

IMPACT OF GUT MICROBIOME ON CARDIOVASCULAR DISEASE: A NARRATIVE REVIEW

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Abstract

Cardiovascular disease (CVD) is the primary cause of morbidity and mortality globally. The role of the gut microbiota in the development and progression of CVD is increasingly appreciated due to its effect on host metabolism, immune regulation and inflammatory responses. The objective of this narrative review is to examine recent findings of the association between gut microbiota and its metabolites on cardiovascular disease and to identify therapeutic possibilities directed at gut microbiota. A narrative literature review was done on the published articles from 2010 to 2025 from the databases of PubMed, Scopus, Google Scholar, and ScienceDirect. Only those articles comprised of relevant reviews, original research articles, and clinical studies were included. Data suggests disruption of intestinal homeostasis and chronic inflammation, endothelial dysfunction, thrombosis, and atherosclerosis are associated with evidence of gut dysbiosis. The metabolites of beneficial microbes, such as bile acids and short-chain fatty acids (SCFAs), can defend cardiovascular health via regulating lipid metabolism, immune and gut barrier functions. On the other hand, toxic metabolites like trimethylamine-N-oxide (TMAO) promote foam cell development, platelet activation, oxidative stress, and vascular inflammation, putting individuals at risk for worse cardiovascular outcomes. Dietary changes, probiotics, prebiotics and other microbiota-targeted interventions have demonstrated potential in restoring the balance of gut microbes and lowering cardiovascular risk. Finally, while further clinical trials and mechanistic studies are needed, gut microbiota and metabolites play a critical role in the pathogenesis of cardiovascular diseases.

INTRODUCTION

Human body has trillions of microbes residing in diverse ecological niches, including the stomach, mouth, and skin, establishing a symbiotic relationship essential for health maintenance. The

microbiota has an important role in digestion, absorption, immune system development, and metabolic control (Xu et al., 2025). The mammalian gut harbors a diverse microbial ecosystem comprising bacteria, archaea, fungus,

helminths, and protozoa collectively known as the “microbiota” whereas their genetic material referred to as “microbiome”. Bacteria are the most prevalent (~10¹² cells/g of stool), followed by fungus (~10⁴ cells per g) and archaea (~10⁹ cells per g). Intestinal microbial community mainly consist of bacteria (Tomasova et al., 2021; Tang et al., 2019).

Microbiota comprises of four distinct types of bacteria *Actinobacteria*, *Firmicutes*, *Proteobacteria*, and *Bacteroides* and these bacteria continuously adjust to lifestyle changes (Canfora, 2017). Bacterial phyla include *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, *Proteobacteria*, *Verrucomicrobia*, *Fusobacteria*. *Firmicutes* phylum is consists of *Lactobacillus*, *Clostridium*, *Enterococcus*, *Bacillus*, *Ruminococcus* genera and *Bacteroidetes* is represented by *Prevotella* and *Bacteroides*. *Actinobacteria* comprise of *Bifidobacterium* genus. Microbiota composition is highly differentiated on the base of gene, sex, age environmental factors such as habitual diet and use of drugs (Jordan et al., 2022). Bacteria reside in gut either temporarily or permanently they are known as transient and persistent microbiota. The resident microbes lives in the intestinal membrane of host while transient microbes stay in food and enter into gastrointestinal system and adhere to gut wall (Yukgehnash et al., 2020).

The microbiota and host exist in a commensal relationship in normal physiological conditions. On the other hand, the host is fed by the intestinal microbes. In contrast, commensal microbes maintain gut homeostasis and metabolize nutrients, bile acids, xenobiotics and toxins. (Hajiagha et al., 2022). Genetics exert a minor role in gut bacteria than do environmental factors such as mode of delivery, nutrition and geography. (Rothschild et al., 2018).

The changes in the composition of normal gut microbiota are denoted as dysbiosis. Frequent studies have presented that microbiota dysbiosis is related to the pathologies of obesity and cardiometabolic diseases, characterized by lower microbial diversity or abnormal microbiota composition (Witkowski, Weeks, & Hazen, 2020). Gut dysbiosis has been shown to be caused by the

majority of CVD risk factors, including ageing, obesity, eating habits, and sedentary lifestyle. Dysbiosis is associated with intestinal inflammation and a weaker gut barrier, which boosts blood levels of bacterial structural elements and microbial metabolites such as trimethylamine-N-oxide and short-chain fatty acids, potentially promoting CVD development. (Novakovic et al., 2020).

Collectively, these alterations in gut microbiota composition and metabolic activity are emerging as one of the most potent risk factors for cardiovascular disease (Schiattarella et al., 2019). According to World Health Organization (WHO), cardiovascular disease account for approximately 17.9 deaths per year and 85% of these deaths are attributed to stroke and heart attack. Arterial hypertension and coronary heart disease reinforces heart failure and cerebrovascular damage at the end (Marzullo, 2020). Metabolic disorders and its cardiovascular consequences are the leading causes of morbidity and mortality in western cultures. Dietary trends have fundamentally changed during the last few decades. The consumption of saturated fat, simple carbohydrates, and salt has increased significantly. Dietary changes are accompanied by a decrease in physical activity. Both of these together are said to disrupt the energy balance in human beings, resulting in a significant rise in the incidence of metabolic and cardiovascular diseases like obesity, diabetes and hypertension. (Sattar et al., 2020).

Growing evidence suggests that alterations in gut microbiota composition (gut dysbiosis) contribute to the development and progression of cardiovascular disease through multiple metabolic and inflammatory pathways. Therefore, this narrative review summarizes the current evidence on the role of gut microbiota, its metabolites, and dysbiosis and therapeutic strategies in cardiovascular disease.

