

The Role of Intestinal Flora and Its Metabolites in Heart Failure

Xueqing Guan, Zhijun Sun

Department of Cardiology, Shengjing Hospital of China Medical University, Shenyang, People's Republic of China

Correspondence: Zhijun Sun, Department of Cardiology, Shengjing Hospital, No. 39 of Huaxiang Road, Tiexi District, Shenyang, 110021, People's Republic of China, Tel +86 18940251218, Fax +86 18940251218, Email sunzhijunszj8@126.com

Abstract: Intestinal flora is a complex collection of microbial communities that participate in the physiological and pathological activities of the human body through various pathways. In recent years, numerous studies have reported that intestinal flora are involved in the occurrence and development of heart failure (HF) and its metabolic products could play an important role in this progression, suggesting a great value in the clinical treatment of this condition. This study reported the interaction between intestinal flora and HF, and with intestinal flora metabolites, such as short-chain fatty acids, trimethylamine N-oxide and bile acids and urotoxins, considered as the starting point, the mechanism of the roles in HF was summarized. Additionally, the current research status and the development prospects of applying flora and metabolites to the clinical therapeutic decision of HF were discussed.

Keywords: intestinal flora, heart failure, trimethylamine N-oxide, inflammation, probiotics, targeted therapy, fecal microbiota transplantation

Introduction

Heart failure is a complex group of clinical syndromes caused by abnormal changes in the structure and/or function of the heart due to multiple causes; it results in impaired ventricular systolic and/or diastolic function, which primarily manifests as dyspnea, fatigue, and fluid retention (pulmonary congestion, systemic circulation congestion, and peripheral edema).¹ HF is characterized by a high incidence and a high mortality rate. Data from developed countries show that the prevalence of HF in the current population is 1.5% to 2.0%, and 5-year mortality rates for inpatients with HF are 10.4%, 22%, and 42.3%, respectively.² Patients with HF often have a decreased cardiac output combined with peripheral circulation congestion, causing intestinal ischemia and edema. In this case, the function of the intestinal barrier is weakened. Increased permeability of the intestinal wall and dislocation of the flora occur since harmful metabolites can enter the bloodstream through the damaged intestinal mucosal barrier, producing more inflammatory stimuli and aggravating HF.³

Intestinal flora is a complex collection of microbial communities which closely connected with the human body through direct or indirect pathways. In one way, intestinal flora can be recognized by intestinal cells and thus act directly. Peptidoglycan, LPS, flagellin, and formyl peptides in bacterial structures, which are called micro-associated molecular patterns (MAMPs), can be selectively recognized by the pattern recognition receptors on the surface of intestinal mucosal cells, such as the host toll-like receptors and receptors containing nucleotide oligomerization domains.⁴ In addition, intestinal flora might also act as an endocrine organ, metabolizing and secreting active substances that indirectly affect other physiological functions of the host through various pathways.

The current research status of the influence of the metabolic secretion products of intestinal flora on HF and its clinical application were summarized in the present study to discuss the possibility of applying the products in the diagnosis and treatment of HF.

Intestinal Flora Alteration Induced by Heart Failure

Patients with HF, especially those with right heart involvement, often have a decreased cardiac output combined with peripheral circulation congestion, causing intestinal ischemia and edema. In this case, the function of the intestinal barrier is weakened. The earliest description of altered intestinal flora in patients with HF was published in 2015, which uncovered that patients with HF had an increased intestinal aggregation of harmful bacteria.⁵ Although limitations existed in the sample collection and data processing, it may still function as an important guide for subsequent investigations. The study revealed that the alpha diversity of the intestinal flora in patients with HF decreased correspondingly with increasing severity of cardiac insufficiency (the New York Heart Association [NYHA] classification), while inflammation and oxidative stress levels increased concurrently.³ In clinical practice, intestinal ischemia can be determined by decreases in intestinal mucosal pH⁶ and passive carrier-mediated d-xylose transport.⁷ Intestinal edema can manifest as a thickening of the intestinal wall. In addition, intestinal permeability can be determined by lactose mannitol and cellobiose tests.^{5,8}

A decrease in the production of short-chain fatty acids (SCFAs) by related flora (eg, *Lachnospiraceae*) has been observed in patients with HF. Among them, the decrease in the abundance of related flora, such as *Faecalibacterium prausnitzii*, *Eubacterium rectale*, and *Roseburia*, with the production of butyrate was more prominent.⁹ The abundance of microbial genes related to the production of LPS and TMA N-oxide (TMAO) was increased. Pasini et al discovered that patients with stable chronic HF with reduced ejection fraction had increased intestinal pathogenic bacteria, including *Candida*, *Campylobacter*, *Shigella*, *Salmonella*, and *Yersinia*, compared with healthy controls⁵ (Figure 1).

