etiology of rotator cuff injuries is a complex interplay of multiple factors, inclusive of age-related degenerative changes, disease progression, and undue physical strain. In the scientific discourse of recent years, a considerable emphasis has been placed on the potential correlation between hyperlipidemia and rotator cuff injuries. This connection was evidenced in a prospectively designed study by Skovgaard et al. (16), wherein hypercholesterolemia surfaced as a factor escalating the risk of upper limb tendon injuries by a factor of 1.5. A similar correlation was delineated in Kara's research (10), where cardiovascular risk elements, including diabetes and hyperlipidemia, were identified as potential precipitators of rotator cuff injuries.

In a parallel vein, Djerbi et al. (22) uncovered a significant correlation between smoking, dyslipidemia, and the incidence rate of rotator cuff tears. An 11-year longitudinal follow-up study conducted by Lin et al. (15) further underscored hyperlipidemia as an independent risk factor for rotator cuff disorders, doubling the risk compared to non-hyperlipidemic cohorts. Recent studies echoed these findings, demonstrating a discernible link between hyperlipidemia and various manifestations of rotator cuff tendon diseases, with hyperlipidemic patients bearing a higher risk of complete tears.

However, it is imperative to note the existence of contrarian views, as several studies (23, 24) reported no significant correlation between dyslipidemia and rotator cuff tears. These incongruities might be attributed to variances in the demographic composition of the study populations, the parameters observed, and the criteria for grouping.

The impact of hyperlipidemia on the efficacy of rotator cuff injury repair

Hyperlipidemia, characterized by elevated lipid levels, has been increasingly identified as a critical factor that correlates not only with the onset of rotator cuff tears but also with the propensity for a re-tear following surgical intervention. This multifaceted influence of hyperlipidemia was substantiated in a large-scale, rigorous study conducted by Cancienne et al. (25). Their research, encompassing an extensive cohort of 30,638 patients subjected to rotator cuff repair, unveiled a significant correlation between perioperative total cholesterol and low-density lipoprotein cholesterol levels, and the rate of revision surgery following the initial repair. This finding underscores the potential for hyperlipidemia to complicate the post-operative trajectory and recovery in patients with rotator cuff tears.

Further amplifying this perspective, Garcia's research (14) revealed a distinct disparity in the risk of re-tear between hyperlipidemic and non-hyperlipidemic patients. The study found that, compared to their non-hyperlipidemic counterparts, patients with hyperlipidemia faced a staggering fourfold increase in the risk of re-tear following rotator cuff repair. This finding is indicative of the profound influence of lipid metabolic disorders on the integrity and healing capacity of rotator cuff tissues.

Complementing these findings, Kim's study (26) further reinforced the role of hyperlipidemia as a significant risk factor for re-tear subsequent to rotator cuff repair. The convergence of these findings across multiple studies underscores the necessity of considering hyperlipidemia in the strategic planning of both preventive and therapeutic interventions for rotator cuff injuries.

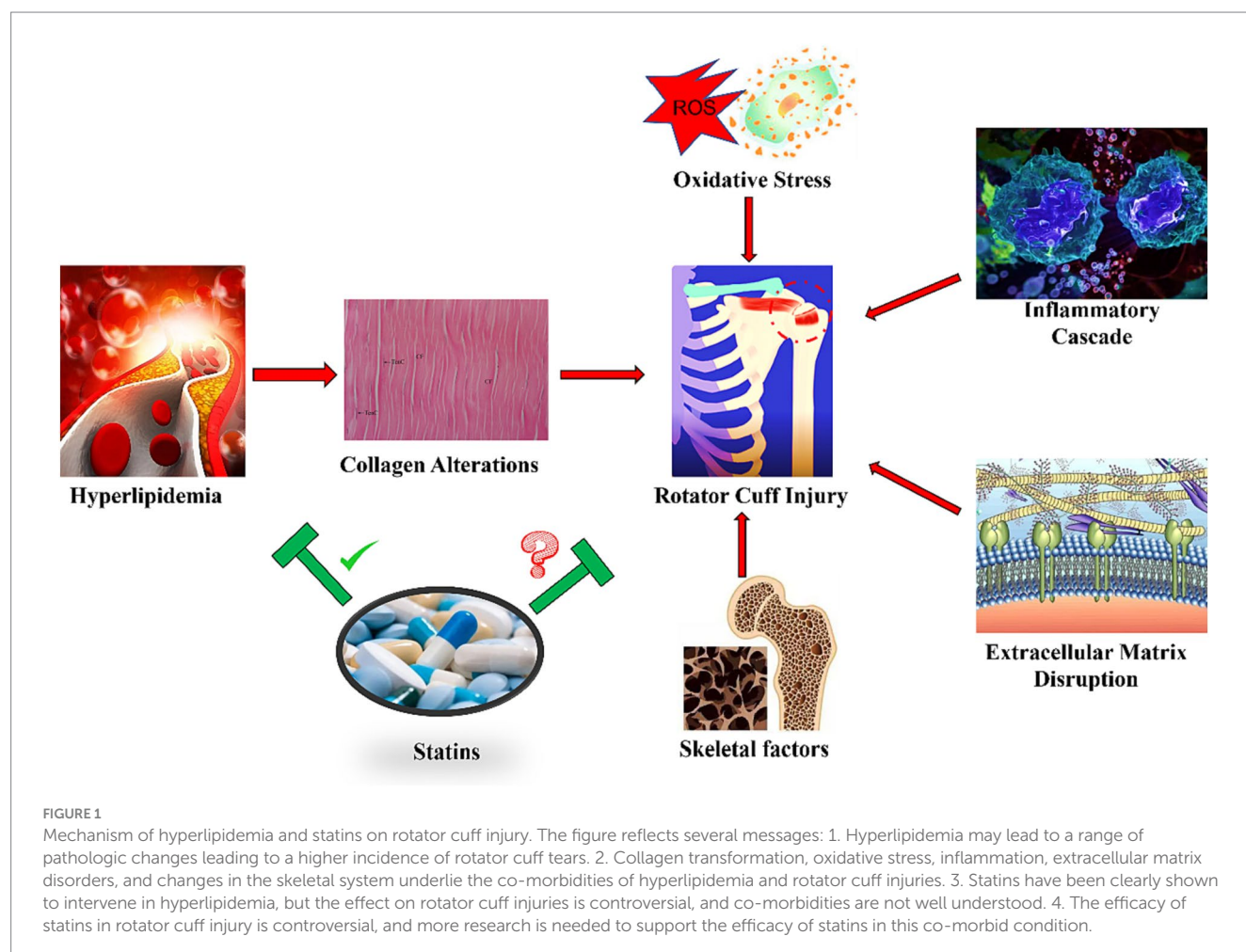
Taking this multifactorial approach a step further, Harada et al. (27) embarked on an investigation of the risk factors for re-tear following rotator cuff repair. The study's findings highlighted that the combination of hyperlipidemia, a tear size of ≥ 40 mm, and a critical shoulder angle of $\geq 37^\circ$ collectively forecasted the highest rate of re-tear. This discovery underscores the importance of a comprehensive, multi-parametric assessment in predicting the risk of re-tear and devising more effective post-operative management strategies.

Molecular mechanism of rotator cuff injury induced by hyperlipidemia

The intricate role of hyperlipidemia in the pathogenesis of rotator cuff injury remains somewhat nebulous, but current research illuminates a series of molecular mechanisms that may underpin the deleterious effects of this metabolic disorder on tendon health (Figure 1).

Oxidative stress

A multitude of studies affirm the primacy of oxidative stress in triggering tendon degeneration, fibrosis, and adhesion (28, 29). Hyperlipidemia, particularly characterized by high cholesterol, can suppress the expression of tendon-related genes in tendon stem/progenitor cells via the reactive oxygen species (ROS)-activated nuclear factor kappa-B (NF- κ B) signaling pathway (30, 31). Concurrently, it can instigate cell apoptosis and autophagy through the ROS-activated AKT/FOXO1 signaling pathway in these cells, culminating in dysfunction and ultimately precipitating tendon degeneration and tendinopathy (32, 33).



Collagen alterations

Normal tendons are predominantly constituted of type I collagen, interspersed with a minor proportion of type III collagen. Aberrant cholesterol deposition in tendon tissues can provoke alterations in collagen synthesis and organization, thereby inducing structural and biomechanical alterations within the tendon matrix (34).

Extracellular matrix disruption

The extracellular matrix (ECM) plays a pivotal role in maintaining tendon homeostasis (35). A hyperlipidemic milieu can induce changes in critical components of the ECM in tendon tissues and cells. The mechanism may involve low-density lipoprotein cholesterol (LDL-C) inducing dysfunction of tendon cells, contributing to alterations in the ECM components (36).

Inflammatory cascade

The inflammatory microenvironment is a key player in tendon degenerative damage (37–39), and hyperlipidemia has been closely linked to systemic inflammation (40). Cholesterol molecules can activate the NF- κ B signaling pathway, augmenting the expression of pro-inflammatory cytokines such as tumor necrosis factor α (TNF- α), interleukin 6 (IL-6) (41–43).

Skeletal factors

Hyperlipidemia can exert a dual detrimental impact on bone health by inhibiting bone formation and accelerating bone resorption, thereby promoting the onset of osteoporosis (44). Notably, osteoporosis has been identified as an independent risk factor for both the genesis of rotator cuff tears and re-tear following surgical repair (45, 46). This underscores the intersection of metabolic, inflammatory, and skeletal factors in the pathogenesis and prognosis of rotator cuff injuries.

Application of lipid-lowering drugs in rotator cuff injuries and repair

Statins, scientifically known as 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase inhibitors, represent the principal lipid-lowering agents in clinical practice (47). By inhibiting HMG-CoA reductase, the rate-limiting enzyme in cholesterol synthesis, statins effectively curtail cholesterol production. This, in turn, upregulates the expression of LDL receptors on the cell surface, thereby accelerating the metabolic clearance of serum LDL. However, the potential influence of statins on rotator cuff injuries and their recovery trajectory engenders a degree of controversy in the current literature.

Several studies have elucidated a beneficial role for statins in the context of rotator cuff injuries and their post-injury repair. Dolkart et al. (48) employed a rat model of rotator cuff tear to probe the impact of atorvastatin on tendon-bone healing following rotator cuff repair

surgery. The experimental findings suggested that atorvastatin could activate the COX2/PGE2/EP4 pathways, thereby fostering tendon cell proliferation, migration, and differentiation, and ultimately bolstering the biomechanical integrity of the tendon-bone interface. Parallel findings were obtained in an animal study conducted by Hao et al. (49), demonstrating that silk protein fortified with simvastatin could stimulate osteogenic differentiation of bone marrow mesenchymal stem cells and collagen synthesis via the β -catenin signaling pathway, thereby enhancing tendon-bone interface healing. Lin et al. (15) conducted an 11-year longitudinal study corroborating that hyperlipidemia constitutes a risk factor for rotator cuff injuries, and statin therapy in hyperlipidemic patients could mitigate this risk. A clinical study by Cancienne et al. (25) revealed a positive correlation between perioperative lipid levels and the rate of revision surgery following rotator cuff repair, suggesting that statin therapy could potentially decrease this revision rate. Similarly, a recent case-control study by Lee et al. (50) incorporated 104 hyperlipidemic patients who underwent arthroscopic rotator cuff repair, among whom 66 individuals were in the statin group and 38 in the non-statin group. The follow-up findings indicated a lower re-tear rate in the statin group.

Conversely, several studies have reported potentially detrimental effects of statins on tendon health. Animal experiments conducted by Oliveira et al. (51, 52) demonstrated that statins could disrupt collagen fiber organization and alter tendon matrix composition, thereby diminishing the biomechanical resilience of the tendon and increasing the risk of rupture. Kaleağasıoğlu et al. (53) discerned that statins could precipitate tendon calcification, which could in turn compromise its biomechanical properties. Animal experiments and clinical cohort studies by Eliasson et al. (54, 55) showed that statins could suppress tendon cell proliferation and elicit deleterious effects on tendon collagen and matrix. Furthermore, some studies found that statins did not improve the prognosis following rotator cuff repair surgery. In a study conducted by Amit et al. (1), 77 hyperlipidemic patients underwent arthroscopic rotator cuff repair, among whom 38 individuals were on statins and 39 were not. The follow-up found no significant differences in shoulder joint function, postoperative fatty infiltration, and re-tear rates between the two groups. Similarly, a study by Zeng et al. (56) found no significant difference in postoperative shoulder function scores between hyperlipidemic patients undergoing arthroscopic rotator cuff repair who were or were not on statin therapy perioperatively.

Potential reasons for the varied outcomes observed across different studies may be due to different baseline population data, different administered doses, and different treatment times, etc. Finally, it should be mentioned that there are still some limitations in the literature cited in this current review. (1) Most of the clinical studies have a low grade of evidence. (2) Animal studies are not sufficiently mechanistically insightful. (3) There is no direct evidence for the effect of statins on co-morbidities, and more clinical and basic experimental evidence is needed to support it.

