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## EDITED BY

Mateusz Szudzik,  
Medical University of Warsaw, Poland

## REVIEWED BY

Piotr Poznanski,  
Institute of Genetics and Animal  
Biotechnology, Polish Academy of Sciences,  
Poland  
Anna Leśniak,  
Medical University of Warsaw, Poland

## \*CORRESPONDENCE

Xinrong Fan

✉ fxr-1003@163.com

Yan Wei

✉ weiy.1111@swmu.edu.cn

<sup>†</sup>These authors have contributed equally to  
this work

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# Novel opportunity of treatment for psycho-cardiologic disease by gut microbiome

Yurui Lai<sup>1,2†</sup>, Chenli Fang<sup>3†</sup>, Yuang Jiang<sup>4</sup>, Chengying Yang<sup>1,2</sup>,  
Qiao Zhou<sup>1</sup>, Yihua Cai<sup>1</sup>, Yan Wei<sup>2\*</sup> and Xinrong Fan<sup>1,2\*</sup>

<sup>1</sup>Department of Cardiology, The Affiliated Hospital, Southwest Medical University, Luzhou, Sichuan, China, <sup>2</sup>Key Laboratory of Medical Electrophysiology, Ministry of Education & Medical Electrophysiological Key Laboratory of Sichuan Province, (Collaborative Innovation Center for Prevention of Cardiovascular Diseases), Institute of Cardiovascular Research, Southwest Medical University, Luzhou, Sichuan, China, <sup>3</sup>Department of Cardiology, Institute of Cardiovascular Disease of Chengdu, The Third People's Hospital of Chengdu, Luzhou, Sichuan, China, <sup>4</sup>Department of Cardiovascular Medicine, The Meishan People's Hospital, Meishan, Sichuan, China

Cardiovascular disease (CVD) patients combined with depression, anxiety, and other psychiatric disorders are becoming a common occurrence. There are many comorbid mechanisms, and CVD patients with psychiatric disorders have poor prognosis. Several studies have shown that dysbiosis and metabolite alterations in the gut were major risk factors for CVD and psychosomatic disorders. This review aims to summarize the mechanisms of gut microbiota and its metabolites in psycho-cardiologic disease, and the therapeutic effects of gut microbiota interventions. It is very useful to propose a new direction for the treatment of psycho-cardiologic disease.

## KEYWORDS

gut microbiome, metabolites, psycho-cardiologic disease, relationship, treatment

## Introduction

In contemporary clinical practice, the coexistence of cardiovascular disease (CVD) and psychosomatic disorders, often termed “psycho-cardiological disease” (1), is increasingly prevalent (2). Patients with psycho-cardiological disease frequently present with atypical clinical manifestations of CVD and generally experience suboptimal treatment outcomes (3). Moreover, these patients are more prone to exhibit adverse health behaviors, such as poor adherence to treatment, difficulty in breaking harmful habits, and challenge in adopting a healthy lifestyle (4). Conventional treatment approaches for CVD alone are often insufficient, underscoring the growing importance of comprehensively addressing psycho-cardiological disease (5). Consequently, the condition is receiving growing attention from clinicians. Despite extensive basic and clinical research aimed at elucidating the mechanisms underlying this comorbidity and developing targeted therapies—including combined antipsychotic pharmacotherapy, traditional Chinese medicine interventions, cognitive-behavioral therapy, and exercise rehabilitation—the efficacy of these treatments remains limited due to challenges such as drug side effects, variability in treatment efficacy, and limited therapeutic stability. In recent years, there has been growing interest in the role of gut microbiota and its metabolites in the pathophysiology of both CVD and psychosomatic disorders. Thus, the interest has led to the development of concepts such as “gut-heart axis” and “gut-brain axis” (6), which provide a theoretical framework for using gut-targeted interventions in the prevention and treatment of cardiovascular and cerebrovascular diseases. The article reviews

current researches on gut microbiota and its metabolites in psycho-cardiological disease, aiming to identify new research directions and potential therapeutic applications.

## Psycho-cardiological disease

The concept of psycho-cardiological disease highlights the close relationship between psychological factors and CVD (7). Psycho-cardiology is a discipline grounded in the biopsychosocial model of medicine, which aims to prevent and treat both cardiac and psychological conditions through a holistic approach that integrates physical, psychological, and social dimensions. The historical roots of the concept can be traced back to 1628, when William Harvey proposed the circulatory system as it is understood today, and further emphasized the connection between the mind and the heart. In 1772, William Heberden provided the first detailed description of angina pectoris, noting that it could be exacerbated by mood disorders. However, for nearly two centuries, little attention was given to the potential link between psychology and heart health until a pivotal study by Frasure Smith et al. demonstrated that patients with depression during acute myocardial infarction (MI) had significantly higher mortality rates compared to those without depression (8). Since then, extensive research has been conducted on the relationship between CVD and depression, revealing that depression is highly prevalent among individuals with CVD, affecting approximately 20%–40%, and not only contributes to the onset of CVD but also worsens outcomes in patients with pre-existing heart disease (9). Today, CVD and mood disorders such as anxiety and depression are recognized as leading causes of reduced life expectancy and quality of life worldwide (10). Psychosomatic disorders like depression, have gained increasing attention within the biopsychosocial model of medicine. A current research indicates that the mechanisms underlying the coexistence of CVD and depression include autonomic dysfunction, neuroendocrine imbalance, inflammation, insulin resistance, platelet activation, and lifestyle factors (11). To further elucidate the mechanisms comprehensively, extensive research has focused on identifying potential risk factors through multi-omics data analysis (12).

The gut microbiota plays a crucial role in various aspects of human digestion, nutrient absorption, biological barrier function, immune regulation, and metabolism (13). As the largest and most

complex microecological system in the human body, it comprises over 1,000 different species of bacteria, predominantly from the *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* (14). Maintaining the structural and proportional balance of the community is essential for preserving gut microecological homeostasis. Advances in microbiome research have revealed that disruptions in the gut microbiota can lead to systemic diseases (15), particularly CVD and psychosomatic disorders. The stability of the gut microbiota is crucial for maintaining the physiological integrity of both the circulatory and nervous systems. On the one hand, beneficial gut probiotics produce metabolites, such as short-chain fatty acids (SCFAs), that help prevent CVD and psychosomatic disorders; on the other hand, harmful metabolites produced by certain gut bacteria can be absorbed into the circulatory system, triggering inflammatory responses and contributing to the development of systemic diseases (16).

## Gut microbiota and metabolites in CVD

Earlier sequencing studies identified bacterial DNA in human atherosclerotic plaques, but whether the DNA originated from viable bacteria within the artery wall remains inconclusive. The majority of studies on trimethylamine N-oxide (TMAO) have been pioneering in revealing the potential causal association of gut microbiome and its metabolomics with CVD. TMAO is a bioactive gut microbial metabolite produced from protein-derived foods, such as carnitine and choline found in meat and seafood, which are metabolized by gut microorganisms and subsequently oxidized in the liver. ApoE knockout mice exhibited increased aortic damage following dietary TMAO supplementation (17). *In vitro* studies have demonstrated that TMAO can stimulate platelet aggregation by enhancing calcium release from the platelet endoplasmic reticulum, thereby exerting a prothrombotic effect (18). Clinical trials have also indicated that choline supplementation can elevate fasting TMAO levels and augment platelet aggregation (19). Additionally, TMAO has been shown to activate signaling pathways in vascular smooth muscle cells and endothelial cells, leading to upregulation of inflammatory genes, increased leukocyte adhesion to endothelial cells, and elevated expression of scavenger receptors CD36 and SR-A1, thereby enhance the uptake of modified low-density lipoproteins by macrophages, subsequently promoting foam cell formation (20). Notably, Wang et al. revealed a dose-dependent association between TMAO and cardiovascular disease (CVD) (20). Furthermore, studies have demonstrated significant differences in serum TMAO concentrations among patients with varying severities of coronary atherosclerosis, and plasma TMAO may promote the progression of coronary atherosclerosis to ACS, suggesting its potential role in determining CVD severity and prognosis (21). Another study similarly demonstrated a positive correlation between TMAO levels and atherosclerotic plaque burden (22); however, the precise mechanisms underlying the association remain to be fully elucidated. With the continuous advancement of research, numerous gut microbial metabolites, such as lipopolysaccharide (LPS), SCFAs, and bile acid (BA),

### Abbreviations

CVD, cardiovascular disease; MI, myocardial infarction; SCFAs, short-chain fatty acids; TMAO, trimethylamine N-oxide; LPS, lipopolysaccharide; BA, bile acid; HF, art failure; STEMI, ST-segment elevation myocardial infarction; ACS, acute coronary syndrome; CAD, coronary artery disease; RCT, randomized controlled trial; IL-1 $\beta$ , interleukin-1 beta; TGF- $\beta$ , transforming growth factor-beta; B/E ratio, *Bifidobacterium*-to-*Enterobacteriaceae* ratio; DEP-HTN, depressive-epidemic hypertension; hs-CRP, high-sensitivity C-reactive protein; MedDiet, mediterranean diet; FMT, fecal microbiota transplantation; KO, knockout; CUMS, chronic unpredictable stress; SGLT1, sodium glucose cotransporter protein inhibitor; IHD, Ischemic heart disease; SGLT1/2, sodium glucose cotransporter 1 and 2; DCA, deoxycholic acid; TUDCA, tauroursodeoxycholic acid; CUS, chronic unpredictable stress; AIS, acute ischemic stroke.

have been demonstrated to significantly impact the occurrence and progression of CVD by modulating inflammation, immune response, lipid metabolism, oxidative stress, and insulin resistance (23).