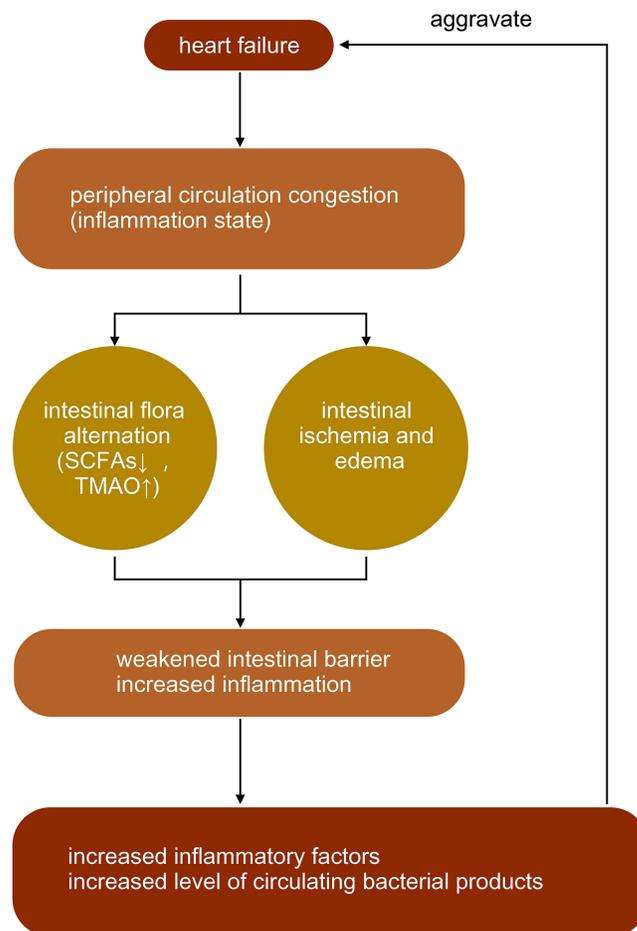


Figure 1 The interaction between heart failure and intestinal flora.

Note: ↑ mean increase, ↓ mean decrease.

Intestinal Flora in Human Body

A Close Relationship of Symbiosis

There are approximately 3.8×10^{13} microbial cells in each human body, far exceeding the number of human cells.¹⁰ Most of these microorganisms are present in the intestinal tract, especially the colon, and some are also distributed in the nasopharynx, mouth, lungs, skin, and cervix. These microbes are called “human microbiota” and consist of approximately 3.3 million microbial genes, which exceeds the number of human genes (approximately 25,000).¹¹ Intestinal flora starts to colonize from birth and increases rapidly after two to three years of age; then, it maintains a dynamic balance under the influence of genes, the environment, and diet for most of a person’s life span. It tends to decrease again when an individual ages to a certain level or develops a serious disease.¹² The intestinal microbiota varies from person to person and even between locations within the same individual, and some of the flora that perform major metabolic functions, which are known as core flora, are similar. The intestinal microbial community is composed of four main phyla: *Bacteroidetes*, *Firmicutes*, *Actinobacteria*, and *Proteobacteria*.¹³ The flora in these four major groups contains most of the dominant flora, which plays an important role in supporting the physiological functions of the host and determines the physiopathological significance of the flora to the host. Of these phyla, *Bacteroidetes* and *Firmicutes* account for 90% of the total bacterial population in a healthy intestine.

The Functions of Intestinal Flora

Intestinal flora is involved in many metabolic processes in the body, including the absorption of indigestible fibers (eg, polysaccharides and resistant starches of plant cell walls) and energy utilization, the production of vitamins and amino acids, and the metabolism of drugs. In addition to acting directly with intestinal cells through substances such as LPS in the structure, intestinal flora might also act as an endocrine organ, metabolizing and secreting active substances that indirectly affect other physiological functions of the host through various pathways. The details of these actions including: a) promote gut mucus barrier, modulate the immune activation and against restrain inflammatory via SCFA pathways,^{14,15} b) participate in the formation of atherosclerotic plaques via TMA and TMAO pathways,^{16,17} c) act on HF through primary and secondary bile acid (BA) pathways,^{18,19} and d) regulate the mitochondrial function in cardiomyocytes and influence myocardial contractility via the urotoxin (eg, indole-3-propionic acid) pathways.²⁰

Intestinal Flora Acts on Heart Failure Through Metabolic Secretory Pathways

Short-Chain Fatty Acids

Short-chain fatty acids are the end products of dietary fiber fermentation by gut microbiomes such as *Bacteroides*, *Bifidobacterium* and *Faecalibacterium*,^{21,22} they are produced primarily by the glycolytic metabolic pathway and the protein metabolic pathway and include various ammonias, amines, thiols, etc. Short-chain fatty acids, such as acetic acid, propionic acid, and butyric acid, produced by the catabolism of glucose are the main sources of energy for colonocytes (which maintain the intestinal mucosal barrier) and are closely associated with the promotion of intestinal immune function. It has been proved that SCFAs act not only as energy sources, but also as ligands and act in various pathways. SCFAs mainly combine with G protein-coupled receptors (GPCRs), including GPR41, GPR43 and GPR109a. They can also recognize with Olfr78, and inhibit the activation of histone deacetylase.²³ Butyrate induces the proliferation of Forkhead box P3+ regulatory T cells and activates G protein-coupled receptors to inhibit the production of Th17 cells, thus producing anti-inflammatory effects.²⁴ In addition, butyrate helps maintain the relative physiological hypoxia of the colonic epithelial mucosa by activating hypoxia-inducible factors, which are essential for maintaining the function of the intestinal barrier.²⁵ In terms of immunity, butyric acid promotes the maturation of T cells on the surface of the intestinal mucosa, which is involved in chronic immune activation and is beneficial in suppressing ventricular remodeling (VR)²⁶.