Summary and perspectives

The significance of hyperlipidemia in the context of rotator cuff injuries is progressively gaining momentum in medical research. The intricate interplay between hyperlipidemia and these injuries remains

somewhat enigmatic, necessitating large-scale, multicentric prospective studies to conclusively ascertain whether hyperlipidemia augments the susceptibility to such injuries. The molecular pathways through which hyperlipidemia instigates rotator cuff injuries are yet to be fully elucidated, thereby requiring a more comprehensive exploration through animal models and cellular experiments.

Moreover, the influence of statins on rotator cuff injuries and the subsequent healing of the tendon-bone interface post-surgery continues to be a subject of debate (57). The impact of other widely used lipid-lowering therapeutics, such as ezetimibe and probucol, as well as novel lipid-lowering agents, on tendon health remains nebulous and warrants a more thorough investigation.

The unraveling of the mechanistic role of hyperlipidemia in rotator cuff diseases, coupled with a deeper understanding of the potential therapeutic benefits of lipid-lowering drugs, could potentially offer transformative insights into the etiological basis and clinical management of rotator cuff injuries. Such insights could pave the way for more personalized and effective therapeutic regimens, enhancing the prognosis for patients with these injuries.

Author contributions

YQ: Investigation, Methodology, Project administration, Resources, Writing – original draft, Writing – review & editing. HH: Conceptualization, Data curation, Investigation, Writing – original draft, Writing – review & editing. RW: Investigation, Methodology, Visualization, Writing – original draft, Writing – review & editing. YZ: Conceptualization, Data curation, Formal analysis, Writing – original draft. XF: Data curation, Formal analysis, Writing – original draft. FX: Funding acquisition, Supervision, Validation, Writing – review & editing. ZL: Conceptualization, Supervision, Validation, Visualization,

Writing – original draft, Writing – review & editing. QW: Conceptualization, Funding acquisition, Resources, Supervision, Validation, Visualization, Writing – original draft.

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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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Multifaceted oncostatin M: novel roles and therapeutic potential of the oncostatin M signaling in rheumatoid arthritis

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Rheumatoid arthritis (RA) is a self-immune inflammatory disease characterized by joint damage. A series of cytokines are involved in the development of RA. Oncostatin M (OSM) is a pleiotropic cytokine that primarily activates the Janus kinase (JAK)/signal transducer and activator of transcription (STAT) signaling pathway, the mitogen-activated protein kinase (MAPK) signaling pathway, and other physiological processes such as cell proliferation, inflammatory response, immune response, and hematopoiesis through its receptor complex. In this review, we first describe the characteristics of OSM and its receptor, and the biological functions of OSM signaling. Subsequently, we discuss the possible roles of OSM in the development of RA from clinical and basic research perspectives. Finally, we summarize the progress of clinical studies targeting OSM for the treatment of RA. This review provides researchers with a systematic understanding of the role of OSM signaling in RA, which can guide the development of drugs targeting OSM for the treatment of RA.

KEYWORDS

oncostatin M (OSM), rheumatoid arthritis (RA), fibroblast-like synoviocytes (FLS), cytokines, cartilage and bone destruction, CD4⁺ T cell, pannus formation

1 Introduction

Rheumatoid arthritis (RA) is an autoimmune disease of unknown etiology, which is believed to be associated with genetic, environmental, and immunological factors (1). The primary clinical manifestation of RA is symmetrical joint inflammation, which is based on synovitis, bone, and cartilage destruction (2). Cytokines play a crucial role in the pathogenesis of RA and are of paramount importance in RA pathology (3, 4). Cytokines

such as tumor necrosis α (TNF- α), interleukin 6 (IL-6), IL-1, IL-17, and IL-10 promote or inhibit the occurrence and development of RA. Fibroblast-like synoviocytes (FLS) and synovial macrophages in the joint cavity of RA patients secrete a large number of pro-inflammatory cytokines and chemokines, which are important mechanisms leading to joint inflammation, bone destruction, and angiogenesis in RA patients (5–7). Therefore, ongoing research is revealing the relationship between cytokines and RA, with the aim of further exploring the molecular mechanisms underlying RA, discovering new disease activity biomarkers, and even finding new targets for treating RA.

As a member of the IL-6 family, oncostatin M (OSM) has gradually received attention for its role and mechanism in the occurrence of rheumatoid arthritis (RA) (8). OSM is a pleiotropic cytokine that participates in the regulation of multiple signaling pathways and plays an important role in the pathogenesis of various autoimmune diseases (9). It has been observed that RA patients have high levels of OSM in their synovial fluid, and further research has found that OSM can promote the occurrence and development of RA through multiple pathways (9, 10). The present paper intends to introduce the research progress of OSM at the current stage from the aspects of OSM and its receptor complex, OSM signal transduction, OSM's biological functions, and the relationship between OSM and the pathogenesis of RA.

2 OSM and OSM receptor complex

The IL-6 cytokine family is one of the largest cytokine families, and the common feature of cytokines in this family is the presence of the signal receptor subunit gp130 in their receptor complexes. These cytokines include IL-6, IL-11, ciliary neurotrophic factor (CNTF), leukemia inhibitory factor (LIF), OSM, IL-12, cardiotrophin-1 (CT-1), cardiotrophin-like cytokine factor 1 (CLCF1), and IL-27 (11). It is

worth noting that the receptor complex of the cytokine IL-31 contains a gp130-like receptor (GPL), so some researchers consider IL-31 as part of the IL-6 cytokine family. OSM is an important member of the IL-6 family of cytokines, first discovered by Zarling et al. in the U-937 human lymphoma cell line (12). The human OSM gene is located in the chromosome 22q12.2 region, and the OSM polypeptide transcribed from the human OSM gene includes 252 amino acid residues, with N- and C-terminals consisting of 25 and 32 amino acid residues, respectively. After proteolytic processing, only 195 amino acid residues are retained. The mature human OSM protein has a molecular weight of 28 kDa, and its structure consists of four α -helices arranged in an “up-up-down-down” topology (13–15). OSM is widely expressed *in vivo*, and many immune cells such as T cells, monocytes/macrophages, and neutrophils can express OSM (16–19).

As mentioned earlier, the receptor complexes of the IL-6 family of receptors all contain the gp130 subunit (20). The receptor complexes of OSM are all heterodimers, and depending on the different second subunits in the receptor complexes, the receptor complexes can be divided into two types: type I and type II (21). The type I OSM receptor complex is composed of the α subunit gp130 and the β subunit LIFR β (LIF receptor β subunit), while the type II OSM receptor complex is composed of the α subunit gp130 and the β subunit OSMR β (OSM receptor β subunit) (Figure 1) (22). To avoid confusion, in this article, OSMR specifically refers to the β subunit of the type II OSM receptor complex, while OSM receptor refers to both type I and type II OSM receptor complexes.

It is worth noting that the two subunits of the OSM receptor complex exist separately in the resting state. When both OSM and the two subunits of the OSM receptor complex are present, OSM first forms a low-affinity heterodimer with gp130, and then this heterodimer recruits OSMR or LIFR and binds to it (9). Further research through computational simulations has identified several key amino acid residues involved in the binding process between OSM and OSMR (23). Additionally, research using computational

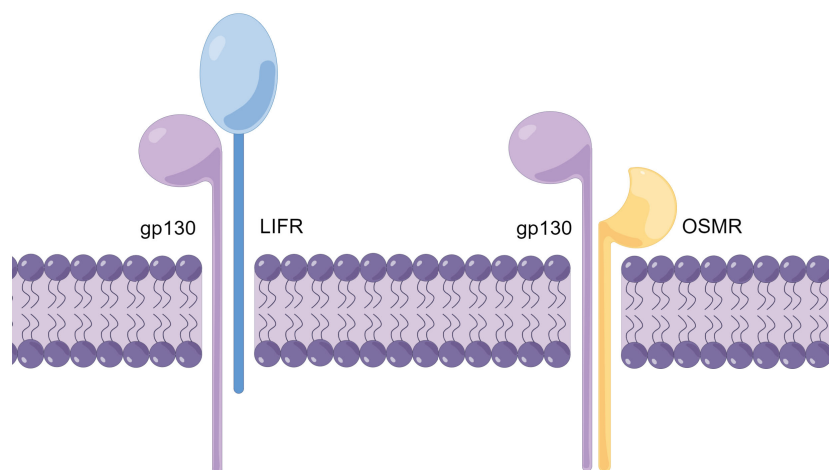


FIGURE 1

Schematic diagram of the OSM receptor complex structure (By Figdraw.). The OSM receptor complex is a heterodimer and can be classified into two types (Type I and Type II), with different subunits comprising each receptor complex. The Type I OSM receptor complex is composed of gp130 and LIFR, while the Type II OSM receptor complex is composed of gp130 and OSMR. The schematic diagram illustrates the structure of the OSM receptor complex.

simulations has revealed that the phenomenon of OSM and LIF sharing the LIFR receptor is related to the structural similarity between OSM and LIF (24). The binding of OSM and the OSM receptor complex is species-specific, and OSM from mice generally only binds to type II OSM receptor complexes. Only high concentrations of mouse-derived OSM can weakly activate LIFR, but there is also a single report that mouse-derived OSM can activate LIFR in mouse osteoblasts (Figure 2) (9, 25, 26). In contrast, OSM from rats or humans can bind to type I or type II OSM receptor complexes of the same species (27). Overall, OSMR as a unique subunit in the OSM receptor complex enables type II OSM receptor complexes to activate downstream pathways different from other IL-6 family signaling pathways, thereby exerting its unique biological functions.

3 OSM signaling transduction

The two subunits of the OSM receptor, like other members of the IL-6 family of receptors, have transmembrane structures. When the extracellular region binds to OSM, the intracellular region recruits and activates the Janus kinase (JAK) family. After binding to its receptor complex, the OSM receptor complex can activate JAK1 through gp130, and promote the phosphorylation and dimerization of the transcription factor signal transducer and activator of transcription (STAT), which is the downstream of JAK (20). The STAT protein then enters the nucleus and regulates the expression of target genes. In addition, OSM signaling can also trigger the RAS/mitogen-activated protein kinase (MAPK)

signaling pathway, the c-Jun N-terminal kinase (JNK)/p38 MAPK signaling pathway, and the phosphatidylinositol 3-kinase/serine-threonine kinase (PI3K/AKT) signaling pathway (28, 29). It is worth noting that the OSM receptor complex of type II OSM receptor complex has the subunit OSMR, which is only present in the OSM receptor, unlike other cytokines in the IL-6 family. Therefore, OSM can exert its unique biological regulatory function through the type II OSM receptor complex. Like type I receptor complexes, type II receptor complexes of OSM can also bind and activate JAK, but the binding affinity of OSM's type II receptor complex with JAK1 or JAK2 is equivalent, while type I receptor complexes of OSM can bind JAK1 with high affinity (30).

4 The physiological functions of OSM signaling

The physiological functions of OSM were first identified in the human lymphoma cell line U-937, and it was subsequently found to have growth-inhibitory effects on melanoma cells, which led to its naming (12). OSM can regulate cell proliferation by controlling cell cycle checkpoints. The cell cycle refers to the entire process between two cell divisions, which can be divided into the mitotic phase and interphase, which is further divided into the G1 phase, S phase, and G2 phase. In eukaryotes, cell cycle checkpoints regulated by cyclins and cyclin-dependent kinases (CDKs) control whether cells can progress from G1 phase to S phase (31). In breast cancer cell lines treated with OSM, the number of cells before S phase significantly

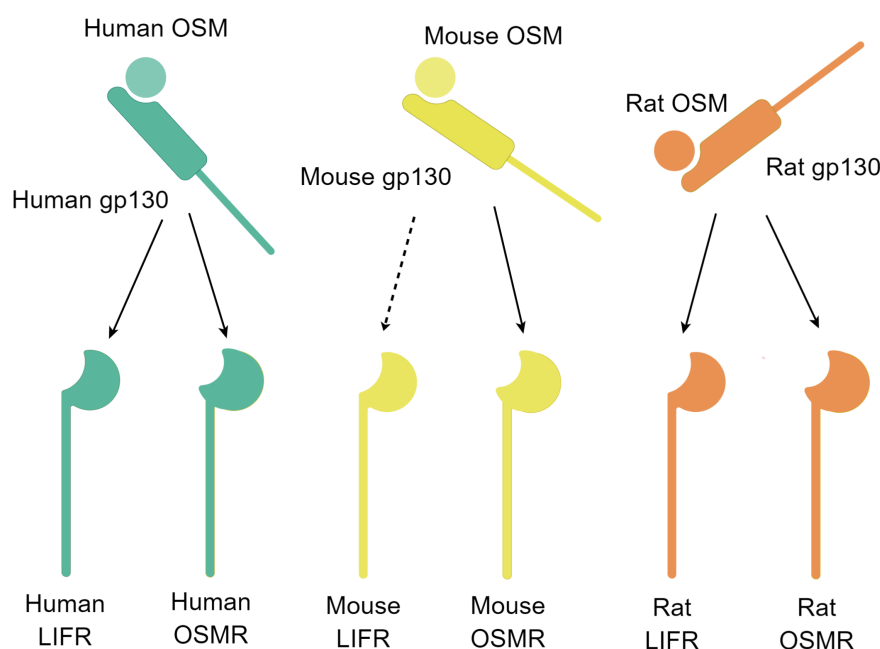


FIGURE 2

Schematic diagram of the OSM and receptor complex binding (By Figdraw.). Free OSM initially binds to gp130 and subsequently binds to another subunit, LIFR or OSMR. The binding ability of OSM and the two receptors differs among different species. The OSM-gp130 complex in humans and rats can bind to LIFR or OSMR of the same species, whereas in mice, the OSM-gp130 complex can bind to OSMR, and at high concentrations, it can also bind to LIFR (dashed line marked). The schematic diagram depicts the binding of the OSM and receptor complex.

increased, while the number of cells in S phase significantly decreased (32). Additionally, OSM treatment altered the levels of cyclins in breast cancer cell lines, indicating that OSM regulates the cell cycle by controlling cyclin levels, causing cells to stay at the cell cycle checkpoint and inhibiting the division of breast cancer cell lines. Furthermore, OSM can inhibit tumor cell division by regulating the expression levels of CDKs in melanoma cell line A375 and liver cancer cell line HepG2, hindering the tumors from progressing through the cell cycle checkpoint (33, 34). However, during liver regeneration, OSM promotes liver cell proliferation by promoting STAT3 phosphorylation (35). These studies suggest that the regulatory effects of OSM on cell proliferation are context-dependent and cannot be generalized.