The relationship between the host and gut microbiota is not unidirectional but rather mutually dependent and synergistic (24). Studies have shown that patients with decompensated heart failure (HF) have higher LPS concentrations compared to those with stable HF, and the progression of HF is associated with an increase in inflammatory markers such as soluble (s) CD14, tumor necrosis factor (TNF) $\alpha$ , and interleukin 6 (IL-6) (25, 26). Multiple studies have demonstrated that HF patients experience alterations in gut barrier integrity, with elevated blood levels of pro-inflammatory cytokines correlating with symptom severity and poorer prognosis (27). A recent animal study confirmed that gut barrier function in mice was impaired following MI, leading to bacterial translocation and LPS entry into the bloodstream, which triggers inflammation and adversely affects prognosis (28). The study observed that serum LPS levels in STEMI patients peaked on the second day after symptom onset. Intriguingly, polymyxin B treatment in myocardial infarction (MI) models reduced infarct size compared to controls, implicating gut microbiota translocation and elevated LPS in post-MI inflammation and adverse cardiovascular events (28). Emerging evidence indicates that lipopolysaccharide (LPS) accelerates atherosclerotic progression through TLR4/NF- $\kappa$ B axis-mediated upregulation of adipose differentiation-related protein (ADRP) in adventitial fibroblasts. This molecular cascade drives pathological lipid deposition and subsequent foam cell formation, a hallmark of atherogenesis (29). It is reported that SCFAs are closely linked to cardiovascular health. Animal studies indicate that SCFAs modulate blood pressure via receptors GPR41 and Olfr78. GPR41-knockout mice exhibited higher systolic blood pressure than wild-type counterparts (30). Additional research highlights SCFAs' critical role in maintaining intestinal barrier integrity and preventing heart failure progression (31).

Disruptions in gut microbial metabolites are associated with gut dysbiosis. A meta-analysis revealed significant differences in the composition of gut microbiota between patients with coronary artery disease (CAD) and those without CAD (32). Notable distinctions included decreased levels of the genera *Bacteroides* and *Lachnospira*, alongside increased levels of the genera *Enterobacteriaceae*, *Actinobacteria*, and *Verrucomicrobia* in CAD patients. These bacterial genera are linked to altered concentrations of metabolites such as LPS, TMAO, SCFAs, and BA (32). Modulating gut microbiota dysbiosis may help reverse metabolic disorders and improve patient outcomes. In a randomized controlled trial (RCT), participants taking *Lactobacillus rhamnosus* for 12 weeks exhibited significantly reduced levels of interleukin-1 beta (IL-1 $\beta$ ) and LPS compared to those receiving a placebo (33). Another RCT demonstrated that *Bifidobacterium lactis* supplementation for 6 months in CAD patients increased *Bacteroides* abundance, decreased *Enterobacteriaceae* levels, and reduced TMAO levels compared to placebo. Furthermore, the symptoms of angina pectoris were also significantly improved in the probiotic group (34).

The translocation of gut microbial metabolites into the circulatory system has been associated with elevated inflammatory markers and increased ischemia-reperfusion injury severity in patients with MI (35). Probiotic supplementation has demonstrated the potential to lower transforming growth factor-beta (TGF- $\beta$ ) and TMAO levels, suggesting therapeutic benefits for myocardial remodeling (35). Animal studies have indicated that modulating gut microbiota can restore immune cell proportions in bone marrow, reducing early inflammatory responses following MI and improving cardiac outcomes (36). In a rat model of MI, supplementation with *Lactobacillus rhamnosus* GR-1 significantly improved left ventricular ejection fraction, reduced left ventricular mass, and decreased brain natriuretic peptide levels (37). Conversely, cardiomyocyte necrosis, apoptosis, and macrophage infiltration post-MI were significantly increased in mice fed TMAO-supplemented diets (38). Additionally, chronic-phase plasma TMAO levels were associated with coronary plaque progression and increased cardiovascular event rates in patients following ST-segment elevation MI (39). Furthermore, supplementation with urolithin A, a gut microbiota-derived metabolite, was found to inhibit myocardial fibroblast transformation and improve myocardial remodeling post-MI (40). These findings underscore the potential of gut microbiota and its metabolites to enhance post-MI cardiac remodeling, providing compelling evidence for the development of gut-based therapies for CVD. In addition to CAD and MI, the composition of intestinal flora in patients with other cardiovascular diseases also changes, including atrial fibrillation, HF, and Hypertension et al. As summarized in Table 1, we have delineated the changes in gut microbiota composition associated with cardiovascular diseases.

In conclusion, disturbances in gut microbiota and its metabolites are associated with increased susceptibility to CVD and adversely affect prognosis. Modulation of metabolite imbalances through gut microbiota interventions holds potential for improving cardiovascular pathology. These findings provide robust evidence supporting the use of gut microbiota interventions in CVD patients; however, large-scale, long-term clinical trials are necessary to further validate their efficacy.

## Gut microbiota and metabolites in psychiatric disorders

By 1980, studies had identified polypeptide hormones produced by specific secretory cells in the gastrointestinal tract which were also present in nerve and brain cells, leading to the development of the "gut-brain axis" concept. The concept has since been evolved into the "microbiome-gut-brain axis," highlighting the interconnections of the nervous, endocrine, immune, and inflammatory systems, along with the gut microbiota and its metabolites (92). In depressed mice, significant reduction of SCFAs in fecal samples, as well as decreases in hypothalamic 5-hydroxytryptamine and neurotransmitter levels, were closely linked to alterations in gut microbial composition (93). Another study demonstrated that gut

TABLE 1 Changes of Gut Microbiota composition in different cardiovascular diseases.

Cardiovascular disease (CVD)	Increased Taxa	Decreased Taxa	References
Acute Coronary Syndrome (ACS)	Proteobacteria (phylum), Streptococcus (genus), Enterobacteriaceae (family); et al.	Faecalibacterium (genus), Bacteroides (genus); et al.	(7, 41–91)
Atherosclerosis (AS)	Clostridiaceae (family), Lactobacillus (genus); et al.	Bacteroidetes (phylum), Roseburia (genus), Faecalibacterium (genus); et al.	(7, 41–91)
Atrial Fibrillation (AF)	Megamonas (genus), Proteobacteria (phylum); et al.	Bacteroidetes (phylum), Roseburia (genus), Blautia (genus); et al.	(7, 41–91)
Coronary Artery Disease (CAD)	Proteobacteria (phylum), Lactobacillus (genus), Enterobacteriaceae (family); et al.	Lachnospira (genus), Faecalibacterium (genus), Bacteroides (genus); et al.	(7, 41–91)
Heart Failure (HF)	Proteobacteria (phylum), Streptococcus (genus), Alistipes (genus); et al.	Prevotella (genus), Roseburia (genus); et al.	(7, 41–91)
Hypertension (HTN)	Streptococcus (genus), Enterococcus (genus); et al.	Faecalibacterium (genus), Bacteroides (genus), Butyrivibrio (genus); et al.	(7, 41–91)
Stroke	Enterobacteriaceae (family), Lactobacillaceae (family), Proteobacteria (phylum); et al.	Faecalibacterium (genus), Roseburia (genus), Bacteroidetes (phylum); et al.	(7, 41–91)

microbes from depressed mice could induce depressive symptoms and alter gut microbiota composition in other mice (94). After ingesting the microbes, the recipient mice developed depressive symptoms and exhibited elevated levels of inflammatory markers. However, the symptoms and cytokine levels were mitigated when subdiaphragmatic vagotomy was performed, providing strong evidence for the bidirectional communication within the microbiome-gut-brain axis. A recent large-scale clinical study found that patients with depression had significantly reduced levels of *Faecalibacterium* and *Coprococcus* bacteria characterized by butyrate production, which are associated with a better quality of life (95). Butyrate, an SCFA, helps improve gut barrier function, reduces inflammation, and promotes neurogenesis (96). A meta-analysis revealed that levels of *Faecalibacterium* and *Coprococcus* were decreased in patients with major depressive disorder, bipolar disorder, psychosis, schizophrenia, and anxiety, suggesting these diseases are characterized by a reduction in anti-inflammatory, butyrate-producing bacteria and an increase in pro-inflammatory genera (97). The finding supports the potential for gut microbiota interventions in treating psychological disorders. In a recent 6-month clinical trial, patients who received *Bifidobacterium lactis* supplementation showed significant improvements in depression and anxiety levels compared to the placebo group (34). Another systematic review highlighted that interventions with polyunsaturated fatty acids may prevent acute mood changes, inhibit inflammation, and alleviate stress-related psychological disorders such as depression and post-traumatic stress disorder (98). The underlying mechanism behind the effect may be that gut microbiota influences brain function by regulating brain areas, neurotransmitters and neuropeptides involved in mood and appetite, and probably also impacts mood and behavior (98). While the use of probiotics and/or prebiotics for treating depression and anxiety is supported by existing evidence, there is currently a lack of corresponding clinical research. Moreover, the current understanding of the bidirectional effects of the “microbiome-gut-brain axis” is predominantly based on animal studies, with a shortage of large-scale clinical trials to confirm therapeutic efficacy.