It was found that SCFAs appeared to promote post-infarction cardiac repair by inducing the infiltration of CX3CR1+ monocytes in the peri-infarct zone.²⁷ Pluznick et al stated that SCFAs (acetic acid/propionic acid) inhibited myocardial fibrosis and suppressed VR. Short-chain fatty acids also play a role in other cardiovascular diseases; for example, SCFAs including acetic, propionate as well as butyrate are involved in the regulation of blood pressure^{23,28} (Table 1 and Figure 2).

Table 1 Microbial Metabolites and Heart-Failure-Related Research Reference

Metabolites	Author and Years	Research Object	Main Findings	Reference	
SCFAs	Carrillo-Salinas et al (2020)	WT mice T cell-deficient mice (Tcra ^{-/-}) mice	Cardiac pressure overload induced gut dysbiosis and T cell immune responses contribute to adverse cardiac remodeling.	[24]	
	Kelly et al (2015)	Germ-free Mice	1. Bacteria-derived butyrate affects epithelial O ₂ consumption and results in stabilization of hypoxia-inducible factor (HIF), a transcription factor coordinating barrier protection. 2. Antibiotic-mediated depletion of the microbiota reduces colonic butyrate and HIF expression, both of which are restored by butyrate supplementation.	[25]	
	Vijay et al (2021)	Healthy participants	Dietary interventions can alter validated biomarkers linked to cardiovascular risk via the gut microbiome composition and its metabolic functions.	[26]	
	Tang et al (2019)	C57BL/6j mice	Gut microbiota-derived SCFAs play an important role in maintaining host immune composition and repair capacity after MI.	[27]	
	Pluznick et al (2013)	WT mice Olfcr78 ^{-/-} mice	SCFAs produced by the gut microbiota modulate blood pressure via Olfcr78 and Gpr41.	[28]	
TMA/TMAO	Suzuki et al (2019)	HF patients	1. TMAO levels were associated with adverse outcomes (mortality and/or rehospitalisation) in BIOSTAT-CHF, and did not respond to guideline-based pharmacological treatment in contrast to BNP levels which did as expected. 2. Lower TMAO levels were associated with favourable outcome regardless of treatment.	[33]	
	Tang et al (2014)	Stable HF patients healthy individuals without known cardiac disease	High TMAO levels were observed in patients with HF, and elevated TMAO levels portended higher long-term mortality risk independent of traditional risk factors and cardiorenal indexes.	[34]	
	Trøseid et al (2015)	Patients with chronic HF patients with stable CAD without HF Healthy individuals	TMAO levels were elevated in patients with HF and associated with NYHA class, ischaemic aetiology and adverse outcomes.	[35]	
	Zhang W et al (2013)	ApoE KO mice on C57BL/6j background	The inhibition of TMAO production attenuated CKD development and cardiac hypertrophy in mice.	[38]	
	Wang et al (2020)	C57BL/6j mice	3,3-dimethyl-1-butanol (DMB) can reduce plasma TMAO levels.	[59]	
	BA	Mayerhofer et al (2017)	Patients with chronic HF Healthy control subjects (age- and sex-matched)	Levels of primary BAs were reduced and specific secondary BAs increased in patients with chronic HF. This pattern was associated with reduced overall survival in univariate analysis, but not in multivariate analyses.	[40]
		Xu J et al (2019)	Adult male Sprague-Dawley rats	Multiple bile acids were biomarkers of heart failure and may participate in the development of heart failure.	[44]
Liu S et al (2020)		Adult male Sprague-Dawley rats	Bile acid metabolism disorder occurred in chronic heart failure.	[45]	
Von Haehling S et al (2012)		Male patients with CHF	Ursodeoxycholic acid improved endothelial function and inflammatory markers in patients with CHF.	[46]	
Eblimit Z et al (2018)		Male C57BL/6j mice	Bile acids, specifically TGR5 agonists, induce cytoprotective changes in the heart and improve myocardial response to physiologic, inotropic, and hemodynamic stress in mice.	[48]	

(Continued)

Table 1 (Continued).

Metabolites	Author and Years	Research Object	Main Findings	Reference
Urotoxins	Gesper et al (2021)	1. Murine cardiomyocytes (HL-1) Human hepatoma cell line (Huh7) Human umbilical vein endothelial cells (HUVEC)	Microbial tryptophan derivative indole-3-propionic acid could be identified as a modulator of mitochondrial function in cardiomyocytes. While acute treatment induced enhancement of maximal mitochondrial respiration, chronic exposure led to mitochondrial dysfunction in cardiomyocytes.	[20]
	Lekawanvijit et al (2010)	2. C57BL/6j mice Neonatal rat cardiac myocytes (NCMs) Fibroblasts (NCFs) Human leukaemia monocytic cell line (THP-1) cells	Indoxyl sulfate significantly increased neonatal rat cardiac fibroblast collagen synthesis and myocyte hypertrophy.	[53]
	Yang et al (2015)	Neonatal rat cardio myocytes (NCMs)	1. IS induces ROS generation in cardiomyocytes by down-regulation of UCP2. 2. UCP2 attenuates IS-induced cardiomyocyte hypertrophy by inhibiting ROS production. 3. AMPK inactivation contributes to IS-induced UCP2 down-regulation.	[54]
	Yang et al (2015)	1. CKD patients 2. WT mice kl/+ mice	Klotho, a putative antiaging gene, is an endogenous protector against IS-induced LVH, and the imbalance between Klotho and IS may contribute to the development of LVH in CKD.	[55]