In addition to its role in regulating cell proliferation, OSM also plays a regulatory role in many physiological processes, including inflammation, immune regulation, and hematopoiesis. As previously mentioned, OSM can activate inflammatory signaling pathways such as JAK/STAT and PI3K/AKT. In human vascular smooth muscle cells and mouse fibroblasts, OSM can also induce the expression of pro-inflammatory cytokine IL-6 (36, 37).

OSM also exhibits complex immunomodulatory effects. OSM has been shown to enhance innate immunity. Treatment of Huh7 liver cancer cells with OSM upregulates the expression of related innate immune molecules, intracellular adhesion molecule-1 (ICAM-1), and IL-15 receptor and enhances interferon- α -induced gene transcription, thereby enhancing interferon- α 's ability to combat hepatitis A and B viruses (38). Additionally, OSM inhibits naive CD4⁺ T cell differentiation into Th17 cells by activating suppressors of cytokine signaling 3 (SOCS3), STAT3, and STAT5 through cytokine signaling transduction (39). These findings demonstrate that OSM regulates both the innate and adaptive immune systems.

OSM is also closely related to hematopoiesis. OSMR^{-/-} mice exhibit reduced numbers of peripheral circulating red blood cells and platelets, as well as a corresponding decrease in megakaryocyte-erythroid progenitor cell (MEP) numbers in the bone marrow (8, 40). During embryonic development in vertebrates, the fetal liver is a natural site for the expansion of hematopoietic stem cells, and in mice, approximately half of the hematopoietic cells reside in the liver during embryonic development. At the end of hematopoiesis, hepatic hematopoietic cells express OSM and act on OSM receptors on the fetal liver stromal cells, promoting the maturation of the fetal liver and the loss of hematopoietic support function (41).

5 OSM signaling and diseases

Abnormal levels of OSM are associated with various inflammatory diseases. Compared to healthy controls, OSM levels are elevated in the peripheral blood plasma of patients with coronavirus disease 2019 (COVID-19), and are associated with the severity of the disease (42). Colonic and serum OSM levels are not only elevated in patients with inflammatory bowel diseases (IBD) who experience postoperative recurrence, but also high levels of OSM in colonic tissue often indicate poor prognosis or insensitivity to biologic therapy in IBD patients (43).

Previously, it was mainly believed that OSM mainly affects the development of many diseases by promoting inflammation. For example, researchers have found that lipopolysaccharide (LPS) produced by respiratory microbiota imbalance can promote OSM secretion by macrophages in the respiratory tract, which not only promotes airway inflammation and mucus secretion in patients with severe asthma. However, blocking the OSM signal with OSM-specific antibodies can alleviate asthma-related pathological features without affecting important antibacterial immune responses in the body (44). In addition, OSM can also promote the expression of inflammatory factors CC chemokine ligand (CCL) 2, IL-6, and vascular endothelial growth factor (VEGF) by inducing human aortic adventitial fibroblasts and smooth muscle cells in synergy with LPS, ultimately promoting the development of atherosclerosis (45). However, some studies have shown that OSM can play an anti-inflammatory role in certain diseases. For example, OSM treatment inhibited the expression of TNF- α induced by lipopolysaccharide (LPS) in septic mice and reduced their mortality (46). OSM also exerts an anti-inflammatory effect by promoting macrophage polarization towards the M2 type in adipose tissue (47). Therefore, the regulatory effect of OSM on inflammation is quite complex, and it may have opposite effects in different diseases. It is a pleiotropic cytokine.

In addition, OSM can also affect the progression of diseases by regulating fibrosis through various pathways. Overexpression of OSM in mouse liver tissue leads to upregulation of the expression of the profibrotic cytokine transforming growth factor- β (TGF- β) in liver macrophages, which promotes liver tissue fibrosis (48). Tissue inhibitor of matrix metalloproteinase (TIMP) can inhibit the expression of matrix metalloproteinase (MMP) 1. In cardiac fibroblasts, OSM inhibits the expression of TIMP1, which promotes the deposition of local extracellular matrix, leading to tissue fibrosis (49). Some studies have also found that OSM directly binds to the extracellular matrix, which may increase the stability of the extracellular matrix and promote its deposition, indicating that OSM may directly promote fibrosis (50). The profibrotic effect of OSM may also be beneficial for disease recovery. *In vitro* studies have shown that OSM can accelerate wound healing by promoting collagen and glycosaminoglycan production in fibroblasts at the site of diabetic foot ulcers (51). Further animal experiments have found that local treatment with OSM promotes wound healing in diabetic mice (52).

Recent studies suggest that OSM may have a role in the development and progression of other diseases beyond regulating inflammation and fibrosis. For instance, OSM secreted by T cells and monocytes in the dermis may enhance the sensitivity of sensory neurons to pruritogens, leading to increased itchiness in inflammatory skin lesions (53).

It is evident that OSM, a pleiotropic cytokine, plays a crucial role in the pathogenesis of many inflammatory diseases. Numerous studies have demonstrated the significant involvement of OSM levels in rheumatic diseases. Single nucleotide polymorphisms (SNP) rs22922016 related to OSMR gene has been found to associated to systemic lupus erythematosus (SLE) (54). Moreover, OSM signaling pathway was identified as a potential pathway which related to SLE by analyzing transcriptomic and genome-wide

association studies data (55). Systemic sclerosis (SSc), a rheumatic disease characterized by skin thickening, hardening, and visceral fibrosis, is also associated with OSM signaling. Diffuse cutaneous systemic sclerosis (dcSSc) patients showed significantly elevated levels of OSM in their serum, and OSM and OSM-regulated genes were upregulated in dcSSc skin (56). Fibroblasts positive for OSM and pSTAT3 were increased in affected skin compared to unaffected skin. These findings suggest that OSM signaling activation in the skin of dcSSc patients may be one of the causes leading to downstream STAT3 signaling activation (56). In addition to SLE and SSc, there is also a close association between the OSM signaling pathway and RA. Subsequently, this article will focus on the relationship between OSM and the development of RA.

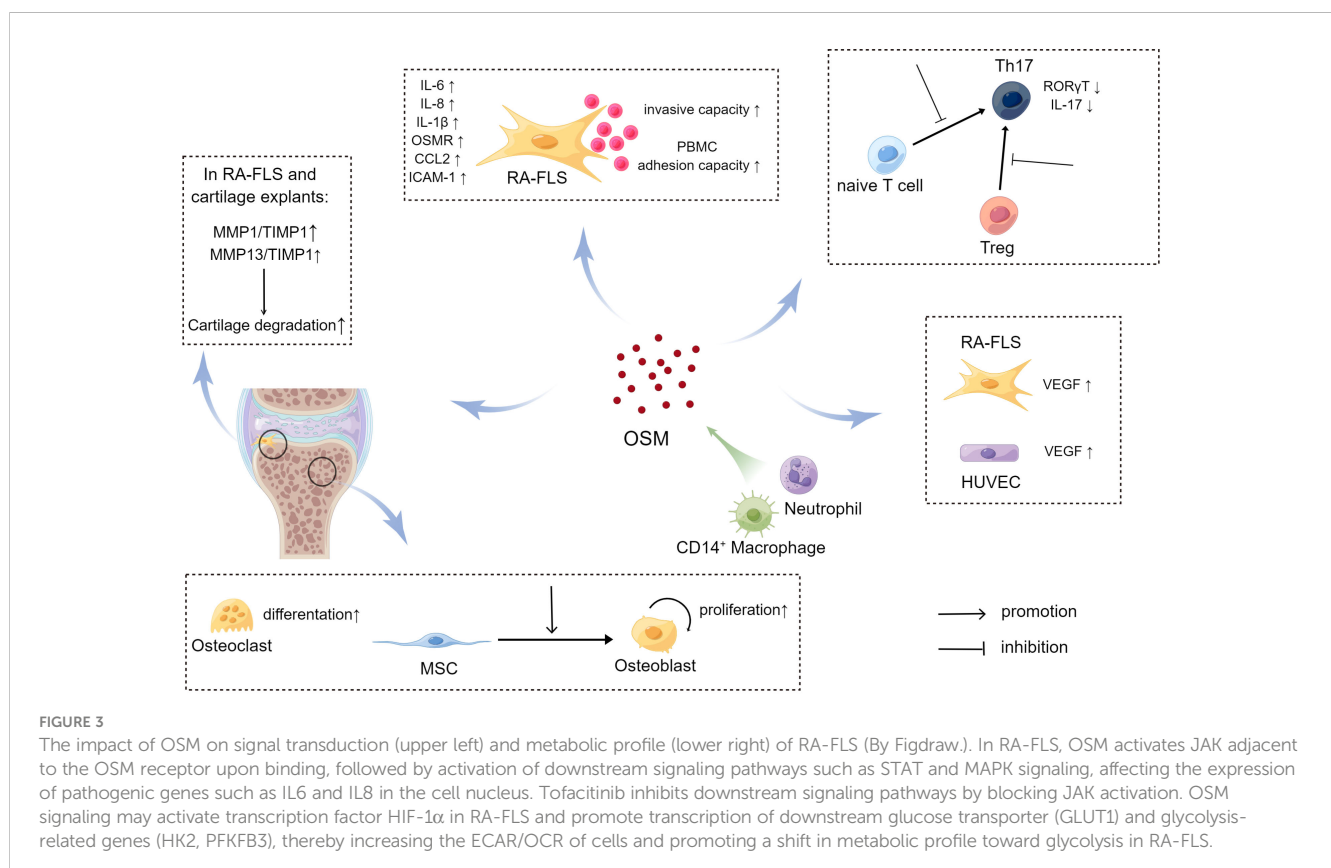
6 The clinical correlation of OSM signaling with RA

Hui et al. first investigated the levels of OSM in synovial fluid from RA patients and found that OSM was detected in 18 out of 20 RA samples, while it was not detected in 10 osteoarthritis (OA) samples used as controls. Additionally, they observed a positive correlation between OSM levels and synovial fluid white blood cell counts (57). Similarly, Cawston et al. detected elevated OSM levels only in RA patients but not in OA or healthy control samples (58). Manicourt et al. later reported a positive correlation between OSM levels in synovial fluid from RA patients and the levels of pro-inflammatory cytokines IL-6 and TNF- α , with a larger sample size

(59). OSM in the joint cavity of RA patients could be derived from macrophages and neutrophils. Cawston et al. confirmed that CD14⁺ macrophages were the primary source of OSM in synovial tissue from RA patients using immunohistochemistry (58). Cross et al. found that neutrophils from peripheral blood of RA patients rapidly expressed and released OSM upon stimulation with granulocyte-macrophage colony-stimulating factor (GM-CSF), while neutrophils from synovial fluid did not respond to GM-CSF stimulation (18). Considering that OSM is a secreted protein, neutrophils in synovial fluid from RA patients may have already released a significant amount of OSM in the joint cavity. Furthermore, genomic studies have shown that the T allele of the OSMR gene promoter region (rs22922016 locus) has a protective effect on RA patients (54). These findings suggest a close relationship between the OSM signaling pathway and the development of RA.

7 Potential effects of OSM signaling on the pathogenesis of RA

As previously mentioned, evidence from both tissue and blood samples of RA patients suggests that OSM may be involved in the pathogenesis of RA. In fact, OSM is not just a bystander in the pathogenesis of RA, but it also participates in regulating RA development through various mechanisms (Figure 3). The following section will focus on elucidating the molecular biological mechanisms through which OSM may impact RA.



7.1 The impact of OSM signaling on RA-FLS

The synovium is a connective tissue that attaches to the surrounding cartilage of the joint and is an essential component of the joint. The synovium not only provides direct physical connections to the musculoskeletal system but also reduces friction between joints by secreting synovial fluid, provides nutrition to other tissues within the joint, and is critical for maintaining normal physiological function (60). Histologically, the human synovium can be divided into two layers: the synovial lining layer near the joint cavity and the sublining layer beneath the lining layer. Under normal conditions, the synovial lining layer consists of only 2-3 cell layers, mainly composed of synovial macrophages (SMs) and FLSs. Synovitis is one of the major pathological changes in RA, and FLSs play a key role in the pathogenesis of RA synovitis (61). After being stimulated by a series of pro-inflammatory cytokines, such as TNF- α , in the joints of RA patients, RA-FLS continue to produce inflammatory factors to maintain chronic inflammation in the synovium, while also proliferating, migrating, and invading to destroy joint cartilage tissue (62, 63).