## Gut microbiota and metabolites in psycho-cardiological disease

Given the substantial evidence linking alterations in gut microbiota and its metabolites to the pathogenesis of CVD and psychological disorders, recent basic and clinical research has increasingly focused on the role of gut microbiota in the development and prognosis of psycho-cardiological diseases. Zhang et al. conducted a comparative analysis of the gut microbiota in patients with comorbid depression and CAD, those with depression alone, and healthy individuals (99). The study found significantly elevated levels of *Enterobacterium* and *Enterococcus* in patients with both depression and CAD, while *Bifidobacterium*, *Lactobacillus*, and the *Bifidobacterium*-to-*Enterobacteriaceae* ratio (B/E ratio) were markedly lower compared to the other two groups. Moreover, logistic regression analysis identified the B/E ratio as an independent predictor of prognosis in patients with depression and CAD. In a recent cross-sectional study, fecal microbiota metagenomic and untargeted metabolomic analyses were performed on patients with heart failure (HF) and depression, patients with HF alone, and healthy individuals (100). The study revealed significant increases in the gut bacteria *Mediterranea*, *Tolomonas*, and *Parabacteroides* in patients with both HF and depression, alongside notable decreases in *Pedobacter*, *Azospirillum*, and *Ruminiclostridium*. Additionally, reduced levels of anti-inflammatory mediators (abietic acid, quinic acid, and linoleic acid) and neurotransmitters (serotonin, tryptamine, and phenylethylamine) were observed in these patients. Enrichment analysis demonstrated a strong correlation between gut microbiota and the functional pathways of metabolites, particularly those related to amino acid metabolism, fatty acid metabolism, and cAMP signaling pathways, suggesting the pathways may play a crucial role in the comorbidity of depression and HF (100). The pathophysiology of hypertension is also closely linked to psychological disorders. A novel subtype of hypertension, termed “depressive-epidemic hypertension” (DEP-HTN), was proposed in a Florida hypertension study, where individuals with DEP-HTN exhibited a distinct gut

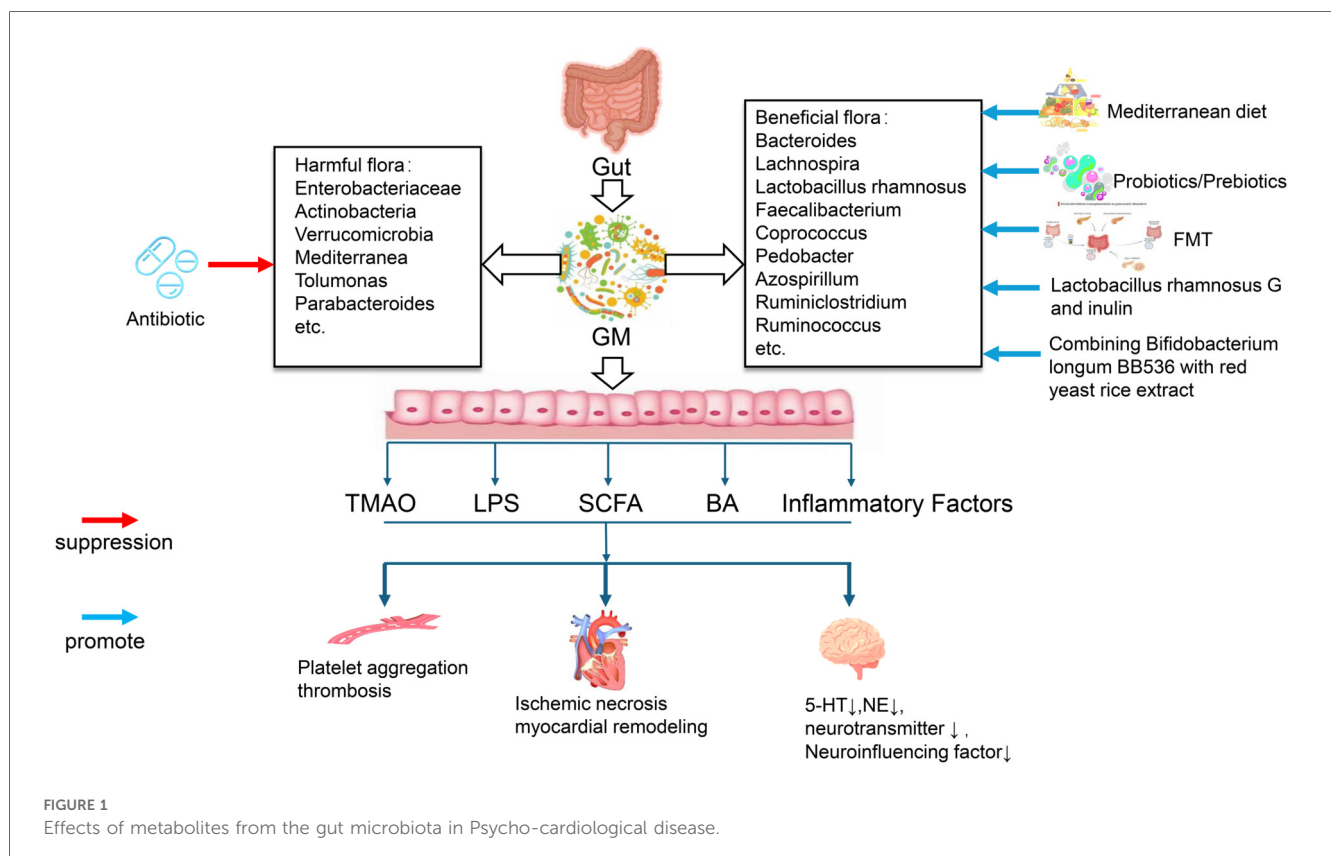
microbiota composition compared to those with either hypertension or depression alone (101). The DEP-HTN model integrates microbial taxa and functional genomics to explore the complex interactions between gastrointestinal pathophysiology and the central regulation of blood pressure and mood. Furthermore, modulating gut microbiota has shown promise in alleviating psychological symptoms in CVD patients. In an RCT, patients with CAD who received an 8-week co-supplementation of probiotics and prebiotics (*Lactobacillus rhamnosus* G and inulin) experienced significant improvements in anxiety, depression, serum high-sensitivity C-reactive protein (hs-CRP), LPS, and tumor necrosis factor-alpha levels compared to those who received a placebo (102). Notably, the combination of inulin with probiotic supplementation was more effective in improving psychological symptoms and inflammatory biomarkers than either supplement alone. Figure 1 summarized the role of the above gut microbiota metabolites in Psycho-cardiological disease. In summary, the disruption of the gut microecosystem is closely associated with the co-occurrence of CVD and psychological disorders, offering new insights into the “microbiota-gut-heart/brain axis” and presenting novel opportunities for gut microbiota-based interventions in psycho-cardiological diseases.

## Interventions targeting gut microbiota

The gut, functioning as a bridge between the body’s internal and external environments, is profoundly influenced by diet. Diet can

modulate the growth and activity of specific microorganisms within the gut microbiota by providing essential nutrients, thereby potentially impacting human health (103). The Mediterranean diet (MedDiet) is a predominantly plant-based dietary pattern characterized by: (a) high levels of unsaturated fatty acids, fiber, vitamins, and minerals derived from fruits, vegetables, nuts, seeds, olive oil, and whole grains; and (b) low consumption of saturated fats, meat, and dairy products (104). Numerous meta-analyses and prospective clinical trials have consistently demonstrated the cardiovascular benefits of the MedDiet (105, 106). Multi-omics studies have shown that the MedDiet is associated with the abundance of gut microbiota, such as *Faecalibacterium*, *Ruminococcus*, and *Bacteroides*, and is positively correlated with higher concentrations of SCFAs in feces (107). Additionally, several clinical trials have demonstrated that adherence to the MedDiet can effectively alleviate depressive symptoms and enhance the quality of life in patients (108, 109). Given the distinct effects of various components of the MedDiet on gut microbiota, further multidisciplinary and multi-omics research is warranted to elucidate the specific impacts of individual dietary components on gut microbial composition and function.

Compared to the complexities of dietary regulation, modulating gut microbiota through probiotics and/or prebiotics offers a more practical approach. Prebiotics are substances that stimulate microbial growth and can be fermented by gut bacteria to produce SCFAs (110), which enhance gut barrier function, and regulate metabolism, immunity, and inflammation. Additionally, probiotics promote the growth of beneficial bacteria while inhibiting the



proliferation of pathogenic bacteria (111). A clinical trial demonstrated that combining *Bifidobacterium longum* BB536 with red yeast rice extract significantly improved the atherogenic lipid profile in patients with low cardiovascular risk (112). Furthermore, after 3 months of probiotic supplementation in patients with MI, significant reductions in TGF- $\beta$ , TMAO, and hs-CRP levels were observed compared to the placebo group (113). These findings suggest that probiotics may positively impact cardiac remodeling in MI patients. Another study found that patients with CAD, taking *Bifidobacterium lactis*, experienced significant improvements in angina, depression, and anxiety compared to those who received a placebo (34).

Fecal microbiota transplantation (FMT) is primarily used as a therapeutic approach for recurrent refractory *Clostridium difficile* infections (114). Recently, FMT has also been applied in the management of conditions such as ulcerative colitis and irritable bowel syndrome (115, 116). As of May 23, 2025, only four clinical trials have been registered on <http://www.clinicaltrials.gov> using “FMT” and “CAD” as keywords. Additionally, only twelve trials have been registered using the terms “FMT” and “Depression.” Current research on the application of FMT in psycho-cardiological disease is largely limited to animal studies. For instance, significant differences in gut microbial composition have been observed between NLRP3 knockout (KO) mice and wild-type mice, particularly in the relative abundance of *Firmicutes*, *Proteobacteria*, and *Bacteroidetes* (117). Furthermore, transplantation of gut microbiota from NLRP3 KO mice into recipient mice significantly improved depressive behaviors induced by chronic unpredictable stress (CUMS). Conversely, when gut microbiota from CUMS model mice were transplanted into normal recipient mice, higher levels of anxiety, depressive behaviors, and inflammatory factors were observed in the recipients (117).

The use of antibiotics in treating psycho-cardiological diseases has a long-established history. As early as the 1970s, tetracycline was found to readily bind to ischemic myocardial cells, and radiolabeled tetracycline was widely employed as a diagnostic tool for identifying MI areas. Minocycline, a member of the tetracycline family, has garnered significant attention as a potential therapeutic agent for CVD due to its anti-inflammatory, anti-apoptotic, and antioxidant properties (118). These beneficial effects have been demonstrated in both preclinical animal models of cardiac disease (118) and clinical trials in neurological conditions (119, 120). Additionally, research has shown that minocycline can prevent depression- and anxiety-like behaviors in animals following a stroke (119). Furthermore, hippocampal neurodegeneration was notably reduced in stroke animals treated with minocycline, suggesting that minocycline may mitigate post-stroke depression and anxiety through its neuroprotective effects following cerebral ischemia (119). However, some clinical studies have reported that minocycline does not significantly improve symptoms in patients with depression or bipolar disorder (121). Thus, further clinical research is necessary to establish the efficacy of antibiotics in treating psycho-cardiological diseases. Table 2 showed some of the above clinical trials results of interventions targeting the gut microbiota.