Abbreviations: SCFAs, short chain fatty acids; MI, myocardial infarction; WT, wild type; TMAO, trimethylamine N-oxide; HF, heart failure; CHF, chronic heart failure; DMB, 3,3-dimethyl-1-butanol; BIOSTAT-CHF, BIOlogy Study to TAilored Treatment in Chronic Heart Failure; BAs, bile acids; CKD, chronic kidney disease; IS, indoxyl sulfate; LVH, left ventricular hypertrophy; ROS, reactive oxygen species; UCP2, uncoupling protein 2.

The abilities of intestinal regulation and anti-inflammatory of short-chain fatty acids have been demonstrated. However, its more direct protective effect on the heart in heart failure, such as anti-myocardial fibrosis, needs further experiments to support it. At present there are only animal trials of short-chain fatty acids can reduce myocardial fibrosis and lack enough supports from clinical trials.

Trimethylamine N-Oxide

Trimethylamine N-oxide is primarily derived during the process of digestion and the decomposition of food. During digestion process food can be broken down into choline and L-carnitine, which are later fermented by intestinal microbiota such as *Firmicutes* and *Proteobacteria* into TMA.²⁹ TMA is then absorbed into the blood and transported to the liver, where it is catalyzed by flavin-containing monooxygenases and consequently metabolised to TMAO.

It has been verified that TMAO may be directly involved in the generation of coronary atherosclerotic plaques.^{30,31} In HF, TMAO was determined to be associated with an increased 5-year mortality rate in patients with HF, a poor prognosis in acute HF, and a higher NYHA classification.^{32,33} Trimethylamine N-oxide is correlated with b-type natriuretic peptide and the echocardiographic indicators of diastolic function (eg, E/Ea and left atrial volume index), while patients with high TMAO levels had worse left ventricular diastolic insufficiencies and clinical prognoses than those with low TMAO levels. However, TMAO is not correlated with systolic function, such as left ventricular ejection fraction.^{34,35} The observation results of choline-fed mice showed a direct effect of elevated TMAO levels on the activation of the myocardial pro-fibrotic pathway.³⁶

Trimethylamine N-oxide also plays a role in kidney injury in addition to promoting myocardial fibrosis and participating in VR. In a cardiac study including 1434 participants without chronic kidney disease (CKD) at the baseline, it was revealed that the levels of choline and TMAO were independent predictors of future CKD.³⁵ In animal

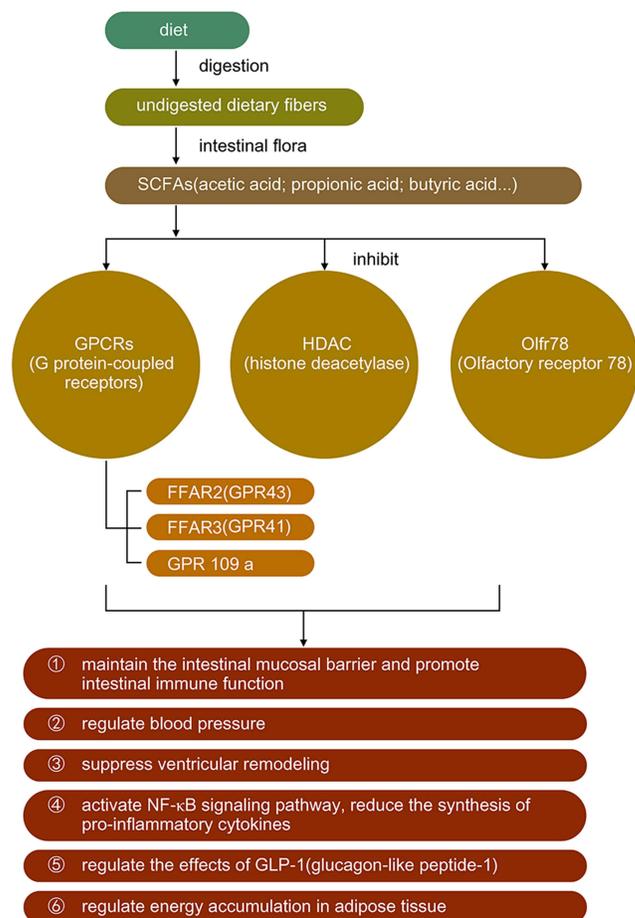


Figure 2 The synthesis of short-chain fatty acids and its effects.

experiments, mice fed with choline or TMAO had increased renal fibrosis and elevated markers of kidney injury, such as cysteine inhibitor-c.³⁶ In one study, the development of CKD and cardiac hypertrophy was delayed in mice fed with iodomethylcholine, an inhibitor of TMA production.³⁷ These results further supported the close relationship between TMAO and CKD (Table 1 and Figure 3).