Studies have shown that OSM can affect RA-FLS through multiple pathways. Migita et al. found *in vitro* that OSM treatment promoted JAK/STAT pathway activation by inducing JAK and STAT phosphorylation in RA-FLS, and also induced RA-

FLS to secrete the pro-inflammatory cytokine IL-6 by activating the MAPK pathway (64). The JAK inhibitor tofacitinib was able to inhibit the aforementioned changes induced by OSM. A more in-depth study by Hanlon et al. found that OSM treatment not only promoted RA-FLS to secrete IL-6, but also promoted RA-FLS to secrete the pro-inflammatory cytokines IL-8, chemokine C-C Motif Chemokine Ligand 2 (CCL2), and adhesion molecule ICAM-1 (65, 66). Using mouse FLS, Goff et al. demonstrated that OSM can synergistically enhance the expression of IL-6 with other pro-inflammatory cytokines, such as TNF- α and IL-1 β (67). Furthermore, OSM treatment increased the expression of OSMR and IL-1 β receptors (IL-1 β R) in human RA-FLS and wild-type mouse FLS, which further activated the inflammatory signaling pathway in FLS through positive feedback. Therefore, OSM stimulation of RA-FLS by inducing the secretion of a series of pro-inflammatory cytokines and chemokines aggravates synovitis and angiogenesis in RA (Figure 4). In addition to inducing RA-FLS to secrete cytokines and their receptors, OSM also increases the invasive ability of RA-FLS and the adhesion of peripheral blood mononuclear cells (PBMCs) to RA-FLS (65).

Interestingly, OSM also causes changes in the metabolic pathways of RA-FLS, known as metabolic reprogramming (Figure 4). Oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) are metrics used to measure mitochondrial respiration and glycolysis, respectively. After OSM treatment, the ECAR/OCR ratio in RA-FLS

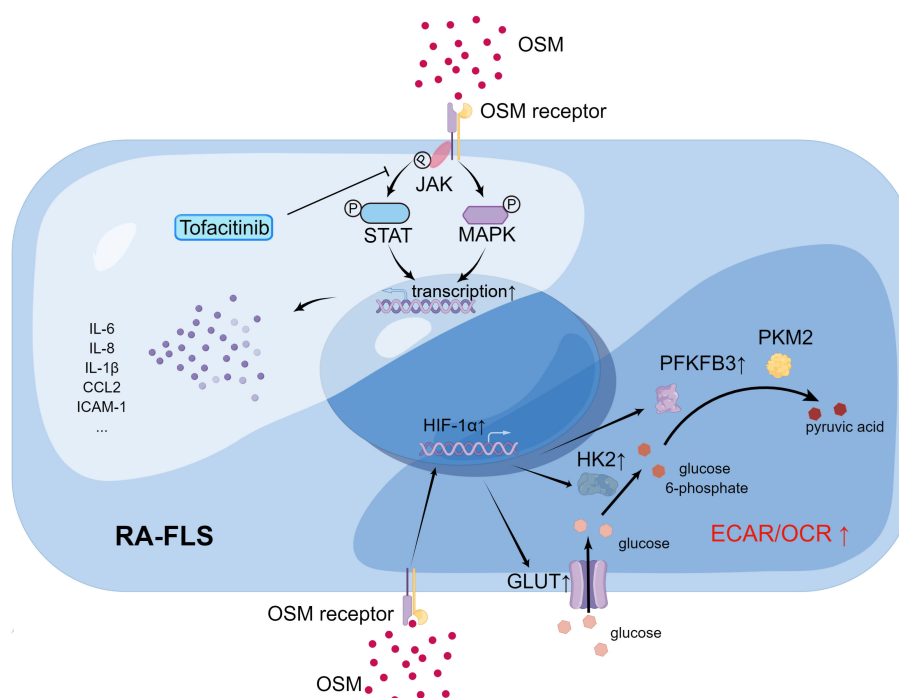


FIGURE 4

The source and pathogenic role of OSM in rheumatoid arthritis (RA) joints (By Figdraw.). In RA joints, CD14⁺ macrophages and neutrophils are potential major sources of Oncostatin M (OSM), which plays a regulatory role in RA-FLS, bone and cartilage, pannus formation, and T cell differentiation. Through these pathways, OSM may impact the development of RA. In the case of RA-FLS, OSM promotes secretion of relevant cytokines, increases the invasive ability of RA-FLS, and enhances adhesion of RA-FLS and PBMC to promote joint damage. OSM also affects bone and cartilage metabolism. For instance, OSM enhances differentiation of MSC to osteoblasts, promotes the proliferation of osteoblasts, and stimulates the differentiation of osteoclasts. Additionally, OSM increases the secretion of MMPs, which further enhances cartilage degradation. OSM inhibits the differentiation of naive T cells to Th17 cells by suppressing the expression of ROR γ T. It also reduces the conversion of Treg to Th17 and decreases the secretion of IL17 from Th17 cells. Moreover, OSM promotes the secretion of VEGF, which facilitates formation of pannus.

cells increased, and OSM induced the expression of glucose transporters (GLUT)-1, hexokinase 2 (HK2), 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), and hypoxia-inducible factor (HIF)-1 α in RA-FLS, indicating that OSM promotes glycolytic metabolism in RA-FLS (65). It is worth noting that most tumor cells also rely on glycolysis to produce energy, and glycolysis-related metabolic intermediates promote the invasion and metastasis of tumor cells (68). As mentioned earlier, OSM treatment also enhances the invasive ability of RA-FLS, which is similar to tumor cells. Therefore, OSM is likely to enhance the intra-articular invasive ability of RA-FLS by promoting glycolytic metabolism in RA-FLS.

7.2 OSM signaling and bone homeostasis and cartilage metabolism

Under normal circumstances, a balance between osteoblast-mediated bone formation and osteoclast-mediated bone resorption maintains bone homeostasis. However, in patients with rheumatoid arthritis (RA), increased osteoclast generation and activity, as well as suppressed osteoblast-mediated bone formation, disrupts the normal bone homeostasis, leading to bone and cartilage destruction and bone loss (69). OSM has biological functions that regulate bone metabolism, which can be seen in its regulation of mesenchymal stem cell osteogenic differentiation and its modulation of osteoblast and osteoclast-mediated bone formation and resorption.

Studies have found that OSM is capable of promoting mesenchymal stem cell differentiation into osteoblasts. It has been shown that treatment with OSM can activate JAK, MAPK and other signaling molecules, promoting osteogenic differentiation of human or mouse adipose-derived mesenchymal stem cells (70, 71). Similarly, in mouse fibroblast cell line C3H10T1/2, OSM treatment can induce osteogenic differentiation and promote terminal calcium deposition and mineralized nodule formation (72). Synovial-derived mesenchymal stem cells (SMSCs) in synovial fluid also have the potential to differentiate into osteoblasts, and studies have attempted to induce SMSCs to differentiate in a directed manner for the treatment of joint bone defects (73). Therefore, it is reasonable to assume that higher levels of OSM in RA joints can promote osteogenic differentiation of SMSCs.

OSM also has the ability to promote the proliferation and osteogenic differentiation of osteoblasts. OSM can promote osteogenic differentiation of mouse embryo osteoblast precursor cells MC3T3-E1 by regulating CCL2 (74). Additionally, OSM can promote osteoclast differentiation. Studies have found that OSM, in combination with pro-inflammatory cytokines TNF- α or IL-1 β , can activate the RANKL-RANK signaling pathway and significantly increase the number of TRAP-positive cells (i.e. osteoclasts) in mouse joints (75).

The aforementioned studies collectively indicate that OSM has a promoting effect on both bone formation and bone resorption. Therefore, *in vivo* studies exploring the comprehensive effects of OSM on bone formation and resorption are necessary. Previous studies have found that injection of OSM into mice with tibial injury can induce intra-membrane bone formation, suggesting that

OSM promotes bone formation in mice (76). However, in a mouse model of arthritis, adenoviral overexpression of joint OSM promotes bone erosion, suggesting that excessive OSM can also contribute to pathological bone destruction (8, 75). Taken together, these two studies suggest that OSM may overall promote bone destruction in the inflammatory environment of arthritis.

Joint damage in RA patients is also closely related to cartilage destruction. High levels of MMPs in the joint cavity of RA patients can degrade the extracellular matrix and absorb cartilage, thereby promoting joint destruction (77). OSM can also regulate cartilage metabolism. Collagen fibers and proteoglycans are the main structural substances of joint cartilage. Clinical studies have found a positive correlation between OSM levels in the synovial fluid of RA patients and the levels of antigenic keratan sulfate (Ag KS) and D-pyridinoline (D-Pyr), suggesting that OSM may promote the degradation of proteoglycans and collagen in joint cartilage of RA patients (59). *In vitro* experiments have shown that OSM treatment of pig joint cartilage explants increases the release of proteoglycans while inhibiting synthesis (78). MMPs can degrade cartilage by cleaving collagen. Using co-cultures of RA-FLS and normal human joint cartilage explants, Fearon et al. found that OSM treatment increased the levels of MMP1 and the MMP inhibitor TIMP1, both of which can degrade the extracellular matrix (79). However, the ratio of MMP1 to TIMP1 increased after OSM treatment, and compared to the use of a single cytokine, the combined use of OSM and IL-1 β significantly increased the ratio of MMP1 to TIMP1 and MMP13 to TIMP1. These results suggest that in an inflammatory environment, OSM can promote cartilage degradation.

7.3 OSM signaling and pannus formation

Pannus formation is another major pathological change in RA. As synovitis progresses in RA patients, a large number of immune cells infiltrate, the synovial lining layer proliferates and transforms into pannus, extending and adhering to cartilage, promoting the degradation of cartilage and bone tissue (80). Pannus consists of neovascularization, proliferating synovial cells, immune cells, and fibrinoid deposits, and angiogenesis mediated by cell factors such as VEGF is one of the important factors in angiogenesis formation (81, 82). Hanlon et al. found that OSM treatment not only promotes RA-FLS and human umbilical vein endothelial cells to secrete pro-inflammatory cytokines such as IL-6 and CCL2, but also promotes the expression of VEGF (65). Furthermore, OSM and IL-1 β combined treatment significantly upregulated the levels of VEGF in the co-culture supernatant of RA-FLS and normal human joint cartilage explants (79). Therefore, it can be seen that OSM can enhance angiogenesis by promoting the expression of VEGF, thus exacerbating the formation of angiogenesis in synovial tissue of RA.

7.4 OSM signaling and CD4⁺ T cells

The imbalance of CD4⁺ T cell subsets also plays a significant role in the pathogenesis of RA. Among the various CD4⁺ T cell

subsets, the imbalance between the pro-inflammatory Th17 subset and the immunosuppressive regulatory T (Treg) subset is closely related to the development and progression of RA. Currently, there are not many studies on the effects of OSM on CD4⁺ T cell differentiation and function. One study found that OSM treatment inhibited the differentiation of CD4⁺ T cells from mouse spleen into Th17 cells, suppressed Th17-related cytokine IL-17, and the Th17-specific transcription factor retinoic acid-related orphan receptor γ t (ROR γ t) expression (39). Further research found that OSM inhibited CD4⁺ T cell differentiation into Th17 cells by activating STAT3, STAT5, and suppressor of cytokine signaling (SOCS) 3 signaling in a dose-dependent manner. In addition, OSM also inhibited the proliferation of Th17 cells and the conversion of Treg cells into Th17 cells. Similarly, Shirshv et al. found that combined treatment with sex hormones and OSM increased the ratio of Treg cells in CD4⁺ T cells derived from PBMCs, which helps to maintain pregnancy-related immune tolerance (83).

From the perspective of the effect of OSM on CD4⁺ T cell subset differentiation, OSM can alleviate RA inflammatory responses. However, this contradicts many clinical studies and animal experiments. Considering that OSM is a pleiotropic cytokine, we speculate that although OSM inhibits Th17 cell differentiation, it also has the effect of promoting the secretion of inflammatory cytokines, promoting bone destruction and angiogenesis in RA. Overall, OSM still promotes the pathogenesis of RA.

8 The OSM signaling pathway in arthritis animal models

The aforementioned studies suggest that OSM is a pleiotropic cytokine, thus it is necessary to examine its overall regulatory effect in animal models of arthritis. Currently, most studies on animal models of arthritis suggest that OSM promotes the onset and progression of arthritis. In mice with collagen-induced arthritis (CIA), the mRNA levels of OSM in joint tissues are elevated, and the severity of arthritis and histopathological changes can be improved by neutralizing OSM with antibodies (84). In mice with pristane-induced arthritis (PIA), preemptive OSM neutralization with antibodies can prevent the onset of arthritis symptoms (84). Local overexpression of OSM in mouse joints using adenoviral vectors leads to synovial hyperplasia, mononuclear cell infiltration, and cartilage damage (85). In mice with antigen-induced arthritis (AIA), the expression levels of OSM and its type I and II receptors are elevated (67). In a rat model of peptidoglycan-polysaccharide (PGPS)-induced arthritis, OSM levels in the synovial membrane are higher than those in the control group, and the levels of OSM in the knee joints of rats are positively correlated with the Krenn score (used to evaluate synovitis histopathology) and the Mankin score (used to evaluate cartilage damage) (86). However, some studies have also shown that OSM can improve joint lesions in animal models of arthritis. Wahl et al. used four different monoclonal antibodies against collagen and LPS to construct a mouse model of

arthritis and found that the mice in the arthritis group exhibited joint pathology changes such as angiogenesis, cartilage and bone erosion, while the joint pathology changes in the OSM-treated group were minimal (46). This result is obviously contradictory to other relevant studies. However, it is worth noting that Wahl et al. used human OSM in their study, which cannot bind to mouse OSMR and activate downstream signaling pathways, but can bind to receptors such as LIFR in mice and exert anti-inflammatory effects (9, 29).