Accumulating evidence indicates that Sodium glucose cotransporter protein inhibitor (SGLTi) plays an extremely

important role in the treatment of IHD (Ischemic heart disease), and its protective effects mainly involve modulating energy metabolism, anti-inflammation, anti-fibrosis and improving the expression and function of ion channels (126). Recently, our animal study showed that sotagliflozin (SOTA), an approved sodium glucose cotransporter 1 and 2 (SGLT1/2) inhibitor for diabetes, not only improves the cardiac function of mice with MI, but also ameliorates the depression-like behaviors in the mice (127). The study also suggested that SOTA protected the heart mainly through regulating the composition of the gut microbiota, and found that *Alloprevotella*, *Prevotellaceae* UCG-001, and *Prevotellaceae* NK3B31 group may be important contributors to the SOTA treatment effects in MI mice. Meanwhile, the study further confirmed the beneficial effects of SOTA on cardiac function and depression-like behaviors in MI mice through FMT. These findings indicate that both SGLTi and FMT can ameliorate cardiac function and depression-like behaviors by modulating the gut microbiota, which provides a new direction for treating depression-like behaviors in patients with MI and promoting the recovery of cardiac function after MI. At present, however, no study has found the specific mechanism of SGLT modulating or altering the gut microbial communities of MI mice, as well as the current study is still in the animal research stage, and relevant clinical studies are also needed to evaluate the specific efficacy of SGLTi and FMT intervention on psycho-cardiological diseases.

During the development of psycho-cardiological diseases, the reduction of some gut microbiota metabolites is closely related to the progress of the disease. Supplementing relevant gut microbiota metabolites is also a potential therapeutic strategy. Recent studies have found that supplements of native metabolites of intestinal flora is also beneficial to the treatment of double heart disease. A study found that DCA (a secondary bile acid metabolized by intestinal flora) was significantly reduced in patients with AMI by analyzing the bile acid metabolism in the serum of patients with AMI and the control group (128). The study also found that compared with the control group, the ischemic damage to cardiac function of MI mice treated with DCA was reduced, and the main mechanism was to reduce inflammation through *dca-tgr5* signaling pathway to improve cardiac function after myocardial infarction. Another animal study found that TUDCA, (a bile acid, which has attracted much attention because of its protective effect on Alzheimer’s disease and other brain disorders (129) reduced the increase of inflammasome and microglial activation markers in CUS mice, including interleukin- $\beta$ , and nod like receptor protein 3 et al. (130). In addition, Relevant studies have proved that microglial dysfunction is closely related to the occurrence and development of neurodegenerative diseases and mental diseases (131). A prospective observational study found that SCFA producing bacteria and fecal SCFA levels in AIS patients were significantly reduced, suggesting that SCFA is a marker of the severity and prognosis of AIS, and may also be a potential therapeutic target (132). A study pointed out that transplantation of SCFA rich fecal microbiota or butyrate supplementation is an effective method for the treatment of ischemic stroke (133), but a large number of relevant clinical studies are still needed to clarify the

Table 2 Clinical trial results of intervention targeting Gut Microbiota for psycho-cardiological disease.

Type of trial	Intervention	Major findings	References
Randomized, crossover Study	Vegetarian diet	Of 150 eligible patients, 31 (21%) agreed to participate, and 27 (87%) participants completed the study. Mean oxidized LDL-C ( $-2.73$ U/L), total cholesterol ( $-5.03$ mg/dl), LDL-C ( $-3.87$ mg/dl), and body weight ( $-0.67$ kg) were significantly lower with the VD than with the MD. Differences between VD and MD were observed in the relative abundance of several microbe genera within the families Ruminococcaceae, achnospiraceae, and Akkermansiaceae. Plasma metabolites, including l-carnitine, acylcarnitine metabolites, and phospholipids, differed in subjects consuming VD and MD. The effect on oxidized LDL-C in response to the VD was associated with a baseline gut microbiota composition dominated by several genera of Ruminococcaceae.	(122)
Randomized controlled trial	MED, Green-MED	Both MED diets and Green-MED induced substantial changes in the community structure of the gut microbiome, with the Green-MED diet leading to more prominent compositional changes, largely driven by the low abundant, "non-core," microorganisms. The Green-MED diet was associated with specific microbial changes, including enrichments in the genus <i>Prevotella</i> and enzymatic functions involved in branched-chain amino acid degradation, and reductions in the genus <i>Bifidobacterium</i> and enzymatic functions responsible for branched-chain amino acid biosynthesis.	(123)
Randomized, double-blind clinical trial	Co-supplementation of probiotics and inulin	Probiotic-Inulin, Co-supplementation significantly decreased BDI ( $-11.52 \pm 0 + 3.20$ vs. $+ 2.97 \pm 0.39$ , $P = 0.001$ ), STAI-state ( $-17.63 \pm 3.22$ vs. $-0.60 \pm 0.33$ , $P = 0.021$ ), and STAI-trait ( $-24.31 \pm 7.41$ vs. $-1.45 \pm 0.66$ , $P = 0.020$ ) scores, hs-CRP ( $-1.69 \pm 0 + 66$ vs. $+ 0.82 \pm 0.39$ mg/dl, $P = 0.020$ ), LPS [ $-22.02 \pm 5.40$ vs. $+ 0.31 \pm 0.18$ (EU/L), $P = 0.047$ ], and TNF-alpha [ $-25.05 \pm 7.41$ vs. $+ 0.79 \pm 0.71$ (ng/L), $P = 0.032$ ] in comparison to placebo.	(124)
Observational trial	FMT, probiotic supplementation	Gut microbiota of patients with inflammatory depression exhibits higher <i>Bacteroides</i> and lower <i>Clostridium</i> , with an increase in SCFA-producing species with abnormal butanoate metabolism. After FMT, the gut microbiota of the inflammatory depression group shows increased peripheral and central inflammatory factors and intestinal mucosal permeability in recipient mice with depressive and anxiety-like behaviors. <i>Clostridium butyricum</i> administration normalizes the gut microbiota, decreases inflammatory factors, and displays antidepressant-like effects in a mouse model of inflammatory depression.	(125)
Double-blind, 12-week, randomised, placebo-controlled trial	Minocycline, celecoxib	From baseline to week 12, depressive symptoms as per HAMD-17 reduced in all four groups (from 24.5–25.2 to 11.3–12.8), but these reductions did not differ significantly between the groups. In terms of main effects, reductions in HAMD-17 did not differ for patients treated with minocycline [mean adjusted difference vs non-minocycline 1.48 (95% CI $-0.41$ to 3.36); $p = 0.123$ ] or for celecoxib [mean adjusted difference vs non-celecoxib $-0.74$ ( $-2.61$ to 1.14); $p = 0.443$ ]. Rates of serious adverse effects did not differ between groups (31 participants had a manic switch, two self-harmed, and one died in a motor vehicle accident).	(121)

LDL-C, low-density lipoprotein cholesterol; VD, vegetarian diet; MD, meat diet; MED, Mediterranean diet; Green-MED, Green-Mediterranean diet; SCFA, short chain fatty acid; FMT, fecal microbiota transplantation; HAMD-17, hamilton depression scale.

effectiveness of this treatment strategy. In conclusion, intestinal flora plays an important role in psycho-cardiological diseases, and dysbiosis is inseparably connected with different level of microbiota metabolites. Therefore, in psycho-cardiological diseases, supplementing beneficial metabolites may also be an effective intervention. In the future, a large number of studies are needed to clarify the relevant mechanisms and therapeutic targets.

## Future perspectives

Previous studies have established a link between gut microbiota and psycho-cardiological diseases; however, the understanding of their interactions and the underlying molecular mechanisms remains limited. Additionally, many fundamental questions about the use of gut microbiota as a therapeutic intervention remain unresolved, which include identifying the specific microbial species involved, determining the optimal dosage and duration of interventions, standardizing treatment protocols, assessing the frequency of administration, evaluating potential side effects, addressing microbial dysbiosis, and elucidating the physiological mechanisms underpinning the "microbiota-gut-heart/brain axis." Despite these gaps in knowledge, current researches indicate that metabolites produced by gut microbiota, such as SCFAs, BA,

LPS, and TMAO, play significant roles in the pathogenesis of psycho-cardiological diseases. Future researches should prioritize elucidating the mechanisms and interrelationships of gut microbiota and its metabolites through both basic and clinical studies. Such efforts are essential for effectively realizing the concept of "intestinal therapy for heart and brain diseases."

## Author contributions

YL: Writing – original draft. CF: Writing – original draft, Data curation, Resources. YJ: Writing – original draft, Data curation, Resources. CY: Writing – review & editing, Supervision, Validation. QZ: Writing – review & editing, Validation. YC: Writing – review & editing, Supervision, Validation. YW: Writing – review & editing, Supervision, Validation, Conceptualization. XF: Writing – original draft, 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.

## Generative AI statement

The author(s) declare that no Generative AI was used in the creation of this manuscript.