Given that patients with chronic heart failure are often combined with renal dysfunction while TMAO is associated with kidney injury, it may lead to a decline in the prognosis ability of TMAO in patients with HF and CKD. In addition, interindividual dietary differences and ethnic differences would also make it more difficult to set a standard for TMAO and its application in clinical practice needs more in-depth research.

Bile Acids

The physiological function of BA is to promote the absorption of dietary fat, fat-soluble molecules, and cholesterol and gut bacteria such as Bacteroides, Clostridium, and Lactobacillus could affect bile salt hydrolase gene expression.³⁸ However, recent studies have found that BA not only has physiological significance but also plays a role in diseases such as HF.³⁹ Farnesoid X receptors are highly expressed in the liver and ileum and negatively regulate BA synthesis by regulating different transcriptional networks.^{40,41} Tauro- β -muricholic acid is an abundant primary BA produced by intestinal flora, which upregulates the size and composition of the BA library and acts as a farnesoid X receptor antagonist. The ratio of the secondary to primary BAs in the blood was increased in patients with chronic HF, and a univariate analysis revealed that this ratio might be correlated with a decrease in overall survival.^{39,42} Multiple metabolomic studies also showed that the mechanism of HF was closely related to the metabolic disorder of bile

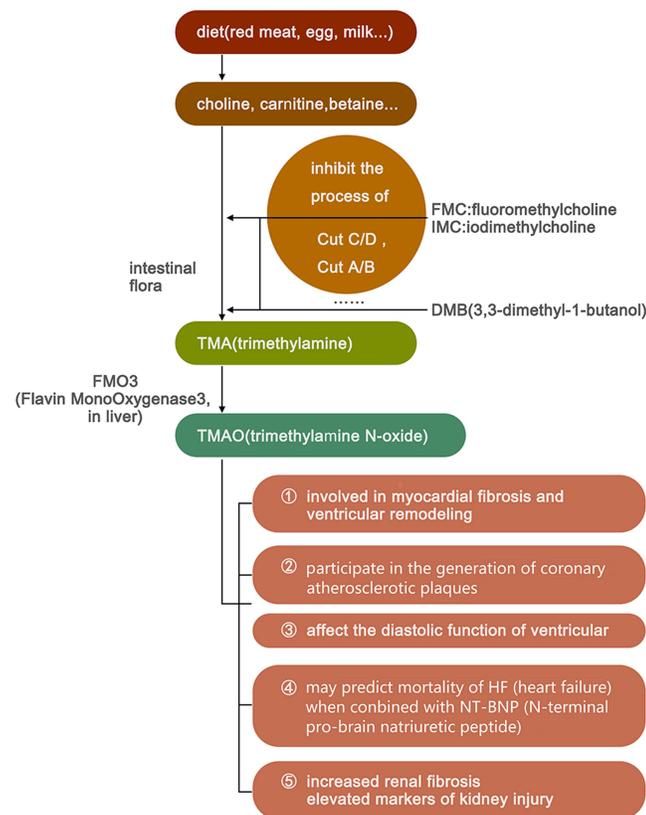


Figure 3 The synthesis of trimethylamine N-oxide and its effects.

acids.^{43,44} Some bile acids, such as ursodeoxycholic acid found to be significantly reduced in HF, have been proved to be beneficial to improving the peripheral blood flow of patients with HF and protecting the heart from reperfusion injury.⁴⁵ The discovery of bile acid receptors has greatly expanded the understanding of the role of bile acids in HF, such as farnesoid X receptor (called FXR) and G-protein coupled bile acid receptor 1 (called TGR5). Farnesoid X receptors are highly expressed in the liver and ileum and negatively regulate BA synthesis by regulating different transcriptional networks.^{40,41} FXR activation can improve bile acid ratio and inhibit NF- κ b, thereby reducing inflammation and improving myocardial function.⁴⁶ Bile acids, especially TGR5 agonists, can induce protective changes in cardiac cells and improve the myocardial response of mice to physiological, positive muscle force and hemodynamic stress.⁴⁷ These results suggested that BA metabolism might be regulated by intestinal flora, thus slowing the progression of HF (Table 1 and Figure 4).

Urotoxins

Tryptophan is derived from dietary protein and is metabolized by intestinal microorganisms to produce a variety of indole derivatives.⁴⁸ Indole may be involved in a variety of normal physiological activities as a signaling molecule, such as affecting intestinal colony distribution, regulating gene expression in intestinal epithelial cells that affect barrier function, regulating glucagon-like peptide-1 secretion, and regulating anti-inflammation and antioxidation. However, some tryptophan metabolites, such as indole sulfate (IS), may have negative effects on the organism. Indole sulfate is metabolized from indole in the liver under the action of cytochrome P450 enzymes. In patients with renal insufficiency, urinary excretion is reduced, and IS accumulates in the body as a urotoxin, inducing tubulointerstitial fibrosis, glomerulosclerosis, and oxidative stress in the endothelial cells.^{49–51} In cardiovascular disease, IS may activate p38 mitogen-activated protein kinase, p42/44 mitogen-activated protein kinase, and nuclear factor- κ B pathways, thereby stimulating the myocardial fibroblasts and collagen synthesis and resulting in adverse cardiac remodeling. In vitro studies also confirmed