9 Research on targeted OSM signaling therapy for patients with RA

There have been studies attempting to treat RA patients by antagonizing OSM signaling. Choy et al. attempted to construct a humanized monoclonal antibody against OSM (GSK315234) and conducted a Phase II clinical trial to test its efficacy for treating RA patients (87). The results showed that RA patients had good tolerance to GSK315234, and common adverse events included aggravation of RA, elevated alanine aminotransferase, fever, headache, hypertension, and diarrhea, but no one withdrew from the study due to adverse events. However, the therapeutic effect of GSK315234 on RA was not very satisfactory. In the multi-dose, intravenous infusion trial, GSK315234 improved the disease activity score using 28 joint counts (DAS28) in RA; in the single-dose, intravenous infusion control trial, there was no difference in DAS28 between the treatment group and the placebo group; in the single-dose, subcutaneous injection trial, there was a statistically significant difference in DAS28 between the treatment group and the placebo group. In all three clinical trials, there was no statistically significant difference in erythrocyte sedimentation rate or C-reactive protein between the treatment group and the placebo group. Pharmacokinetic and pharmacodynamic analyses revealed that the low affinity of GSK315234 for OSM may be the main reason for its unsatisfactory therapeutic effect on RA.

Besides GSK315234, there are other monoclonal antibodies targeting the OSM signaling pathway. GSK2330811, another anti-OSM monoclonal antibody, has demonstrated sufficient affinity and good tolerability in healthy individuals and has been explored for the treatment of SSc and Crohn's disease (88). In a completed multicenter, randomized, double-blind, placebo-controlled clinical trial, GSK2330811 was administered at doses of 100 mg or 300 mg weekly for 12 weeks in the treatment of SSc. However, the trial found that changes in inflammation or fibrosis biomarkers in SSc subjects following GSK2330811 treatment were not ideal. Additionally, GSK2330811 led to dose-dependent decreases in hemoglobin or platelet counts in 39% and 26% of the subjects, respectively. Overall, GSK2330811 does not appear to be an ideal choice for treating SSc. Another multicenter, randomized clinical trial (NCT04151225), which aimed to use GSK2330811 for the treatment of Crohn's disease, has been canceled by the sponsor due to a potentially narrow therapeutic window, and no relevant study data have been disclosed.

There are also studies attempting to target OSMR (OSM receptor β subunit) for the development of monoclonal antibodies to treat related diseases. Vixarelimab, also known as KPL-716, is a monoclonal antibody developed against OSMR. It has shown significant reduction in skin itchiness and improvement in quality of life caused by prurigo nodularis in clinical trials (89). Vixarelimab also demonstrated notable improvements in excessive skin keratinization and nodules in prurigo nodularis subjects. Furthermore, compared to the placebo group, the vixarelimab-treated group did not exhibit an increased incidence of overall infections, immune reactions, liver function abnormalities, hematological changes, malignancies, injection site reactions, or drug-related adverse events related to cardiac toxicity. However, the vixarelimab-treated group had a higher incidence of upper respiratory tract infections. Overall, vixarelimab, targeting OSMR, has shown significant efficacy and relatively sufficient drug safety for the treatment of prurigo nodularis, making it a potential emerging therapy for this condition. The relevant information of existing monoclonal antibodies targeting OSM has been summarized in Table 1.

It is worth mentioning that researchers are also developing small molecule drugs targeting OSM and OSMR. SMI-10B is a small molecule drug predicted through screening to target the OSM signaling pathway (90). The drug developers claim that further experiments have shown that this small molecule can significantly reduce OSM-induced STAT3 phosphorylation in cancer cells. Recently, additional unbiased molecular dynamics studies have revealed that SMI-10B can spontaneously bind to OSM (91). Compared to monoclonal antibodies, small molecule inhibitors, as clinical drugs, generally exhibit lower toxicity and antigenicity, as well as better patient compliance when administered orally. Therefore, it is promising to expect the use of small molecule inhibitors targeting the OSM signaling pathway in RA or other related diseases, although further clinical trials are needed to evaluate their therapeutic efficacy.

10 Conclusions

OSM, a secreted cytokine, can regulate JAK/STAT, RAS/MAPK, JNK/p38 MAPK, and PI3K/AKT signaling pathways.

TABLE 1 Monoclonal antibody drugs targeting Oncostatin M signaling.

Name	Target	Diseases	National Clinical Trial number
GSK315234	OSM	rheumatoid arthritis	NCT00674635
GSK2330811		systemic sclerosis	NCT03041025
		Crohn's disease	NCT04151225
Vixarelimab/ KPL-716	OSMR	prurigo nodularis	NCT03816891

OSM, Oncostatin M; OSMR, Oncostatin M receptor β subunit.

OSM can regulate physiological processes such as cell proliferation, inflammation, immune response, and hematopoiesis, and is associated with the pathogenesis of various diseases. In RA patients, the gene polymorphism of OSMR is related to disease activity, and OSM levels in synovial fluid and synovium are higher than those in healthy controls. Existing research indicates that OSM mainly affects the occurrence and development of RA by promoting the secretion of pro-inflammatory cytokines and chemokines by RA-FLS, enhancing the invasive ability of RA-FLS, promoting the adhesion of other immune cells to RA-FLS, regulating bone formation and bone destruction in RA joints, promoting angiogenesis, and regulating the differentiation of CD4⁺ T cells. Although OSM has pleiotropic effects, considering clinical studies and animal models of arthritis, it is clear that OSM overall promotes the occurrence and development of RA.

However, it should be noted that the binding of OSM to its receptor has species specificity, which has affected some previous related studies. Currently, research on RA still cannot avoid animal models of arthritis, and the issue of OSM species specificity will be difficult to avoid in the future. Therefore, future researchers should provide detailed information on the species of the reagents used in experiments, and the interpretation of research results should also consider the species specificity of OSM.

Although the clinical study of the anti-OSM monoclonal antibody GSK315234 for treating RA patients did not achieve good results, this is related to the low affinity of GSK315234 for OSM. Future clinical trial research should learn from this lesson and develop anti-OSM antibodies and small molecule inhibitors with high affinity for use in clinical trials to better explore the potential of antagonizing OSM signaling for treating RA and provide new tools for clinical drug treatment of RA.

Author contributions

LH: Data curation, Investigation, Writing – original draft. JY: Investigation, Visualization, Writing – review & editing. TL: Investigation, Visualization, Writing – review & editing. WL: Investigation, Writing – review & editing. YaH: Writing – review & editing, Funding acquisition. PS: Writing – review & editing, Funding acquisition. XB: Writing – review & editing. YiH: Writing – review & editing, Funding acquisition. KQ: Writing – review & editing, Funding acquisition. YG: Visualization, Writing – review & editing. HW: Visualization, Writing – review & editing. KZ: Visualization, Writing – review & editing. YL: Writing – review & editing. YW: Writing – review & editing. ZC: Writing – review & editing, Funding acquisition. ST: Supervision, Writing – review & editing, Funding acquisition.

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GPR35 acts a dual role and therapeutic target in inflammation

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GPR35 is a G protein-coupled receptor with notable involvement in modulating inflammatory responses. Although the precise role of GPR35 in inflammation is not yet fully understood, studies have suggested that it may have both pro- and anti-inflammatory effects depending on the specific cellular environment. Some studies have shown that GPR35 activation can stimulate the production of pro-inflammatory cytokines and facilitate the movement of immune cells towards inflammatory tissues or infected areas. Conversely, other investigations have suggested that GPR35 may possess anti-inflammatory properties in the gastrointestinal tract, liver and certain other tissues by curbing the generation of inflammatory mediators and endorsing the differentiation of regulatory T cells. The intricate role of GPR35 in inflammation underscores the requirement for more in-depth research to thoroughly comprehend its functional mechanisms and its potential significance as a therapeutic target for inflammatory diseases. The purpose of this review is to concurrently investigate the pro-inflammatory and anti-inflammatory roles of GPR35, thus illuminating both facets of this complex issue.

KEYWORDS

GPR35, pro-inflammatory, anti-inflammatory, inflammatory diseases, therapeutic target

Introduction

Inflammation is a multifaceted physiological reaction that serves a critical role in the immune response against infection, tissue injury, and other provocations. It orchestrates a series of cellular and molecular activities with the ultimate goals of eradicating pathogens, repairing damaged tissues, and reinstating homeostasis (1). However, a dysregulated or persistent inflammatory response can pave the way for numerous diseases, encompassing autoimmune disorders where the body mistakenly attacks its cells, chronic inflammatory conditions that endure over extended periods, and even cancer where abnormal cells

proliferate uncontrollably (2–4). The link between inflammation and such diverse diseases underscores the importance of understanding and effectively managing inflammation.

G protein-coupled receptors (GPCRs) constitute a vast family of cell surface receptors that fundamentally mediate cellular responses to a myriad of stimuli, including inflammatory (5, 6). Among these receptors, GPR35 has recently drawn considerable interest due to its suspected role in inflammatory processes. Discovered in 1998, GPR35 is highly expressed in the intestine and various immune cells. Owing to its wide expression and the significance of its function, it is perceived as a prospective therapeutic target for various diseases (7–9).

The involvement of GPR35 in inflammation is complex and context-dependent, demonstrating both pro-inflammatory and anti-inflammatory effects in disparate cellular and tissue settings. GPR35 has been implicated in modulating an array of inflammatory responses, including the activation of immune cells, production of cytokines, and chemotactic movements (10–12). It interacts with several signaling pathways, such as MAPK, NF- κ B and others, thereby modulating inflammatory signaling dynamics. Furthermore, the functionality of GPR35 can be influenced by various ligands, ranging from endogenous metabolites to synthetic compounds, thus impacting its downstream effects in the inflammation process (13). Through these complex interactions and functions, GPR35 illustrates the multifactorial nature of inflammation and the intricate molecular dance that enables the body to respond appropriately to internal and external stressors. Yet, it also underscores the delicate balance that must be maintained, as dysregulated signaling via pathways involving GPR35 could potentially lead to pathological inflammation, underscoring the need for further research to elucidate its precise role and regulatory mechanisms.

In this comprehensive review, we explored the current understanding of GPR35, with a particular focus on its role in inflammation. We began by presenting a detailed overview of GPR35, discussing aspects such as its expression pattern, signaling mechanisms, and the variety of ligands it interacts with. From there, we investigated the pro-inflammatory role of GPR35, and its activation influences the immune response, including the impact on immune cell activation, cytokine production, and chemotactic activity within various immune cells such as neutrophils, macrophages, and invariant natural killer T (iNKT) cells. Subsequently, we discussed an in-depth examination of the anti-inflammatory role of GPR35 and covered aspects such as its impact on immune cell signaling, cytokine generation, and the resolution of inflammation. In addition, we explored the intricate signaling pathways and mechanisms underpinning the pro-inflammatory and anti-inflammatory effects that are triggered following GPR35 activation. This comprehensive exploration will serve as a map guiding us through the complicated roles of GPR35 in inflammation, shedding light on its significance and potential therapeutic value.

Expression pattern of GPR35

GPR35 is classified as a class A orphan GPCR comprising nearly 85% of all GPCRs. GPCRs play a pivotal role in metabolite sensing within the intestine, acting as a significant connector linking the microbiota, immune system, and intestinal epithelium (14).

Most GPCRs are predicted to be responsible for encoding olfactory receptors, while the rest are divided between receptors that bind with recognized endogenous compounds and those termed as orphan receptors because their specific endogenous activators remain unidentified (15).

Despite various endogenous ligands of GPR35, a definitive endogenous activator has not yet been firmly established, which maintains its status as an orphan receptor (13). Human GPR35 gene is transcribed and translated into three distinct variants (16). Both variants 2 and 3 encode the longer isoform GPR35b, which diverges from GPR35a by possessing an extended N-terminal sequence of 31 additional amino acids, thereby lengthening its extracellular domain. Despite this distinction, the subsequent sequences of the two isoforms are identical. mRNA expression of GPR35a and GPR35b have been identified in human tissues. Notably, GPR35b, which is highly expressed in gastric and colon cancer tissues, may have associations with carcinogenesis (17). Intriguingly, GPR35b demonstrates a lower agonist response efficacy than GPR35a (18). It was reported that the elongated N-terminus of the longer isoform may constrain G protein activation while boosting the interaction with β -arrestin (19).