## References

- Lai M, Shen T, Cui H, Lin L, Ran P, Huo P, et al. Clinical outcomes and survival analysis in patients with psycho-cardiological disease: a retrospective analysis of 132 cases. *J Int Med Res.* (2021) 49(3):300060521990984. doi: 10.1177/0300060521990984
- Sun Z, Ping P, Zhang P, Yao Y, Huang Z, Zhao Y, et al. Associations between cardiac structure and function and depressive disorder: a centenarian study in China. *Heliyon.* (2023) 9(2):e13233. doi: 10.1016/j.heliyon.2023.e13233
- Goldfarb M, De Hert M, Detraux J, Di Palo K, Munir H, Music S, et al. Severe mental illness and cardiovascular disease: JACC state-of-the-art review. *J Am Coll Cardiol.* (2022) 80(9):918–33. doi: 10.1016/j.jacc.2022.06.017
- Al-Zaru IM, Shahrour G, Masha'al D, Hayajneh AA. Depression and adherence to healthy lifestyle behaviors among patients with coronary artery diseases in Jordan. *Heliyon.* (2022) 8(7):e09752. doi: 10.1016/j.heliyon.2022.e09752
- You Y, Shou X, Zhang X, Fan S, Chai R, Xue W, et al. Psycho-Cardiological disease: a bibliometric review from 2001 to 2021. *Front Cardiovasc Med.* (2022) 9:890329. doi: 10.3389/fcvm.2022.890329
- Chen F, Dong X, Yu Z, Zhang Y, Shi Y. The brain-heart axis: integrative analysis of the shared genetic etiology between neuropsychiatric disorders and cardiovascular disease. *J Affect Disord.* (2024) 355:147–56. doi: 10.1016/j.jad.2024.03.098
- Zuo K, Yin X, Li K, Zhang J, Wang P, Jiao J, et al. Different types of atrial fibrillation share patterns of gut Microbiota dysbiosis. *mSphere.* (2020) 5(2). doi: 10.1128/mSphere.00071-20
- Frasure-Smith N, Lespérance F, Talajic M. Depression following myocardial infarction. Impact on 6-month survival. *JAMA.* (1993) 270(15):1819–25. doi: 10.1001/jama.1993.03510150053029
- Gutlapalli SD, Prakash K, Swarnakari KM, Bai M, Manoharan MP, Raja R, et al. The risk of fatal arrhythmias associated with sertraline in patients with post-myocardial infarction depression. *Cureus.* (2022) 14(9):e28946. doi: 10.7759/cureus.28946
- Vos T, Lim SS, Abbafati C, Abbas KM, Abbasi M, Abbasifard M, et al. Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: a systematic analysis for the Global Burden of Disease Study 2019. *Lancet.* (2020) 396(10258):1204–22. doi: 10.1016/S0140-6736(20)30925-9
- Li Y, Cen J, Wu J, Tang M, Guo J, Hang J, et al. The degree of anxiety and depression in patients with cardiovascular diseases as assessed using a mobile app: cross-sectional study. *J Med Internet Res.* (2023) 25:e48750. doi: 10.2196/48750
- Torgersen K, Rahman Z, Bahrami S, Hindley GFL, Parker N, Frei O, et al. Shared genetic loci between depression and cardiometabolic traits. *PLoS Genet.* (2022) 18(5):e1010161. doi: 10.1371/journal.pgen.1010161
- Liu L, Zou Z, Yang J, Li X, Zhu B, Zhang H, et al. Jianpi jieyu decoction, an empirical herbal formula, exerts psychotropic effects in association with modulation of gut microbial diversity and GABA activity. *Front Pharmacol.* (2021) 12:645638. doi: 10.3389/fphar.2021.645638
- Almeida A, Nayfach S, Boland M, Strozzi F, Beracochea M, Shi ZJ, et al. A unified catalog of 204,938 reference genomes from the human gut microbiome. *Nat Biotechnol.* (2021) 39(1):105–14. doi: 10.1038/s41587-020-0603-3
- Xu Q, Ni JJ, Han BX, Yan SS, Wei XT, Feng GJ, et al. Causal relationship between gut Microbiota and autoimmune diseases: a two-sample Mendelian

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## Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fcvm.2025.1604962/full#supplementary-material>

- randomization study. *Front Immunol.* (2021) 12:746998. doi: 10.3389/fimmu.2021.746998
- Shi N, Li N, Duan X, Niu H. Interaction between the gut microbiome and mucosal immune system. *Mil Med Res.* (2017) 4:14. doi: 10.1186/s40779-017-0122-9
- Gregory JC, Buffa JA, Org E, Wang Z, Levison BS, Zhu W, et al. Transmission of atherosclerosis susceptibility with gut microbial transplantation. *J Biol Chem.* (2015) 290(9):5647–60. doi: 10.1074/jbc.M114.618249
- Wang X, Li X, Dong Y. Vitamin D decreases plasma trimethylamine-N-oxide level in mice by regulating gut Microbiota. *Biomed Res Int.* (2020) 2020:9896743. doi: 10.1155/2020/9896743
- Zhu W, Wang Z, Tang WHW, Hazen SL. Gut microbe-generated trimethylamine N-oxide from dietary choline is prothrombotic in subjects. *Circulation.* (2017) 135(17):1671–3. doi: 10.1161/CIRCULATIONAHA.116.025338
- Wang Z, Klipfell E, Bennett BJ, Koeth R, Levison BS, Dugar B, et al. Gut flora metabolism of phosphatidylcholine promotes cardiovascular disease. *Nature.* (2011) 472(7341):57–63. doi: 10.1038/nature09922
- Kong W, Ma J, Lin Y, Chen W. Positive association of plasma trimethylamine-N-oxide and atherosclerosis in patient with acute coronary syndrome. *Cardiovasc Ther.* (2022) 2022:2484018. doi: 10.1155/2022/2484018
- Bogiatzi C, Gloor G, Allen-Vercoe E, Reid G, Wong RG, Urquhart BL, et al. Metabolic products of the intestinal microbiome and extremes of atherosclerosis. *Atherosclerosis.* (2018) 273:91–7. doi: 10.1016/j.atherosclerosis.2018.04.015
- Witkowski M, Weeks TL, Hazen SL. Gut Microbiota and cardiovascular disease. *Circ Res.* (2020) 127(4):553–70. doi: 10.1161/CIRCRESAHA.120.316242
- Jin Y, Gong T, Lu X, Wang Y, Cheng Y. Effects of gut microbiota and metabolites on the host defense peptide expression. *Appl Microbiol Biotechnol.* (2025) 109(1):10. doi: 10.1007/s00253-024-13400-2
- Niebauer J, Volk HD, Kemp M, Dominguez M, Schumann RR, Rauchhaus M, et al. Endotoxin and immune activation in chronic heart failure: a prospective cohort study. *Lancet.* (1999) 353(9167):1838–42. doi: 10.1016/S0140-6736(98)09286-1
- Peschel T, Schönauer M, Thiele H, Anker SD, Schuler G, Niebauer J. Invasive assessment of bacterial endotoxin and inflammatory cytokines in patients with acute heart failure. *Eur J Heart Fail.* (2003) 5(5):609–14. doi: 10.1016/S1388-9842(03)00104-1
- Rauchhaus M, Doehner W, Francis DP, Davos C, Kemp M, Liebenenthal C, et al. Plasma cytokine parameters and mortality in patients with chronic heart failure. *Circulation.* (2000) 102(25):3060–7. doi: 10.1161/01.CIR.102.25.3060
- Zhou X, Li J, Guo J, Geng B, Ji W, Zhao Q, et al. Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction. *Microbiome.* (2018) 6(1):66. doi: 10.1186/s40168-018-0441-4
- Wang J, Si Y, Wu C, Sun L, Ma Y, Ge A, et al. Lipopolysaccharide promotes lipid accumulation in human adventitial fibroblasts via TLR4-NF- $\kappa$ B pathway. *Lipids Health Dis.* (2012) 11:139. doi: 10.1186/1476-511X-11-139