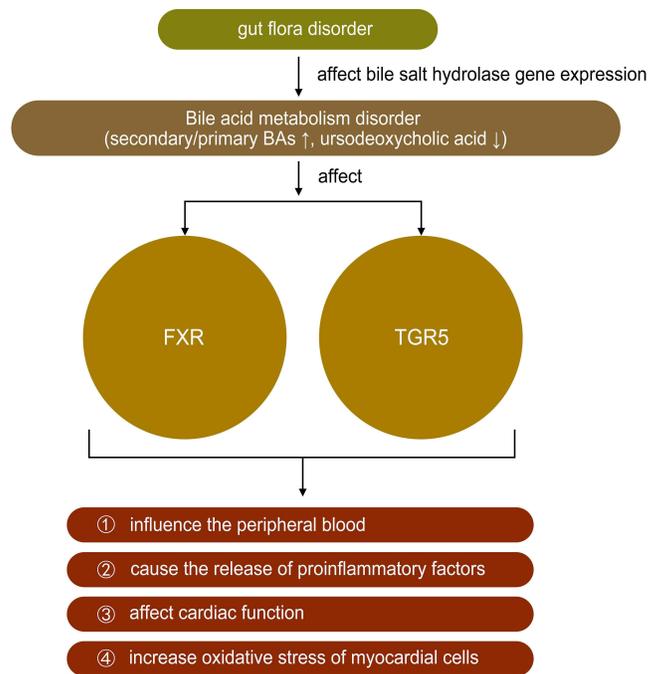


Figure 4 The role of bile acids in heart failure.
Note: ↑ mean increase, ↓ mean decrease.

the direct effect of IS on the induction of cardiomyocytes hypertrophy and collagen synthesis in cardiac fibroblasts.^{49,52,53} A study in 2021 showed that the microbial tryptophan derivative indole-3-propionic acid could be identified as a regulator of mitochondrial function in cardiomyocytes. Acute treatment induced an enhanced maximal mitochondrial respiration, while chronic exposure resulted in mitochondrial dysfunction in cardiomyocytes in isolated perfused hearts of mice. The latter effect could also be observed in human hepatic and endothelial cells²⁰ (Table 1 and Figure 5).

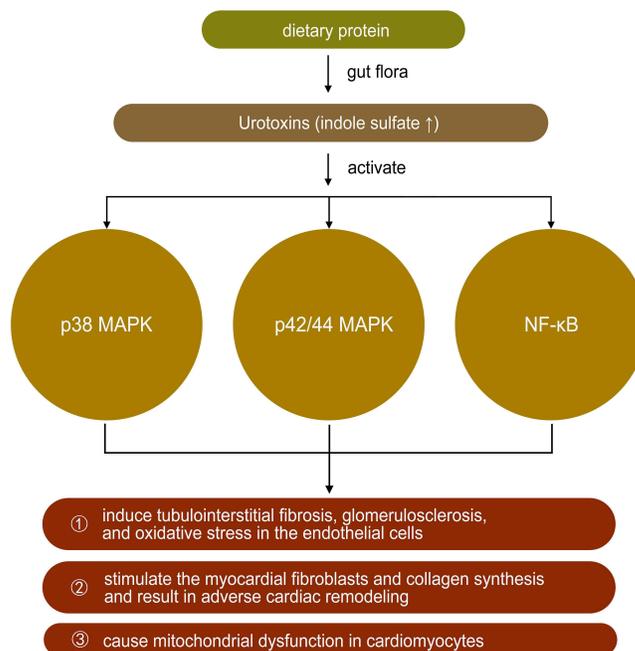


Figure 5 The role of urotoxins in heart failure.
Note: ↑ mean increase.

Based on the effect of IS on cardiac fibrosis and the characteristics of its transrenal metabolism in the above studies, the inhibition of its production or accelerate its clearance to reduce its accumulation in body is essential for patients with heart failure and renal insufficiency in improving their prognosis.

The Clinical Value of Intestinal Flora in Heart Failure (Figure 6)

Potential Predictive Markers

The high mortality rate and poor prognosis of heart failure are still problems to be solved. As for the inner reason, the current lack of understanding of the pathogenesis contributes to the predicament to the same extent as the frequent multi-systemic involvement. In clinical practice, assessing HF disease development requires more abundant, more objective and more accurate indicators. Studies have found that in patients with acute heart failure, TMAO has a significant correlation with renal function (BUN, eGFR) and cannot be used as an independent predictor. However, after combining the clinical algorithm and NT-BNP it can predict mortality during hospital stay and mortality within 1 year.³² In a trial containing a sample of 720 patients, CHF patients had significantly higher TMAO levels and a 3.4-fold increased risk of death when compared with age-, sex-matched non-HF patients. Higher TMAO levels can still predict a 5-year increased risk of mortality even after adjustment for traditional risk factors and cardiorenal index.³³ Furthermore, a multicenter study involving 11 European countries showed that patients with lower TMAO levels at baseline or follow-up had higher survival rates, and persistently elevated TMAO levels before and after treatment were associated with higher mortality.³²