GPR35 expression pattern suggests its pivotal role in immune responses and inflammation. GPR35 expression is particularly prominent in the small intestine and colon, with moderate but noticeable expression in the stomach, liver, spleen, kidney, and sympathetic neurons (20, 21). This widespread presence across various organ systems indicates its broad functionality within the body. Moreover, GPR35 expression is not limited to these organ systems. It also appears in various immune cells, including monocytes (CD14⁺), T-cells (CD3⁺), neutrophils, assorted dendritic cells, and invariant natural killer T cells (22–24), highlighting its integral role in immune responses. Among these, dendritic cells (CD103⁺/CD11b⁺) and macrophage clusters from the lamina propria and Peyer's patch cells in mouse small intestine are noted for their high expression of GPR35 (25).

Furthermore, there is a significant upregulation of GPR35 in neutrophils and intestinal tissues during the invasion of pathogenic microbes, as well as in mast cells during the stimulation of IgE antibodies, indicating a pronounced inflammatory response (21, 26, 27). Additionally, GPR35 presence in epithelial and endothelial cells, which are key participants in the inflammatory response (28), further underscores broad impact across numerous cell types and physiological processes. This ubiquitous distribution and varied presence underscore GPR35 potential as a major player in immune responses and inflammation. GPR35 presents the intriguing features with tissue specificity and different isoforms, taking into consideration when examining the potential of GPR35 as a therapeutic target for inflammation-related conditions.

GPR35 involved inflammation-related pathways

G proteins serve as the primary effector proteins for GPCRs. Typically, G proteins exist as a trimeric complex composed of α , β , and γ subunits. Upon activation of the GPCR, it binds to the G α

subunit and facilitates the exchange of GDP for GTP on $G\alpha$. This process leads to the disassociation of $G\alpha$ from the $G\beta\gamma$ dimer. Following this separation, both $G\alpha$ and $G\beta\gamma$ can independently initiate their respective signaling pathways (29).

Four principal $G\alpha$ protein families exist, and GPR35 has been found to couple predominantly with $G\alpha_{12/13}$ and $G\alpha_{i/o}$ proteins (7, 24, 30) (Figure 1A). $G\alpha_{i/o}$ protein interacts with adenylate cyclase (AC), inhibiting its activity and consequently reducing intracellular cAMP levels, resulting in the dampening of the MAPK/ERK pathway (31). Interestingly, ERK may serve as an anti-inflammatory signal, suppressing the production of NF- κ B dependent inflammatory factors through the inhibition of IKK activity (32). $G\beta\gamma$ dimer can activate phospholipase C beta (PLC β), which results in phosphoinositide generation and activation of the PI3K/AKT pathway. This leads to the activation of a host of downstream transcription factors, notably NF- κ B, a major player in the expression of genes encoding inflammatory factors (33). In the case of $G\alpha_{12/13}$, activation leads to Rho-mediated cytoskeleton reorganization, collaborating with $G\beta\gamma$ to regulate immune cell chemotaxis to inflammation sites - these actions primarily result in pro-inflammatory effects (34, 35). $G\alpha_q$ coupled with GPR35 directly inhibits the PI3K catalytic subunit and then suppresses Akt activation. Additionally, $G\alpha_q$ plays a role in the activation of ERK through the PLC β /Ca²⁺/Src signaling cascade (19, 36).

GPR35 has been demonstrated to directly engage with β -arrestin upon activation by agonists, leading to its internalization and desensitization (37). Beyond that, β -arrestins also function as signaling scaffolds, interacting with various pathways including the c-Jun N-terminal kinase, protein kinase B, and the extracellular signal-regulated kinase (ERK1/2) pathway in a G protein

independent manner, leading to anti-inflammatory effects (38–40). In addition, β -arrestins interact with I κ B α , leading to the suppression of NF- κ B activation (41). It is worth noting that there are certain ligands capable of activating GPR35 without facilitating the interaction between GPR35 and β -arrestin, such as kynurenic acid (19, 42), 5-HIAA (42) and DHICA analogues (43). Moreover, GPR35 interacts with the sodium-potassium pump (Na/K-ATPase), a vital regulator of cellular electrochemical gradients and Src family kinase signaling (44). This interaction enhances Na/K-ATPase pump function, aiding in the regulation of Ca²⁺ homeostasis. Also, Na/K-ATPase directly activates the kinase Src, leading to ERK activation in macrophages and enterocytes (45). Given that elevated cytoplasmic Ca²⁺ levels promote ERK and NF- κ B activation via PKC in inflammation, alterations in Ca²⁺ homeostasis have context-dependent impacts on inflammation (46, 47) (Figure 1B).

Furthermore, GPR35 has also been reported to modulate the production of reactive oxygen species (ROS), key mediators of inflammation. Under mechanical stress, GPR35 activation has been shown to enhance ROS production, and excessive ROS triggers further GPR35 expression (48). Conversely, GPR35 activation with Kynurenic acid in macrophages suppresses NLRP3 inflammasome activation and related inflammation by reducing mitochondrial damage and mitochondrial ROS production (49). These studies, despite showing divergent outcomes, reveal the significant role of GPR35 in modulating inflammation via ROS-mediated pathways.

In sum, a growing body of evidence proposes a sophisticated and intricate role of GPR35 in inflammation. It appears to exert both pro-inflammatory and anti-inflammatory influences, which depend on the type of cell, the specific signaling pathways, and the

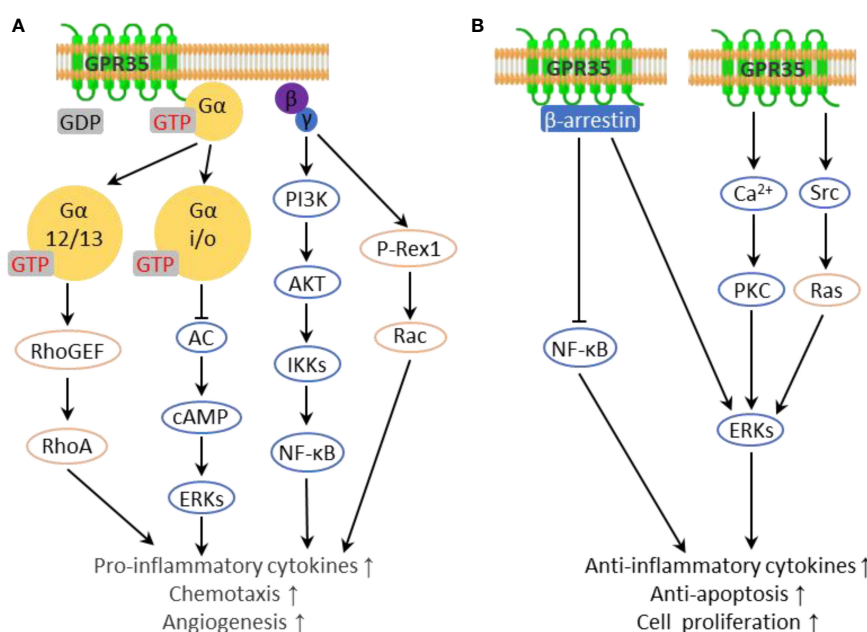


FIGURE 1

Inflammation-related downstream pathways of GPR35. (A) G proteins interacting with GPR35 transmit pro-inflammatory downstream pathways. (B) GPR35 transmits anti-inflammatory downstream pathways.

availability of ligands. The precise mechanisms through which GPR35 impacts inflammation-related pathways, however, remain somewhat elusive. Therefore, it necessitates additional research to comprehensively understand the subtleties of its signaling.

Primary ligands with activity at GPR35

A pivotal element influencing the activity of GPR35 are its ligands, otherwise referred to as agonists and antagonists. Agonists are molecules that initiate signaling by binding to the receptor, thereby triggering downstream cellular responses. Conversely, antagonists exert opposing effects. Furthermore, the activation of receptors is not always fully “on or off” scenario while some agonists can activate the corresponding receptors in a biased manner. For instance, in the case of the kynurenic acid/GPR35 axis, while kynurenic acid triggers the activation of G proteins downstream of GPR35, it scarcely facilitates the interaction between GPR35 and β -arrestin (42, 43).

There are multiple single nucleotide polymorphisms (SNPs) located within the GPR35 gene linked with various immune and inflammation-related diseases, such as inflammatory bowel diseases, ankylosing spondylitis, and primary sclerosing cholangitis (9). One of the most prevalent variants, rs3749171, induces the replacement of a threonine with methionine in transmembrane domain III (T108M), demonstrating a significant correlation with inflammatory bowel disease (50). Although most SNP-induced variations do not significantly affect the potency of agonist ligands, the V76M variant (rs13387859) does exhibit a reduction in agonist potency (51). While this variant is present at a 2% allele frequency, it has not been associated with any disease.

In recent years, a multitude of both endogenous and synthetic GPR35 ligands have been discovered, enriching our understanding of this involvement in inflammation and a host of other biological phenomena (Table 1).

Endogenous agonists

Kynurenic acid, a metabolite derived from tryptophan, is noted for its roles in the central nervous system, as well as anti-inflammatory property (73, 74). Its ability to activate GPR35 is significantly more potent in mice and rats compared to humans, where it requires 40- to 100-fold higher concentrations (20), occasionally failing to activate human GPR35 at high doses (27, 54). This species-selective aspect of the kynurenic acid/GPR35 axis has stirred discussion on whether this interaction is truly physiological, particularly in humans, leaving kynurenic acid as a potential endogenous ligand for GPR35 (7). Recently, it was demonstrated that pre-treatment with kynurenic acid mitigated the injuries sustained by both human iPS-cardiomyocytes and mouse cardiomyocytes following simulated ischemia/reperfusion (I/R) *ex vivo* (8). In mice, kynurenic acid stimulates the migration of CX3CR1⁺/GPR35⁺ macrophages in the small intestine, but not GPR35⁻ macrophages (75).

Lysophosphatidic acid (LPA), an active phospholipid derivative, is present in cell membranes and can be produced extracellularly to activate six known GPCRs including LPAR1-6 (76). It was displayed that the Ca²⁺ response triggered by 2-acyl LPA was significantly stronger in GPR35-expressed HEK293 cells compared to the response in the control cells, which pronounced difference was not observed when 1-acyl LPA was applied (54). GPR35 deficiency was found to inhibit LPA-induced Ca²⁺ signaling in bone marrow-derived macrophages (BMDMs). However, it was posited that GPR35 deficiency might compromise LPA signaling via other LPA receptors (45). Recently, GPR35 was affirmed as a potential LPA receptor linked to an inhibitory G protein (Gi) (27). However, there LPA failed to activate GPR35 in other experimental settings, which leaves the question open on whether LPA acts as an endogenous agonist for GPR35 (26, 77).

CXCL17, a homeostatic chemokine in mucosa, attracts dendritic cells and macrophages but can be expressed elsewhere during inflammation (78). It was reported that CXCL17 influenced GPR35 at nanomolar levels within a physiological range, unlike kynurenic acid (56). However, subsequent studies failed to show that CXCL17 induced migration or signaling responses in GPR35-expressing cells (79, 80). Further, the actions of CXCL17 in a neuropathic pain model in mice were decreased by kynurenic acid and zaprinast, suggesting the presence of a CXCL17 receptor other than GPR35 (81).

Recent findings indicate that 5-Hydroxyindoleacetic acid (5-HIAA), a metabolite of 5-hydroxytryptamine generated by activated platelets and extravascular mast cells, can act as an agonist for GPR35, promoting the recruitment of neutrophils (26) and the migration of eosinophils (82). Interestingly, this perspective offers fresh insight into the role GPR35 regulating pain sensations due to the association of 5-HIAA with pain and sensory neurons (83). Additionally, GPR35 plays a role in modulating cAMP production and inhibiting N-type Ca²⁺ channels in neurons and astrocytes, showcasing its potential involvement in pain management treatments (84). Moreover, other endogenous molecules such as 5,6-dihydroxyindole-2-carboxylic acid (DHICA), reverse T3 (3,3,5- triiodothyronine), and cyclic guanosine 3'-5' monophosphate (cGMP) have demonstrated a degree of activity towards GPR35, albeit with modest potency. However, these observations require further validation (40, 58).

Synthetic agonists

Zaprinast (2-(2-propyloxyphenyl) -8-azapurin-6-one), originally identified as a cGMP phosphodiesterase inhibitor, is one of the earliest discovered GPR35 ligands. Notably, the effects of Zaprinast on GPR35 can be separated from its cGMP phosphodiesterase inhibition properties with the intracellular calcium mobilization (59). With its moderate-to-high potency across human, mouse, and rat orthologs, Zaprinast has established its status as a go-to reference agonist for GPR35 research (30, 72). Its efficacy and wide applicability across different species have aided in comparative studies and offered

TABLE 1 A schematic representation of GPR35 ligands.