30. Mayerhofer CCK, Kummen M, Holm K, Broch K, Awoyemi A, Vestad B, et al. Low fibre intake is associated with gut microbiota alterations in chronic heart failure. *ESC Heart Fail.* (2020) 7(2):456–66. doi: 10.1002/ehf2.12596
31. Natarajan N, Hori D, Flavahan S, Steppan J, Flavahan NA, Berkowitz DE, et al. Microbial short chain fatty acid metabolites lower blood pressure via endothelial G protein-coupled receptor 41. *Physiol Genomics.* (2016) 48(11):826–34. doi: 10.1152/physiolgenomics.00089.2016
32. Choroszy M, Litwinowicz K, Bednarz R, Roleder T, Lerman A, Toya T, et al. Human gut Microbiota in coronary artery disease: a systematic review and meta-analysis. *Metabolites.* (2022) 12(12):1165. doi: 10.3390/metabo12121165
33. Moludi J, Kafil HS, Qaisar SA, Gholizadeh P, Alizadeh M, Vayghan HJ. Effect of probiotic supplementation along with calorie restriction on metabolic endotoxemia, and inflammation markers in coronary artery disease patients: a double blind placebo controlled randomized clinical trial. *Nutr J.* (2021) 20(1):47. doi: 10.1186/s12937-021-00703-7
34. Sun B, Ma T, Li Y, Yang N, Li B, Zhou X, et al. Bifidobacterium lactis probio-M8 adjuvant treatment confers added benefits to patients with coronary artery disease via target modulation of the gut-heart/-brain axes. *mSystems.* (2022) 7(2):e010022. doi: 10.1128/msystems.00100-22
35. Taslim NA, Yusuf M, Ambari AM, Del Rosario Puling IM, Ibrahim FZ, Hardinsyah H, et al. Anti-Inflammatory, antioxidant, metabolic and gut Microbiota modulation activities of probiotics in cardiac remodeling condition: evidence from systematic study and meta-analysis of randomized controlled trials. *Probiotics Antimicrob Proteins.* (2023) 15(4):1049–61. doi: 10.1007/s12602-023-10105-2
36. Tang TWH, Chen HC, Chen CY, Yen CYT, Lin CJ, Prajnamitra RP, et al. Loss of gut Microbiota alters immune system composition and cripples postinfection cardiac repair. *Circulation.* (2019) 139(5):647–59. doi: 10.1161/CIRCULATIONAHA.118.035235
37. Gan XT, Ettinger G, Huang CX, Burton JP, Haist JV, Rajapurohitam V, et al. Probiotic administration attenuates myocardial hypertrophy and heart failure after myocardial infarction in the rat. *Circ Heart Fail.* (2014) 7(3):491–9. doi: 10.1161/CIRCHEARTFAILURE.113.000978
38. Yang W, Zhang S, Zhu J, Jiang H, Jia D, Ou T, et al. Gut microbe-derived metabolite trimethylamine N-oxide accelerates fibroblast-myofibroblast differentiation and induces cardiac fibrosis. *J Mol Cell Cardiol.* (2019) 134:119–30. doi: 10.1016/j.yjmcc.2019.07.004
39. Matsuzawa Y, Nakahashi H, Konishi M, Sato R, Kawashima C, Kikuchi S, et al. Microbiota-derived trimethylamine N-oxide predicts cardiovascular risk after STEMI. *Sci Rep.* (2019) 9(1):11647. doi: 10.1038/s41598-019-48246-6
40. Chen P, Pei J, Wang X, Tai S, Tang L, Hu X. Gut bacterial metabolite urolithin A inhibits myocardial fibrosis through activation of Nrf2 pathway *in vitro* and *in vivo*. *Mol Med.* (2022) 28(1):19. doi: 10.1186/s10020-022-00444-1
41. Calderón-Pérez L, Gosalbes MJ, Yuste S, Valls RM, Pedret A, Llauradó E, et al. Gut metagenomic and short chain fatty acids signature in hypertension: a cross-sectional study. *Sci Rep.* (2020) 10(1):6436. doi: 10.1038/s41598-020-63475-w
42. Chen L, Wang S, Zhang Y, Li Y, Zhang X, Ma J, et al. Multi-omics reveals specific host metabolism-microbiome associations in intracerebral hemorrhage. *Front Cell Infect Microbiol.* (2022) 12:999627. doi: 10.3389/fcimb.2022.999627
43. Cheng Q, Fan C, Liu F, Li Y, Hou H, Ma Y, et al. Structural and functional dysbiosis of gut microbiota in Tibetan subjects with coronary heart disease. *Genomics.* (2022) 114(6):110483. doi: 10.1016/j.ygeno.2022.110483
44. Chiu FC, Tsai CF, Huang PS, Shih CY, Tsai MH, Hwang JJ, et al. The gut microbiome, seleno-compounds, and acute myocardial infarction. *J Clin Med.* (2022) 11(5):1462. doi: 10.3390/jcm11051462
45. Chong Nguyen C, Duboc D, Rainteau D, Sokol H, Humbert L, Seksik P, et al. Circulating bile acids concentration is predictive of coronary artery disease in human. *Sci Rep.* (2021) 11(1):22661. doi: 10.1038/s41598-021-02144-y
46. Choroszy M, Sobieszkańska B, Litwinowicz K, Łączmański Ł, Chmielarz M, Walczuk U, et al. Co-toxicity of endotoxin and indoxyl sulfate, gut-derived bacterial metabolites, to vascular endothelial cells in coronary arterial disease accompanied by gut dysbiosis. *Nutrients.* (2022) 14(3):424. doi: 10.3390/nu14030424
47. Cui X, Ye L, Li J, Jin L, Wang W, Li S, et al. Metagenomic and metabolomic analyses unveil dysbiosis of gut microbiota in chronic heart failure patients. *Sci Rep.* (2018) 8(1):635. doi: 10.1038/s41598-017-18756-2
48. Emoto T, Hayashi T, Tabata T, Yamashita T, Watanabe H, Takahashi T, et al. Metagenomic analysis of gut microbiota reveals its role in trimethylamine metabolism in heart failure. *Int J Cardiol.* (2021) 338:138–42. doi: 10.1016/j.ijcard.2021.06.003
49. Gao J, Yan KT, Wang JX, Dou J, Wang J, Ren M, et al. Gut microbial taxa as potential predictive biomarkers for acute coronary syndrome and post-STEMI cardiovascular events. *Sci Rep.* (2020) 10(1):2639. doi: 10.1038/s41598-020-59235-5
50. Haak BW, Westendorp WF, van Engelen TSR, Brands X, Brouwer MC, Vermeij JD, et al. Disruptions of anaerobic gut Bacteria are associated with stroke and post-stroke infection: a prospective case-control study. *Transl Stroke Res.* (2021) 12(4):581–92. doi: 10.1007/s12975-020-00863-4
51. Han Y, Gong Z, Sun G, Xu J, Qi C, Sun W, et al. Dysbiosis of gut Microbiota in patients with acute myocardial infarction. *Front Microbiol.* (2021) 12:680101. doi: 10.3389/fmicb.2021.680101
52. Hayashi T, Yamashita T, Watanabe H, Kami K, Yoshida N, Tabata T, et al. Gut microbiome and plasma microbiome-related metabolites in patients with decompensated and compensated heart failure. *Circ J.* (2018) 83(1):182–92. doi: 10.1253/circj.CJ-18-0468
53. Huang K, Wang Y, Bai Y, Luo Q, Lin X, Yang Q, et al. Gut Microbiota and metabolites in atrial fibrillation patients and their changes after catheter ablation. *Microbiol Spectr.* (2022) 10(2):e0107721. doi: 10.1128/spectrum.01077-21
54. Huang Y, Shen Z, He W. Identification of gut microbiome signatures in patients with post-stroke cognitive impairment and affective disorder. *Front Aging Neurosci.* (2021) 13:706765. doi: 10.3389/fnagi.2021.706765
55. Ji L, Chen S, Gu G, Zhou J, Wang W, Ren J, et al. Exploration of crucial mediators for carotid atherosclerosis pathogenesis through integration of microbiome, metabolome, and transcriptome. *Front Physiol.* (2021) 12:645212. doi: 10.3389/fphys.2021.645212
56. Ji W, Zhu Y, Kan P, Cai Y, Wang Z, Wu Z, et al. Analysis of intestinal microbial communities of cerebral infarction and ischemia patients based on high throughput sequencing technology and glucose and lipid metabolism. *Mol Med Rep.* (2017) 16(4):5413–7. doi: 10.3892/mmr.2017.7227
57. Jie Z, Xia H, Zhong SL, Feng Q, Li S, Liang S, et al. The gut microbiome in atherosclerotic cardiovascular disease. *Nat Commun.* (2017) 8(1):845. doi: 10.1038/s41467-017-00900-1
58. Karlsson FH, Fåk F, Nookaew I, Tremaroli V, Fagerberg B, Petranovic D, et al. Symptomatic atherosclerosis is associated with an altered gut metagenome. *Nat Commun.* (2012) 3:1245. doi: 10.1038/ncomms2266
59. Katsimichas T, Ohtani T, Motooka D, Tsukamoto Y, Kioka H, Nakamoto K, et al. Non-Ischemic heart failure with reduced ejection fraction is associated with altered intestinal Microbiota. *Circ J.* (2018) 82(6):1640–50. doi: 10.1253/circj.CJ-17-1285
60. Kwun JS, Kang SH, Lee HJ, Park HK, Lee WJ, Yoon CH, et al. Comparison of thrombus, gut, and oral microbiomes in Korean patients with ST-elevation myocardial infarction: a case-control study. *Exp Mol Med.* (2020) 52(12):2069–79. doi: 10.1038/s12276-020-00543-1
61. Li H, Zhang X, Pan D, Liu Y, Yan X, Tang Y, et al. Dysbiosis characteristics of gut microbiota in cerebral infarction patients. *Transl Neurosci.* (2020) 11(1):124–33. doi: 10.1515/tncsi-2020-0117
62. Li J, Zhao F, Wang Y, Chen J, Tao J, Tian G, et al. Gut microbiota dysbiosis contributes to the development of hypertension. *Microbiome.* (2017) 5(1):14. doi: 10.1186/s40168-016-0222-x
63. Li N, Wang X, Sun C, Wu X, Lu M, Si Y, et al. Change of intestinal microbiota in cerebral ischemic stroke patients. *BMC Microbiol.* (2019) 19(1):191. doi: 10.1186/s12866-019-1552-1
64. Li W, Li H, Wang S, Han K, Liu Y, An Z, et al. Regional pattern and signatures of gut microbiota in rural residents with coronary heart disease: a metagenomic analysis. *Front Cell Infect Microbiol.* (2022) 12:1007161. doi: 10.3389/fcimb.2022.1007161
65. Liu C, Sun Z, Shali S, Mei Z, Chang S, Mo H, et al. The gut microbiome and microbial metabolites in acute myocardial infarction. *J Genet Genomics.* (2022) 49(6):569–78. doi: 10.1016/j.jgg.2021.12.007
66. Liu F, Fan C, Zhang L, Li Y, Hou H, Ma Y, et al. Alterations of gut microbiome in Tibetan patients with coronary heart disease. *Front Cell Infect Microbiol.* (2020) 10:373. doi: 10.3389/fcimb.2020.00373
67. Liu L, Luo F. Alterations in the fecal microbiota and serum metabolome in unstable angina pectoris patients. *Front Biosci (Landmark Ed).* (2022) 27(3):100. doi: 10.31083/j.fbl2703100
68. Liu X, Shen M, Yan H, Long P, Jiang H, Zhang Y, et al. Alterations in the gut microbiota and metabolome with newly diagnosed unstable angina. *J Genet Genomics.* (2022) 49(3):240–8. doi: 10.1016/j.jgg.2021.11.009
69. Peng J, Gong H, Lyu X, Liu Y, Li S, Tan S, et al. Characteristics of the fecal microbiome and metabolome in older patients with heart failure and sarcopenia. *Front Cell Infect Microbiol.* (2023) 13:1127041. doi: 10.3389/fcimb.2023.1127041
70. Sawicka-Smiarowska E, Bondarczuk K, Bauer W, Niemira M, Szalkowska A, Raczowska J, et al. Gut microbiome in chronic coronary syndrome patients. *J Clin Med.* (2021) 10(21):5074. doi: 10.3390/jcm10215074
71. Stø K, Valeur J, Ueland T, Malmström GH, Bjerkeli V, Trøseid M, et al. Fecal level of butyric acid, a microbiome-derived metabolite, is increased in patients with severe carotid atherosclerosis. *Sci Rep.* (2022) 12(1):22378. doi: 10.1038/s41598-022-26759-x
72. Sun T, Zhang Y, Yin J, Peng X, Zhou L, Huang S, et al. Association of gut Microbiota-dependent metabolite trimethylamine N-oxide with first ischemic stroke. *J Atheroscler Thromb.* (2021) 28(4):320–8. doi: 10.5551/jat.55962
73. Tabata T, Yamashita T, Hosomi K, Park J, Hayashi T, Yoshida N, et al. Gut microbial composition in patients with atrial fibrillation: effects of diet and drugs. *Heart Vessels.* (2021) 36(1):105–14. doi: 10.1007/s00380-020-01669-y