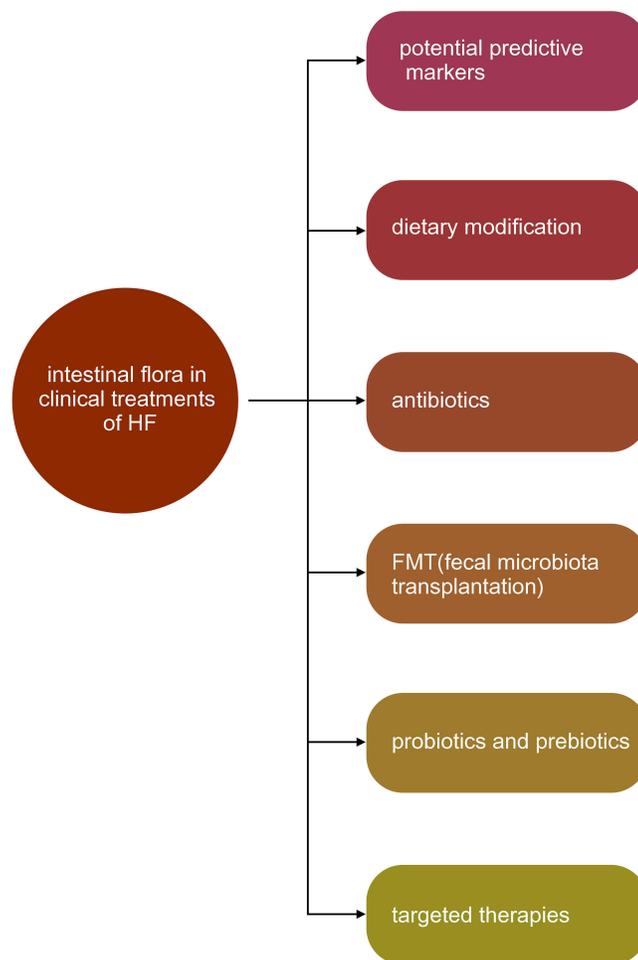


Figure 6 The clinical value of intestinal flora in heart failure.

However, the production of TMAO can be significantly influenced by diet and the level of TMAO in plasma varies in different regions and ethnic groups.⁵⁴ Thus, there are still no specific criteria for the level of elevated TMAO, and further clinical trials are needed to evaluate the effectiveness of combining TMAO and other indicators to predict heart failure.

Feasible Strategies of Treatment

Dietary Modification

Several studies have shown that the consumption of fiber-rich foods is associated with healthier intestinal microbiota and lower mortality rates. A systematic review and meta-analysis of randomized controlled trials showed that the Mediterranean diet reduced the incidence of HF by 70%.⁵⁵ In addition, since TMAO is derived primarily from dietary choline and carnitine, reducing the intake of red meat can also reduce the production of TMAO in the body.⁵⁶ In addition, an ingredient called DMB, which can be found in virgin olive oil can inhibit the production of TMA.⁵⁷ However, due to the complexity of food sources, more precise control of variables is necessary to obtain more definitive results in the investigation of the dietary effects on HF.

Antibiotics

It has been suggested that the oral administration of polymyxin B, which can selectively kill gram-negative bacteria, could reduce the production of pro-inflammatory factors by monocytes in patients with HF, which in turn could improve flow-mediated dilation and improve vascular endothelial function.⁵⁸ However, the results of multiple trials have shown that due to the poor selectivity of antibiotics, although pathogenic flora was removed, the beneficial flora was significantly weakened. Therefore, since the function of the intestinal flora was seriously weakened, an increased risk of cardiovascular disease, diabetes mellitus, and other diseases was revealed, and the long-term disadvantages outweighed the advantages.

Fecal Microbiota Transplantation

The primary function of fecal microbiota transplantation (FMT) is to deliver the intestinal flora from healthy individuals to the intestine of a patient to regulate the balance of their intestinal flora, usually in an endoscopic route. In current clinical circumstances, FMT is often used in the treatment of severe infections or inflammatory bowel diseases (IBD). In heart failure treatments, FMT is adopted as a potential auxiliary therapy. There are several experiments on FMT and its effects on cardiovascular diseases for now. In an experiment on atherosclerosis pathogenesis, fecal microbiota transplanted from WT mice could improve gut microbiome composition and reduce the atherosclerosis level of atherosclerosis-prone CTRP9-KO mice.⁵⁹ Studies also showed that FMT could alleviate inflammatory infiltration, and thus reduce myocardial injury.⁶⁰ However, FMT also carries risk, and in a clinical trial, one of the two patients who accepted a FMT treatment died due to improper donor screening.⁶¹ The procedure and operation of FMT still need further standardization and optimization, including screening for suitable donors, developing gentler non-invasive delivery methods, and extracting more specific ingredients for more individualized therapeutic strategies.