Name	Type	Potency (EC50)	Role in inflammation	References
Kynurenic acid	Metabolite of L-tryptophan	Human: 217 μ M Rat: 66 μ M	Anti-inflammatory	(52, 53)
LPA	Phospholipid derivative	Not reported	Pro-inflammatory	(54, 55)
5-HIAA	Serotonin metabolite	Not reported	Pro-inflammatory in Neutrophils	(26)
CXCL17	Endogenous peptide	Not reported	Anti-inflammatory	(56, 57)
cGMP	Cyclic nucleotide derived from GTP	Human: 131 μ M	No conclusion	(58)
DHICA	Intermediate in the biosynthesis of elanin	Human: 22 μ M	No conclusion	(40)
Reverse T3	Hormone produced in the thyroid gland	Human: 100 μ M	No conclusion	(40)
Zaprinast	Synthetic agonist	Human: 2-8 μ M Mouse: 1 μ M Rat: 100 nM	No conclusion	(59)
Pamoic acid	Synthetic agonist	Human: 30-50 nM Mouse: Inactive Rat: >100 μ M	Anti-inflammatory	(60, 61)
YE120	Synthetic agonist	Human: 30-35 nM	Anti-inflammatory	(62, 63)
Lodoxamide	Synthetic agonist	Human: 4 nM Rat: 13 nM	Allergic inhibition	(51)
Bufrolin	Synthetic agonist	Human: 13 nM Rat: 10 nM	Allergic inhibition	(51)
Compound 1	Synthetic agonist	Human: 26 nM Mouse: 17 μ M Rat: 8 μ M	No conclusion	(64)
PSB-13253	Synthetic agonist	Human: 12 nM Mouse: Inactive Rat: 1.4 μ M	No conclusion	(65)
Amoxanox	Synthetic agonist	Human: 4 μ M Rat: 23 nM	Mast cell stabilizer, anti-asthma and anti-allergy medication	(51)
Cromolyn disodium	Synthetic agonist	Not reported	Mast cell stabilizer, mitigate asthma	(21)
Nedocromil	Synthetic agonist	Human: 0.13 μ M Mouse: 7.3 μ M Rat: 2.7 μ M	Mast cell stabilizer, mitigate asthma	(21)
Doxantrazole	Synthetic agonist	Human: 3.4 μ M Rat: 300 nM	Mast cell stabilizer	(51)
Pemirolast	Synthetic agonist	Human: Inactive Rat: 95 nM	Mast cell stabilizer	(51)
Furosemide	Synthetic agonist	Human: 8.3 μ M	Anti-inflammatory	(66)
Tyrphostin-51	Synthetic agonist	Human: 8 μ M (DMR 120 nM)	No conclusion	(67)
2,3,5-THB	Synthetic agonist	Human: 8.4 μ M (DMR 250 nM)	No conclusion	(68)
Gallic acid	Synthetic agonist	Human: 11.4 μ M (DMR 1.16 μ M)	Anti-inflammatory	(69)
wedelolactone	Synthetic agonist	Human: 1.39 μ M (DMR 2.73 μ M)	Anti-inflammatory	(69)
Ellagic acid	Synthetic agonist	Human: 2.96 μ M (DMR 110 nM)	Anti-inflammatory	(69)

(Continued)

TABLE 1 Continued

Name	Type	Potency (EC50)	Role in inflammation	References
Aminosalicylate	Synthetic agonist	Not reported	Anti-inflammatory	(70)
Compound 50	Synthetic agonist	Human: 5.8 nM	No conclusion	(71)
CID2745687	Synthetic antagonist	Human (Ki): 10–20 nM	No conclusion	(60)
ML-145	Synthetic antagonist	Human (Ki): 25 nM	No conclusion	(72)

insights into the roles GPR35 plays in a myriad of biological processes.

Pamoic acid (5-nitro-2-(3-phenylpropylamino) benzoic acid) emerged as a potential GPR35 ligand following screening exercises within the Prestwick Chemical Library. However, its activity at rat and mouse orthologs of GPR35 is noticeably less potent compared to its interaction with the human version. This lower efficacy significantly impedes its usage in these preclinical studies (30, 60). Despite this limitation, the discovery of pamoic acid interaction with GPR35 has contributed to the expanding catalog of ligands and may potentially prompt further development of more effective analogs, thereby expanding our understanding of GPR35 physiological role.

YE120 (2-(3-cyano-5-(3,4-dichlorophenyl)-4,5-dimethylfuran-2(5H)-ylidene) malononitrile) is another compound that was identified as a GPR35 agonist through dynamic mass redistribution (DMR) assays performed in the native cell line HT-29. Remarkably, it has demonstrated superior potency compared to zaprinast (62). This discovery indicates the continuing progress in our understanding of GPR35, providing a new promising candidate for the functionality and potentially enabling the development of more effective therapeutic strategies targeting GPR35.

Lodoxamide, a widely used anti-inflammatory mast cell stabilizer, is another synthetic agonist that targets GPR35. Its application in the treatment of allergic keratoconjunctivitis attests to its significant role in modulating inflammatory responses. However, despite its high potency towards human and rat GPR35, the effectiveness of lodoxamide is notably diminished to for the mouse orthologue, with its potency being a 100-fold lower (51, 85). This highlights the importance of species-specific investigations in understanding the precise role of GPR35 and its ligands in mediating inflammatory responses. Recently, there was a significant development in understanding the structural attributes of GPR35 through its structure when bound to a GPR35 agonist lodoxamide, which shows a novel site for divalent cation coordination and a distinctive ionic regulatory mechanism. This helps understanding the affinity of GPR35 for other anti-asthma and anti-allergy agents, especially those featuring symmetric diacid structures like lodoxamide, providing a clear pathway for the binding process (86).

Aminosalicylates, a first-line treatment for inflammatory bowel diseases (IBDs), have shown activity on both human and mouse GPR35, although their exact target remains undefined. Of these, the pro-drug olsalazine exhibits the greatest potency in terms of GPR35 agonism, promoting ERK phosphorylation and the translocation of β -arrestin2. Notably, in a model of dextran sodium sulfate (DSS)-induced colitis, the protective effects of olsalazine on disease progression and its inhibitory effect on TNF α mRNA expression,

as well as the NF- κ B and JAK-STAT3 pathways, are significantly reduced in mice with GPR35 knockout, thus suggesting a critical role of GPR35 in these anti-inflammatory actions (70).

Recently, a group of 2H-chromen-2-one derivatives has been identified as agonists for GPR35 using dynamic mass redistribution assays in HT-29 cells. The compound 6-Bromo-7-hydroxy-8-nitro-3-(1H-tetrazol-5-yl)-2H-chromen-2-one (Compound 50) emerged as the most potent GPR35 agonist with an EC50 of 5.8 nM (71). In another development, GPR35 fluorescent probes were designed based on known GPR35 agonists. These serve as valuable tools for GPR35 research and for the discovery of new synthetic GPR35 agonists. The most promising compound from this series exhibited the highest binding potency, along with a minimal nonspecific Bioluminescence Resonance Energy Transfer (BRET) binding signal, with a Kd value of 3.9 nM (87).

Antagonists

CID2745687, known as methyl-5- [(tert-butylcarbamothioyl)hydrazinylidene)methyl] -1-(2,4- difluorophenyl)pyrazole-4-carboxylate, is a well-known antagonist of GPR35. It demonstrates the ability to obstruct the effects of the agonists pamoic acid and zaprinast in cells expressing either variant of human GPR35a or GPR35b. It is estimated that the inhibitor constant Ki is in the range of 10–20 nM, suggesting potential competitive function in a competitive manner (60). CID2745687 has a higher affinity for human GPR35 compared to its mouse and rat counterparts, limiting its application primarily to *in vitro* studies rather than rodent models (88). Another antagonist of GPR35 is ML-145, or 2-hydroxy-4- [4-(5Z)-5-[(E)-2-methyl-3- phenylprop-2-enylidene] -4-oxo-2-sulfanylidene-1,3- thiazolidin-3-yl] butanoylamino] benzoic acid. This compound also demonstrates high affinity for human GPR35 but shows appreciable affinity for the mouse and rat orthologues (72).

These antagonists and their specificity for the human GPR35 over rodent versions provide valuable insights into the diverse functionality and pharmacology of GPR35. They underline the challenges of studying GPR35 across different species but also offer opportunities for the development of novel therapeutic agents targeting the human GPR35 receptor.

Pro-inflammatory roles of GPR35

GPR35 activation has been demonstrated to induce a pro-inflammatory state within cells, leading to increased production

of pro-inflammatory cytokines and chemokines, which act as signal carriers, promoting the recruitment and activation of specific types of immune cells to the inflammation site (Figure 2). This process, in essence, highlights a crucial role of GPR35 in orchestrating immune responses, contributing to the exacerbation of inflammation, and potentially influencing the progression of various inflammatory conditions and diseases. There have been two diseases that are connected to the pro-inflammatory effects of GPR35. GPR35 plays a vital role in detecting bacteroides fragilis toxin and triggering an immune response in bacteroides fragilis toxin-induced colitis (89), and GPR35 loss in nucleus pulposus cells significantly reduces intervertebral disc degeneration typically triggered by inflammation induced by ROS or mechanical stress (49). In addition, encephalomyelitis (EAE) is worsened through the accumulation of GPR35⁺/Ly6C⁺ macrophages in the small intestine, while the blockage of KYNA-GPR35 signaling can alleviate EAE (75).

GPR35 plays a pro-inflammatory role in neutrophils

Neutrophils, the most populous immune cells in human blood, act as first responders in the face of tissue damage and pathogenic infections. The journey of neutrophils from blood vessels to target tissues is complex, traditionally classified into four stages: 1. The egress of neutrophils from bone marrow into the bloodstream. 2. A multi-step adhesion cascade resulting in the congregation of adherent neutrophils in microvessels. 3. Diapedesis of neutrophils across the vascular wall, granting access to the extravascular space. 4. Interstitial migration of neutrophils to their ultimate target sites

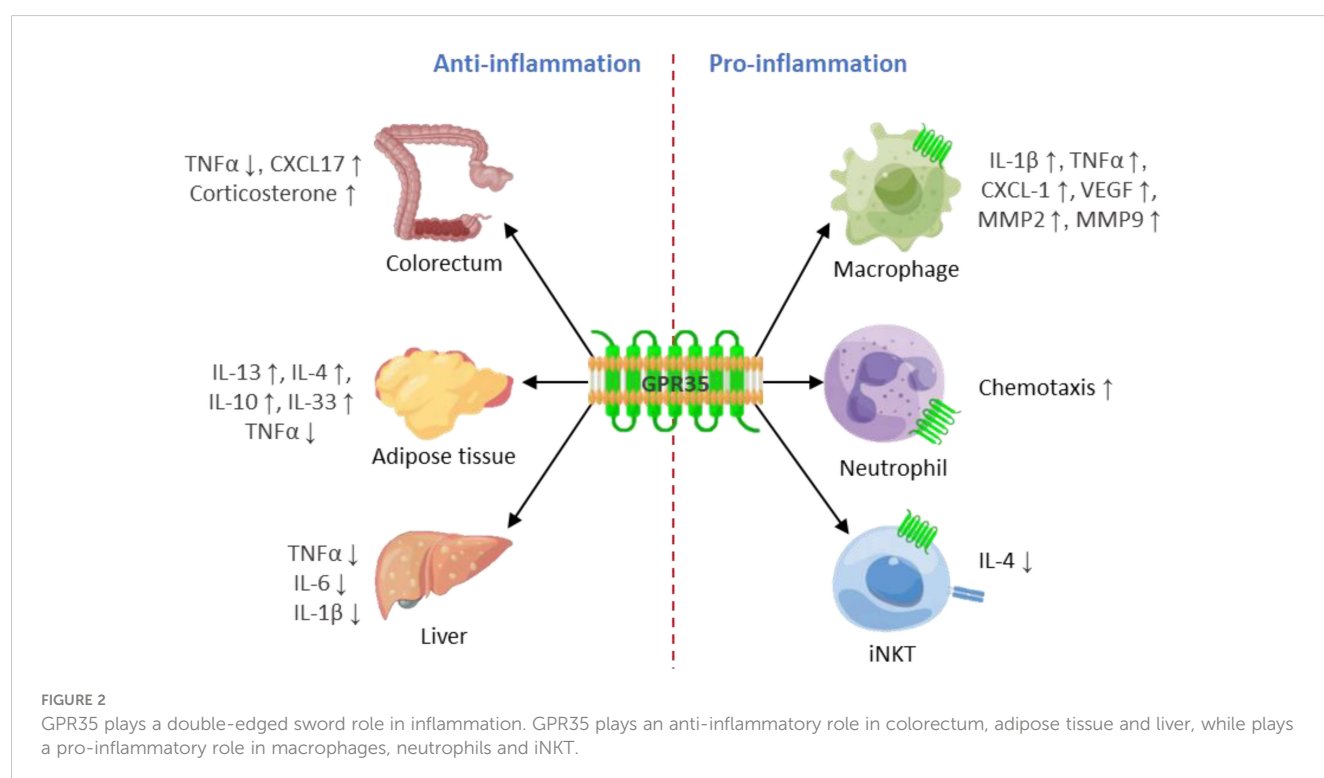
(90). Various small molecules and cytokines orchestrate these stages, resulting in a highly redundant regulatory system, which complicates the task of identifying dominant chemokines (91).

Interestingly, GPR35 expression is observed to be relatively low in inactive neutrophils, while it increases substantially in activated neutrophils, which aligns with the role of GPR35 in promoting neutrophil recruitment to inflammatory tissues (26). While GPR35 deficiency was found to somewhat dampen neutrophil adherence to blood vessel walls, this effect was not significantly observed in animal studies. Nevertheless, the role of GPR35 in neutrophil diapedesis has been identified as non-redundant (92). Moreover, 5-HIAA produced by activated platelets and extravascular mast cells, can activate GPR35 as an agonist, thus encouraging the recruitment of neutrophils (93).