74. Takagi T, Naito Y, Kashiwagi S, Uchiyama K, Mizushima K, Kamada K, et al. Changes in the gut Microbiota are associated with hypertension, hyperlipidemia, and type 2 diabetes Mellitus in Japanese subjects. *Nutrients*. (2020) 12(10):2996. doi: 10.3390/nu12102996
75. Tian R, Liu H, Feng S, Wang H, Wang Y, Wang Y, et al. Gut microbiota dysbiosis in stable coronary artery disease combined with type 2 diabetes mellitus influences cardiovascular prognosis. *Nutr Metab Cardiovasc Dis*. (2021) 31(5):1454–66. doi: 10.1016/j.numecd.2021.01.007
76. Tian R, Liu HH, Feng SQ, Wang YF, Wang YY, Chen YX, et al. Gut microbiota metabolic characteristics in coronary artery disease patients with hyperhomocysteinemia. *J Microbiol*. (2022) 60(4):419–28. doi: 10.1007/s12275-022-1451-2
77. Wang W, Li X, Yao X, Cheng X, Zhu Y. The characteristics analysis of intestinal microecology on cerebral infarction patients and its correlation with apolipoprotein E. *Medicine (Baltimore)*. (2018) 97(41):e12805. doi: 10.1097/MD.00000000000012805
78. Wang Z, Cai Z, Ferrari MW, Liu Y, Li C, Zhang T, et al. The correlation between gut Microbiota and Serum metabolomic in elderly patients with chronic heart failure. *Mediators Inflamm*. (2021) 2021:5587428. doi: 10.1155/2021/5587428
79. Xiang L, Lou Y, Liu L, Liu Y, Zhang W, Deng J, et al. Gut microbiotic features aiding the diagnosis of acute ischemic stroke. *Front Cell Infect Microbiol*. (2020) 10:587284. doi: 10.3389/fcimb.2020.587284
80. Xu DJ, Wang KC, Yuan LB, Li HF, Xu YY, Wei LY, et al. Compositional and functional alterations of gut microbiota in patients with stroke. *Nutr Metab Cardiovasc Dis*. (2021) 31(12):3434–48. doi: 10.1016/j.numecd.2021.08.045
81. Yan Q, Gu Y, Li X, Yang W, Jia L, Chen C, et al. Alterations of the gut microbiome in hypertension. *Front Cell Infect Microbiol*. (2017) 7:381. doi: 10.3389/fcimb.2017.00381
82. Yin J, Liao SX, He Y, Wang S, Xia GH, Liu FT, et al. Dysbiosis of gut Microbiota with reduced trimethylamine-N-oxide level in patients with large-artery atherosclerotic stroke or transient ischemic attack. *J Am Heart Assoc*. (2015) 4(11):e002699. doi: 10.1161/JAHA.115.002699
83. Yoshida N, Emoto T, Yamashita T, Watanabe H, Hayashi T, Tabata T, et al. *Bacteroides vulgatus* and *Bacteroides dozei* reduce gut microbial lipopolysaccharide production and inhibit atherosclerosis. *Circulation*. (2018) 138(22):2486–98. doi: 10.1161/CIRCULATIONAHA.118.033714
84. Yu H, Li L, Deng Y, Zhang G, Jiang M, Huang H, et al. The relationship between the number of stenotic coronary arteries and the gut microbiome in coronary heart disease patients. *Front Cell Infect Microbiol*. (2022) 12:903828. doi: 10.3389/fcimb.2022.903828
85. Zhao L, Wang C, Peng S, Zhu X, Zhang Z, Zhao Y, et al. Pivotal interplays between fecal metabolome and gut microbiome reveal functional signatures in cerebral ischemic stroke. *J Transl Med*. (2022) 20(1):459. doi: 10.1186/s12967-022-03669-0
86. Zheng Q, Chen Y, Zhai Y, Meng L, Liu H, Tian H, et al. Gut dysbiosis is associated with the severity of cryptogenic stroke and enhanced systemic inflammatory response. *Front Immunol*. (2022) 13:836820. doi: 10.3389/fimmu.2022.836820
87. Zheng YY, Wu TT, Liu ZQ, Li A, Guo QQ, Ma YY, et al. Gut microbiome-based diagnostic model to predict coronary artery disease. *J Agric Food Chem*. (2020) 68(11):3548–57. doi: 10.1021/acs.jafc.0c00225
88. Zhong J, Wu D, Zeng Y, Wu G, Zheng N, Huang W, et al. The microbial and metabolic signatures of patients with stable coronary artery disease. *Microbiol Spectr*. (2022) 10(6):e0246722. doi: 10.1128/spectrum.02467-22
89. Zhu Q, Gao R, Zhang Y, Pan D, Zhu Y, Zhang X, et al. Dysbiosis signatures of gut microbiota in coronary artery disease. *Physiol Genomics*. (2018) 50(10):893–903. doi: 10.1152/physiolgenomics.00070.2018
90. Zuo K, Li J, Li K, Hu C, Gao Y, Chen M, et al. Disordered gut microbiota and alterations in metabolic patterns are associated with atrial fibrillation. *Gigascience*. (2019) 8(6):giz058. doi: 10.13241/j.cnki.pmb.2023.08.028
91. Zuo K, Li J, Xu Q, Hu C, Gao Y, Chen M, et al. Dysbiotic gut microbes may contribute to hypertension by limiting vitamin D production. *Clin Cardiol*. (2019) 42(8):710–9. doi: 10.1002/clc.23195
92. Margolis KG, Cryan JF, Mayer EA. The Microbiota-gut-brain axis: from motility to mood. *Gastroenterology*. (2021) 160(5):1486–501. doi: 10.1053/j.gastro.2020.10.066
93. Wu M, Tian T, Mao Q, Zou T, Zhou CJ, Xie J, et al. Associations between disordered gut microbiota and changes of neurotransmitters and short-chain fatty acids in depressed mice. *Transl Psychiatry*. (2020) 10(1):350. doi: 10.1038/s41398-020-01038-3
94. Zheng P, Zeng B, Zhou C, Liu M, Fang Z, Xu X, et al. Gut microbiome remodeling induces depressive-like behaviors through a pathway mediated by the host's metabolism. *Mol Psychiatry*. (2016) 21(6):786–96. doi: 10.1038/mp.2016.44
95. Valles-Colomer M, Falony G, Darzi Y, Tigheelaar EF, Wang J, Tito RY, et al. The neuroactive potential of the human gut microbiota in quality of life and depression. *Nat Microbiol*. (2019) 4(4):623–32. doi: 10.1038/s41564-018-0337-x
96. Cui W, Xu L, Huang L, Tian Y, Yang Y, Li Y, et al. Changes of gut microbiota in patients at different phases of stroke. *CNS Neurosci Ther*. (2023) 29(11):3416–29. doi: 10.1111/cns.14271
97. Nikolova VL, Smith MRB, Hall LJ, Cleare AJ, Stone JM, Young AH. Perturbations in gut Microbiota composition in psychiatric disorders: a review and meta-analysis. *JAMA Psychiatry*. (2021) 78(12):1343–54. doi: 10.1001/jamapsychiatry.2021.2573
98. Bremner JD, Moazzami K, Wittbrodt MT, Nye JA, Lima BB, Gillespie CF, et al. Diet, stress and mental health. *Nutrients*. (2020) 12(8):2428. doi: 10.3390/nu12082428
99. Zhang H, Cao N, Zhang X, Tian L, Liu M. Correlation between intestinal Flora imbalance and prognosis of depression with coronary heart disease. *Progress in Modern Biomedicine*. (2023) 23(8):1541–5. 79.
100. Huang K, Duan J, Wang R, Ying H, Feng Q, Zhu B, et al. Landscape of gut microbiota and metabolites and their interaction in comorbid heart failure and depressive symptoms: a random forest analysis study. *mSystems*. (2023) 8(6):e0051523. doi: 10.1128/msystems.00515-23
101. Stevens BR, Pepine CJ, Richards EM, Kim S, Raizada MK. Depressive hypertension: a proposed human endotype of brain/gut microbiome dysbiosis. *Am Heart J*. (2021) 239:27–37. doi: 10.1016/j.ahj.2021.05.002
102. Moludi J, Khedmatgozar H, Nachvak SM, Abdollahzad H, Moradinazar M, Sadeghpour Tabaei A. The effects of co-administration of probiotics and prebiotics on chronic inflammation, and depression symptoms in patients with coronary artery diseases: a randomized clinical trial. *Nutr Neurosci*. (2022) 25(8):1659–68. doi: 10.1080/1028415X.2021.1889451
103. Nova E, Gómez-Martínez S, González-Soltero R. The influence of dietary factors on the gut Microbiota. *Microorganisms*. (2022) 10(7):1368. doi: 10.3390/microorganisms10071368
104. Morales G, Balboa-Castillo T, Fernández-Rodríguez R, Garrido-Miguel M, Guidoni CM, Sirtoli R, et al. Adherence to the Mediterranean diet and depression, anxiety, and stress symptoms in Chilean university students: a cross-sectional study. *Cad Saude Publica*. (2023) 39(10):e00206722. doi: 10.1590/0102-311xen206722
105. Sofi F, Cesari F, Abbate R, Gensini GF, Casini A. Adherence to Mediterranean diet and health status: meta-analysis. *Br Med J*. (2008) 337:a1344. doi: 10.1136/bmj.a1344
106. Wang DD, Toledo E, Hruby A, Rosner BA, Willett WC, Sun Q, et al. Plasma ceramides, Mediterranean diet, and incident cardiovascular disease in the PREDIMED trial (Prevención con Dieta Mediterránea). *Circulation*. (2017) 135(21):2028–40. doi: 10.1161/CIRCULATIONAHA.116.024261
107. Kimble R, Gouinguet P, Ashor A, Stewart C, Deighton K, Matu J, et al. Effects of a Mediterranean diet on the gut microbiota and microbial metabolites: a systematic review of randomized controlled trials and observational studies. *Crit Rev Food Sci Nutr*. (2023) 63(27):8698–719. doi: 10.1080/10408398.2022.2057416
108. Bayes J, Schloss J, Sibbritt D. The effect of a Mediterranean diet on the symptoms of depression in young males (the “AMMEND: a Mediterranean diet in MEN with depression” study): a randomized controlled trial. *Am J Clin Nutr*. (2022) 116(2):572–80. doi: 10.1093/ajcn/nqac106
109. Parletta N, Zarnowiecki D, Cho J, Wilson A, Bogomolova S, Villani A, et al. A Mediterranean-style dietary intervention supplemented with fish oil improves diet quality and mental health in people with depression: a randomized controlled trial (HELFIMED). *Nutr Neurosci*. (2019) 22(7):474–87. doi: 10.1080/1028415X.2017.1411320
110. Nannini G, Meoni G, Tenori L, Ringressi MN, Taddei A, Nicolai E, et al. Fecal metabolomic profiles: a comparative study of patients with colorectal cancer vs adenomatous polyps. *World J Gastroenterol*. (2021) 27(38):6430–41. doi: 10.3748/wjg.v27.i38.6430
111. Zhu W, Zhou S, Liu J, McLean RJC, Chu W. Prebiotic, immuno-stimulating and gut microbiota-modulating effects of Lycium barbarum polysaccharide. *Biomed Pharmacother*. (2020) 121:109591. doi: 10.1016/j.biopha.2019.109591
112. Ruscica M, Pavanello C, Gandini S, Macchi C, Botta M, Dall'Orto D, et al. Nutraceutical approach for the management of cardiovascular risk—a combination containing the probiotic *Bifidobacterium longum* BB536 and red yeast rice extract: results from a randomized, double-blind, placebo-controlled study. *Nutr J*. (2019) 18(1):13. doi: 10.1186/s12937-019-0438-2
113. Moludi J, Saiedi S, Ebrahimi B, Alizadeh M, Khajebishak Y, Ghadimi SS. Probiotics supplementation on cardiac remodeling following myocardial infarction: a single-center double-blind clinical study. *J Cardiovasc Transl Res*. (2021) 14(2):299–307. doi: 10.1007/s12265-020-10052-1
114. Yang B, Tian H, Ye C, Lin Z, Zhao D, Ma C, et al. The efficacy and safety of fecal Microbiota transplantation combined with biofeedback for mixed constipation: a retrospective cohort study. *Front Med (Lausanne)*. (2021) 8:746990. doi: 10.3389/fmed.2021.746990
115. Kedia S, Virmani S, KV S, Kumar P, Kante B, Sahu P, et al. Faecal microbiota transplantation with anti-inflammatory diet (FMT-AID) followed by anti-inflammatory diet alone is effective in inducing and maintaining remission over 1 year in mild to moderate ulcerative colitis: a randomised controlled trial. *Gut*. (2022) 71(12):2401–13. doi: 10.1136/gutjnl-2022-327811
116. El-Salhy M, Kristoffersen AB, Valeur J, Casen C, Hatlebakk JG, Gilja OH, et al. Long-term effects of fecal microbiota transplantation (FMT) in patients with irritable bowel syndrome. *Neurogastroenterol Motil*. (2022) 34(1):e14200. doi: 10.1111/nmo.14200