Probiotics and Prebiotics

Probiotic therapy is the direct administration of certain beneficial flora, such as *Bifidobacteria*, to promote the balance of intestinal flora. Prebiotics, such as dietary fiber, have certain specific ingredients that can produce a therapeutic effect. The consumption of probiotics or prebiotics can improve the distribution of intestinal flora and reduce the production of related harmful metabolites and inflammatory factors. The results of animal experiments suggested that certain lactic acid bacteria could have cardioprotective effects. Rats were given a supplement containing *Lactobacillus plantarum* 299v, followed by a coronary artery ligation and observation. Reduced myocardial infarct size and improved left ventricular function were observed in rats fed with probiotics.⁶² Another study found that the addition of *L. rhamnosus* GR-1 to a rat model with myocardial ischemia resulted in similar cardioprotective effects.⁶³ In terms of the investigation on prebiotics, a recent randomized controlled trial showed that the addition of inulin or inulin-propionate ester to the diet in experimental animals increased the delivery of SCFAs in the colon.⁶⁴ Although current scientific evidence does not yet support the application of probiotics or prebiotics in the treatment of patients with HF, the production of SCFAs via supplementation with inulin or other prebiotics provides a strategy for the treatment of cardiovascular disease.

Targeted Therapies

There is a broad prospect of taking metabolic products as targeted drug in treatments of cardiovascular diseases. Several inhibitors of enzymes have been tested in trials. Fluoromethylcholine (FMC) and iodomethylcholine (IMC) are inhibitors of cutC/D, a kind of enzyme participants the produce of TMA. They can permanently inactivate cutC/D without affecting the viability of the commensal bacteria. In animal models, FMC and IMC significantly reduced systemic TMAO levels and reversed TMAO-induced platelet hyperactivity as well as thrombosis.⁶⁵ Inhibitors of FMOs in the liver can reduce TMAO generation, but can also cause TMA accumulation and lead to complications such as acute hepatitis.⁶⁶ Short-chain fatty acids entering the systemic circulation were shown to have the ability to regulate cardiovascular disease risk factors, including lowering blood pressure and regulating blood glucose and lipid homeostasis. Oral charcoal adsorbent (AST-120) has been used clinically to remove uremic toxins, such as indoxyl sulfate, in patients with advanced renal failure. Moreover, existing animal trials have shown that AST-120 can prevent the progression of LV hypertrophy and myocardial fibrosis.⁶⁷ At present, most of the studies on the role of metabolites are animal experiments, but it is foreseeable that the application of microbiota metabolic products in the treatment of heart failure is of great value.

Conclusions and Future Perspectives

Heart failure affects intestinal microbiota community structure, leading to the dysfunction of gut microbiota. On the other hand, microbiota dysbiosis and the accumulation of some microbiota-derived metabolites aggravate heart failure progression in multiple aspects. Intestinal flora is similar to an endocrine organ and is involved in many metabolic pathways of the body, both directly and indirectly, that affect the functions of the host. There are emerging evidences that intestinal flora is closely connected with diabetes mellitus, obesity, hypertension and other chronic diseases.

There is quite a lot of clinical data to prove that intestinal microbiota experiences a dysbiosis in patients with heart failure compared to healthy cohorts, even in HFpEF patients.^{68–70} Further studies also uncovered the fact that diets could effect cardiovascular risk factors such as the blood lipid by means of intestinal microbiome.²⁶ In laboratory investigations with rats, we found that the effects of microbiota-derived metabolites on inflammation factors, fibrosis substances and other aspects correlated with heart failure.^{3,71,72} However, the mass insufficiency in the studies for now should not be ignored. On one hand, the superficial analysis of the diversity changes in microbiota is far from enough and specific function of bacterium ought to be explored. Only in that way could we make more precise evaluation on the effects of microbiota and its metabolites. On the other hand, more clinical trials are needed to transmit the achievements in animal studies into practical treatments. Meanwhile, the current clinical outcomes should also be verified with larger scales of experiments. What is more, the effect of medicine applied in current heart failure treatments is an essential part too. For example, the SGLT-2 inhibitors, which are introduced into the clinical treatments in heart failure in recent years seems to share similar accesses with gut microbiota when they come into effect.^{23,73} Therefore, the study on correlations between drugs and microbiota is of great significance. However, it is undeniable that the regulation of the microflora and its metabolites will have an extremely important role in the long-term treatment of heart failure.

Abbreviation

HF, heart failure; LPS, lipopolysaccharide; CRP, C-reactive protein; TNF- α , tumour necrosis factor alpha; VR, ventricular remodeling; pH, potential of hydrogen; TMA, trimethylamine; TMAO, trimethylamine N-oxide; MAMPs, micro-associated molecular patterns; prr, pattern recognition receptors; SCFAs, short chain fatty acids; E/Ea, the ratio of peak velocity of early tricuspid inflow wave (E) to peak velocity of early diastolic wave of the lateral tricuspid annulus (Ea); CKD, chronic kidney disease; IMC, iodomethylcholine; NT-proBNP, N-terminal prohormone of brain natriuretic peptide; GLP-1, glucagon-like peptide 1; IS, Indoxyl sulfate; 16sRNA, 16S ribosomal DNA identification; RCT, randomized clinical trial; FMT, fecal microbiota transplantation; BA, bile acids; DMB, 3,3-dimethyl-1-butanol; IBD, inflammatory bowel diseases; SGLT-2 inhibitors, sodium-glucose cotransporter-2 inhibitors; HFpEF, heart failure with preserved ejection fraction.

Data Sharing Statement

The datasets used and/or analysed during the current study available from the corresponding author on reasonable request.

Disclosure

The authors report no conflicts of interest in this work.

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