In summary, through the complex interactions of these various mechanisms, GPR35 plays a significant role in promoting an inflammatory response in neutrophils by facilitating neutrophil recruitment, reinforcing its central role in the body response to inflammation.

GPR35 plays a pro-inflammatory role in macrophages

Macrophages are specialized cells derived from monocytes in the bloodstream, and they play crucial roles in identifying, engulfing, and destroying bacteria, thereby initiating inflammation. These activated macrophages are classified into two types based on their involvement in inflammation: pro-inflammatory (M1) and anti-inflammatory (M2). M1 macrophages secrete pro-inflammatory cytokines such as IL-1, IL-



6, TNF- α , as well as metalloproteinases MMP-2 and MMP-9, which help to reshape the extracellular matrix at inflammation sites. However, M2 macrophages produce IL-10, PDGF, IGF-1, TGF- β , and other cytokines that suppress inflammation and foster tissue repair (94–96).

In vitro experiments reveal that the absence of GPR35 does not influence the differentiation of macrophages into M1 and M2 subtypes. However, the level of secreted substances such as CXCL-1, VEGF, MMP2, and MMP9 is reduced in GPR35-deficient macrophages derived from mice with GPR35 deletion, specifically the LysM⁺ cells (44, 45). When observing macrophages in the colon, a notable difference in cytokine expression was seen between GPR35^{+/+} and GPR35^{-/-} macrophages. Proinflammatory cytokines like IL-1 and TNF were highly expressed in GPR35^{+/+} macrophages. Moreover, GPR35 was predominantly expressed in monocyte subgroups exhibiting high to medium levels of Ly6C in the intestine, with the level of intestinal TNF significantly dropping in GPR35^{-/-} macrophages (27). Ly6C⁺ macrophages, differentiated from monocytes expressing high to medium levels of Ly6C, are known to be pro-inflammatory (97).

Additionally, GPR35 deficiency hinders the adhesion of human peripheral monocytes induced by kynurenic acid (20). In contrast, the activation of GPR35 elevates the infiltration level of macrophages in gastric tissues (11). Taken together, it becomes evident that GPR35 contributes to the pro-inflammatory phenotype of macrophages.

GPR35 has pro-inflammatory function in iNKT cells

Human iNKT cells constitute a unique subset of T cells that feature an invariant alpha-beta T-cell receptor (TCR) along with numerous surface molecules characteristic of natural killer (NK) cells. These iNKT cells can become activated either directly through the engagement of the invariant TCR with glycolipid antigens and CD1d, or indirectly through activated antigen-presenting cell (98). Notably, iNKT cells are critical immunoregulatory components capable of rapid, abundant cytokine production, thus influencing the behavior of other immune cells (99). iNKT cells have been found to express GPR35 at high levels. Following receptor activation, GPR35 undergoes internalization within these iNKT cells. It has been observed that specific GPR35 agonists significantly decrease the release of Interleukin-4 (IL-4), but not Interferon gamma (IFN- γ) (22). IL-4 secretion by iNKT cells plays a crucial role in anti-inflammatory processes, such as M2 polarization of macrophages, the transition of monocytes (from Ly6C^{hi} to Ly6C^{lo}), and tissue repair, particularly in the liver (100–102). Thus, the activation of GPR35 in iNKT cells, which in turn reduces the release of IL-4, has the potential to stimulate inflammation.

Overall, it is increasingly apparent that GPR35 can play a pro-inflammatory role under certain circumstances. This is evidenced by the role of GPR35 in the stimulation of pro-inflammatory cytokines and chemokines production, the activation of inflammatory signaling pathways, and the amplification of pro-inflammatory responses in particular cell types. However, it is

crucial to emphasize that the pro-inflammatory effects of GPR35 may be modulated by various factors. These include the microenvironment in which the receptor operates, the existence of other receptor types and signaling pathways, as well as the specific cellular type expressing GPR35. Further in-depth research is required to unravel the underlying mechanisms and conclusively establish the exact role of GPR35 within the context of inflammation. The complexity of these dynamics underscores the intricate interplay of processes within our immune responses and the need for a comprehensive understanding of GPR35.

Anti-inflammatory role of GPR35

Although GPR35 is predominantly linked with pro-inflammatory actions across a range of immune cells, recent studies reveal its potential anti-inflammatory capabilities under certain circumstances. This perspective brings to light the anti-inflammatory roles of GPR35 (Figure 2), enriching our understanding of its part in maintaining immune homeostasis and potentially revealing novel therapeutic targets for treating various inflammatory conditions.

GPR35 displays an anti-inflammatory role, particularly in colonic inflammation. It is prominently expressed in the gastrointestinal tract, playing a pivotal role in regulating the healing process of gastrointestinal injuries. This means GPR35 can inhibit inflammation by maintaining gastrointestinal homeostasis. In fact, GPR35 demonstrates protective qualities in scenarios such as DSS-induced colitis (27, 63, 103). GPR35 agonists such as YE120, zaprinast, and pamoic acid have been shown to expedite wound repair in mouse colon epithelial cells by boosting cell migration through the augmentation of fibronectin expression and ERK phosphorylation (63). Interestingly, the recruitment of β -arrestin 2 and the activation of ERK1/2, mediated by pamoic acid, can be obstructed by the GPR35 antagonist CID2745687. The endogenous ligand of GPR35, 5-HIAA, has been recognized to mitigate the symptoms of ulcerative colitis, while the precise role of GPR35 was not delineated further (104). This insight suggests a potential therapeutic strategy, hinting that manipulating the activity of GPR35 could control the inflammatory response in colonic tissues (60).

GPR35 deficiency in intestinal epithelial cells leads to the reduction in both the number of goblet cells and the expression of Muc2, which occurs due to an increase in the pyroptosis of goblet cells (77). Pyroptosis is a form of cell death that contributes to inflammation, thus exacerbating inflammatory conditions. In consequence of this, the epithelial barrier is weakened, leading to increased susceptibility to infections such as those caused by *Citrobacter rodentium* (105, 106). In DSS-induced colitis mouse models, the specific deletion of GPR35 in macrophages resulted in elevated inflammation associated with a decrease in TNF production in macrophages (27). Although TNF is generally recognized for its pro-inflammatory role and is routinely targeted in treatments for IBD (107), it also serves an anti-inflammatory function. Specifically, it can induce the production of corticosterone in intestinal epithelial cells, a hormone that plays a key role in

mitigating inflammation. The interplay between GPR35 and TNF provides new insights into the mechanisms through which inflammation can be regulated and controlled in gastrointestinal disorders (108).

Recently, it was discovered that when GPR35 was eliminated in the liver of non-alcoholic fatty liver disease (NAFLD) mice, there was an increase in inflammatory cytokines such as TNF α , IL6, and IL1 β in the liver. This led to a worsening of hepatitis. However, the overexpression of GPR35 in the liver reversed these effects, hinting at its potential anti-inflammatory role in liver disease (109). Additionally, Kynurenic acid was found to improve energy metabolism and reduce inflammation in mice fed with a high-fat diet. However, TNF in adipose tissue increased in the absence of GPR35, and the anti-inflammatory effects of kynurenic acid were abolished via reducing anti-inflammatory cytokines such as IL-13, IL-4, IL-10, and IL-33 (74). This finding suggests that GPR35 might also exhibit anti-inflammatory effects in adipose tissue. Therefore, understanding the precise function of GPR35 could provide novel insights into inflammation in diseases like NAFLD and obesity. Interestingly, it is worth noting that kynurenic acid is recognized for its anti-inflammatory effects (74, 110, 111). However, kynurenic acid is known to interact with multiple receptors, not just GPR35, including α 7 nicotinic acetylcholine receptor (a7nAChR), the aryl hydrocarbon receptor (AhR), and ionotropic glutamate receptors (112). Therefore, it is challenging to discern the specific influence of GPR35 in the observed anti-inflammatory effects of kynurenic acid.

In various tissues, different types of cells contribute to the anti-inflammatory effects orchestrated by GPR35. In the colorectum, it mainly operates through epithelial cells and goblet cells to exert anti-inflammatory effects. While it is known that GPR35 also facilitates anti-inflammatory in both the adipose tissue and the liver, the specific cell types involved in these processes have yet to be identified. When looking at immune cells, it was highlighted that the activation of GPR35 with kynurenic acid in macrophages leads to the suppression of NLRP3 inflammasome activation, consequently reducing related inflammation (49). Moreover, it was revealed that GPR35, along with its platelet- and mast-cell-derived ligand 5-HIAA, facilitates eosinophils recruitment to the lungs infected with *Cryptococcus neoformans* and exacerbation of disease (82).

Overall, activation of GPR35 has been demonstrated to suppress the production of pro-inflammatory cytokines, stimulate the output of anti-inflammatory cytokines in a variety of tissues and organs, and fortify the integrity of the gut barrier. These findings highlight the multifaceted and context-dependent nature of GPR35 in inflammation. Nonetheless, a full understanding of the intricacies involved in GPR35 in counteracting anti-inflammatory demands further investigation.

Conclusion and discussion

GPR35 is a distinctive G protein-coupled receptor with a significant role in the regulation of inflammation, demonstrating both pro-inflammatory and anti-inflammatory properties. Its pro-

inflammatory effects have been witnessed in neutrophils, macrophages, and iNKT cells, while its anti-inflammatory attributes have been noted in varying contexts, including those in the colorectum, adipose tissue, and liver. Furthermore, GPR35 is increasingly recognized for its role in cancer and the related immune response. It facilitates angiogenesis within the tumor microenvironment, and GPR35 elimination in macrophages results in reduced immune cell infiltration in colon tumors (44). It was found that activating GPR35 in group 2 innate lymphoid cells fosters an immunosuppressive environment in lung cancer, thereby advancing the progression of lung cancer (113, 114). Consequently, GPR35 exhibits promising potential as a therapeutic target in cancer immunotherapy.

The question arises, “Could GPR35 be a potential target for treating inflammation-associated diseases?” The dual role of GPR35 in inflammation could have considerable consequences for devising therapeutic strategies centered on this receptor. For instance, the use of GPR35 agonists or antagonists could serve to regulate inflammatory responses in diverse diseases. In conditions characterized by excessive inflammation, such as IBD, inhibiting the pro-inflammatory actions of GPR35 could be advantageous. Conversely, in conditions requiring inflammation, such as wound healing or tissue repair, augmenting the anti-inflammatory effects of GPR35 activation may be beneficial. However, considering the intricate nature of GPR35 in inflammation, more comprehensive research is required to determine its exact impact and potential as a therapeutic target.

Currently, only two drugs targeting GPR35 have progressed to clinical trials. The first, Lodoxamide, has been employed for the treatment of allergic keratoconjunctivitis (51), while the other, sodium cromoglycate (also known as RVT-1601 or PA101), is being used for treating idiopathic pulmonary fibrosis and chronic cough (115). Despite this, the potential for GPR35-focused treatment remains promising. GPR35 offers several advantages as a therapeutic target. Firstly, as a receptor situated on the cell surface, it is at the top of the signal transduction pathway. This is particularly significant given the numerous redundancies and compensatory mechanisms that exist within inflammation-related signal pathways, which can minimize these effects at the starting point.

Furthermore, GPR35 exhibits a tissue-specific expression pattern with high expression levels observed in immune cells and the gastrointestinal tract. The robust expression of GPR35 in immune cells aligns with its role in the regulation of inflammation. The substantial presence of GPR35 in the gastrointestinal tract, along with the strong correlation between GPR35 mutation and IBD, has led to the consideration of GPR35 as a potential target for IBD treatment. However, it is important to acknowledge the dual role GPR35 plays in IBD. While inhibiting GPR35 activity can diminish the proinflammatory response of macrophages and neutrophils, it may concurrently hinder the repair of gastrointestinal damage. Consequently, the risk-benefit balance of targeting GPR35 for IBD treatment remains somewhat elusive and requires further investigation.

The precise mechanisms driving the dual roles of GPR35 in promoting and inhibiting inflammation across various cells and

tissues remain unclear and necessitate more in-depth research. The effects of GPR35 activation on inflammatory responses are likely shaped by numerous factors. These include cell types, tissue microenvironments, and the co-existence of other signaling pathways. Additionally, the expression levels and functional activity of GPR35 agonists may also be instrumental in steering the direction of the inflammatory response. In conclusion, GPR35 is a versatile receptor that can adopt either pro-inflammatory or anti-inflammatory stances within distinct immune cells and tissues. This warrants additional comprehensive research into GPR35 intricacies. Recently, the unveiling of the first protein structure of GPR35 marked a significant advancement in our understanding of GPR35 (86). As our knowledge of GPR35 deepens, we can anticipate the development and application of a broader range of GPR35-targeted drugs in the future.

Author contributions

YW: Writing – original draft. PZ: Writing – original draft, Writing – review & editing. HF: Writing – review & editing. CZ: Writing – review & editing. PY: Writing – review & editing. XL: Conceptualization, Supervision. YC: Writing – review & editing, Conceptualization, Funding acquisition, Supervision.

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