117. Li N, Wang Q, Wang Y, Sun A, Lin Y, Jin Y, et al. Fecal microbiota transplantation from chronic unpredictable mild stress mice donors affects anxiety-like and depression-like behavior in recipient mice via the gut microbiota-inflammation-brain axis. *Stress*. (2019) 22(5):592–602. doi: 10.1080/10253890.2019.1617267
118. Yoshida T, Das NA, Carpenter AJ, Izadpanah R, Kumar SA, Gautam S, et al. Minocycline reverses IL-17A/TRAF3IP2-mediated p38 MAPK/NF- $\kappa$ B/iNOS/NO-dependent cardiomyocyte contractile depression and death. *Cell Signal*. (2020) 73:109690. doi: 10.1016/j.cellsig.2020.109690
119. Camargos QM, Silva BC, Silva DG, Toscano ECB, Oliveira BDS, Bellozi PMQ, et al. Minocycline treatment prevents depression and anxiety-like behaviors and promotes neuroprotection after experimental ischemic stroke. *Brain Res Bull*. (2020) 155:1–10. doi: 10.1016/j.brainresbull.2019.11.009
120. Murrrough JW, Huryk KM, Mao X, Iacoviello B, Collins K, Nierenberg AA, et al. A pilot study of minocycline for the treatment of bipolar depression: effects on cortical glutathione and oxidative stress *in vivo*. *J Affect Disord*. (2018) 230:56–64. doi: 10.1016/j.jad.2017.12.067
121. Husain MI, Chaudhry IB, Khoso AB, Husain MO, Hodsoll J, Ansari MA, et al. Minocycline and celecoxib as adjunctive treatments for bipolar depression: a multicentre, factorial design randomised controlled trial. *Lancet Psychiatry*. (2020) 7(6):515–27. doi: 10.1016/S2215-0366(20)30138-3
122. Djekic D, Shi L, Brolin H, Carlsson F, Särnqvist C, Savolainen O, et al. Effects of a vegetarian diet on cardiometabolic risk factors, gut Microbiota, and plasma metabolome in subjects with ischemic heart disease: a randomized, crossover study. *J Am Heart Assoc*. (2020) 9(18):e016518. doi: 10.1161/JAHA.120.016518
123. Rinott E, Meir AY, Tsaban G, Zelicha H, Kaplan A, Knights D, et al. The effects of the green-Mediterranean diet on cardiometabolic health are linked to gut microbiome modifications: a randomized controlled trial. *Genome Med*. (2022) 14(1):29. doi: 10.1186/s13073-022-01015-z
124. Liu P, Liu Z, Wang J, Wang J, Gao M, Zhang Y, et al. Immunoregulatory role of the gut microbiota in inflammatory depression. *Nat Commun*. (2024) 15(1):3003. doi: 10.1038/s41467-024-47273-w
125. Alhmoud T, Kumar A, Lo CC, Al-Sadi R, Clegg S, Alomari I, et al. Investigating intestinal permeability and gut microbiota roles in acute coronary syndrome patients. *Hum Microb J*. (2019):13:100059. doi: 10.1016/j.humic.2019.100059
126. Liao L, Wang T, Zhang L, Wei Y, Fan X. Protective mechanisms of SGLT*i* in ischemic heart disease. *J Cardiovasc Transl Res*. (2024) 17(5):1018–35. doi: 10.1007/s12265-024-10513-x
127. Liao L, Zhang L, Yang C, Wang T, Feng L, Peng C, et al. Sotagliflozin attenuates cardiac dysfunction and depression-like behaviors in mice with myocardial infarction through the gut-heart-brain axis. *Neurobiol Dis*. (2024) 199:106598. doi: 10.1016/j.nbd.2024.106598
128. Wang J, Zhang J, Lin X, Wang Y, Wu X, Yang F, et al. DCA-TGR5 signaling activation alleviates inflammatory response and improves cardiac function in myocardial infarction. *J Mol Cell Cardiol*. (2021) 151:3–14. doi: 10.1016/j.yjmcc.2020.10.014
129. Lo AC, Callaerts-Vegh Z, Nunes AF, Rodrigues CM, D'Hooge R. Tauroursodeoxycholic acid (TUDCA) supplementation prevents cognitive impairment and amyloid deposition in APP/PS1 mice. *Neurobiol Dis*. (2013) 50:21–9. doi: 10.1016/j.nbd.2012.09.003
130. Lu X, Yang RR, Zhang JL, Wang P, Gong Y, Hu WF, et al. Tauroursodeoxycholic acid produces antidepressant-like effects in a chronic unpredictable stress model of depression via attenuation of neuroinflammation, oxido-nitrosative stress, and endoplasmic reticulum stress. *Fundam Clin Pharmacol*. (2018) 32(4):363–77. doi: 10.1111/fcp.12367
131. Abdel-Haq R, Schlachetzki JCM, Glass CK, Mazmanian SK. Microbiome-microglia connections via the gut-brain axis. *J Exp Med*. (2019) 216(1):41–59. doi: 10.1084/jem.20180794
132. Tan C, Wu Q, Wang H, Gao X, Xu R, Cui Z, et al. Dysbiosis of gut Microbiota and short-chain fatty acids in acute ischemic stroke and the subsequent risk for poor functional outcomes. *JPEN J Parenter Enteral Nutr*. (2021) 45(3):518–29. doi: 10.1002/jpen.1861
133. Chen R, Xu Y, Wu P, Zhou H, Lasanajak Y, Fang Y, et al. Transplantation of fecal microbiota rich in short chain fatty acids and butyric acid treat cerebral ischemic stroke by regulating gut microbiota. *Pharmacol Res*. (2019) 148:104403. doi: 10.1016/j.phrs.2019.104403