Methodology

This narrative review aimed to review the available evidence regarding the contribution of gut microbiota to cardiovascular disease. Electronic databases such as PubMed, Scopus, Google

Scholar and ScienceDirect were used for a comprehensive literature search. The articles searched covered the time period from 2010 to 2025, and focus on the most recent reviews, original research articles and clinical studies. The search used various combination of the following keywords: gut microbiota, gut microbiome, gut dysbiosis, cardiovascular disease, atherosclerosis, trimethylamine N-oxide (TMAO), short-chain fatty acids (SCFAs), bile acids, uremic toxins, inflammation, endothelial dysfunction, and thrombosis.

Only full-text articles published in English and relevant to the aim of this review were included. Editorials, abstracts from conferences, duplicate publications, studies not related to the gut microbiota or cardiovascular diseases, as well as articles not published in English were excluded. Selected literature was critically reviewed and synthesized to give a refreshed picture of the mechanisms underlying the connection between gut microbiota and cardiovascular disease and the therapeutic direction that could be taken in targeting the gut microbiota.

Results

Various environmental factors influence the composition of gut microbiome including mode of transmission and diet (Cao et al., 2022). Many changes occur in gut microbiome due to antibiotics the resulting disruption is determined by age, time, and route of treatment. Moreover, post antibiotic environment impact microbiota composition after treatment due to exposure of pathogenic and beneficial microbes (Schwartz, Langdon, & Dantas, 2020). Gut microbiome composition is also affected because of pollutants and smoking (Allais et al., 2016). Diet abundant in indigestible carbohydrates regulate gut microbiome in older adult. (Ghosh et al., 2020). Essential nitrogen source for bacteria are dietary proteins (Holmes et al., 2017). Gut microbes remain in symbiotic relationship within host gut that affect the bioavailability and absorption of Primarily SCFAs produced in colon. By colonocyte butyrate is used as major source of energy while acetate and propionate travel through portal vein into liver. After entering

many oral drugs which enhance production of active metabolites and leads to toxicities or have unfavorable effects on host (Xu et al., 2020). The use of antibiotic destroys both pathological and beneficial microbes with the loss of gut microbiota known as dysbiosis and produce unwanted microbes (Hasan & Yang, 2019).

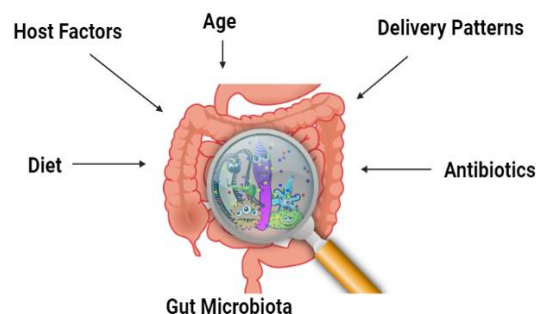


Figure 1: Factors affecting gut microbiota (Hasan and Yang 2019)

Gut microorganisms differentiated on the basis of their site mainly in ascending colon. Microbiota which colonizes gastrointestinal tract especially colon entitle as anaerobic primary microbiota. By saccharolytic and proteolytic pathways nutrients are take-up by colonies of microbes in the intestine (Rahman et al., 2022).

1. In saccharolytic pathway, sugar broken down by gut microbiota and are accountable for the formation of short chain fatty acids (SCFAs)
2. Proteolytic pathway also generates short chain fatty acids (SCFAs) and other co-metabolites such as thiol, phenol, indol, amines (Tang, Kitai, & Hazen, 2017)



Figure 2: Saccharolytic and Proteolytic fermentation in host gut (Jordan et al., 2022)

systematic circulation acetate reach the peripheral tissues which gives metabolic and satiety related effects. SCFAs can adhere to G protein-coupled receptors (Jordan et al., 2022).

These bioactive molecules Trimethylamine N-oxide, uremic toxin, short-chain fatty acids (SCFAs), and bile acids, anthocyanins, phytoestrogens can accumulate in blood (Wang & Zhao, 2018). Different families of colon bacteria produce urease (*Clostridiaceae*, *Enterobacteriaceae*), tryptophanase (*Clostridiaceae*, *Verrucomicrobia*, *Enterobacteriaceae*), short chain fatty acids (*Bifidobacteriaceae*, *Prevotellaceae*, *Lactobacillaceae*) (Yang et al., 2017).

These bacteria act on producing enzyme which activates blood clotting factors. Uremic toxin indoxyl sulphate bounded to albumin increases the response to thrombin and collagen by enhancing platelet activities which leads to thrombosis. Changes in microbiome have a very great impact in the development of thrombosis and cardiovascular disease within host body (Lichota, Gwozdinski, Szewczyk, 2020). Vascular thrombosis occurs when platelet activation increases which leads to acute coronary syndrome (Korzonek-Szlacheta et al., 2018).

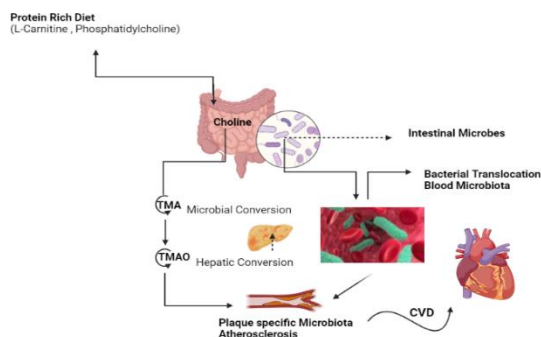


Figure 2: Procedure of microbiota interaction in host gut (Tang & Hazen, 2017)

In liver, synthesis of bile acids occur from cholesterol referred as primary bile acids. After meal, they are release in duodenum for emulsification of dietary fats and oils. Conjugated bile acid in ileum reabsorbed and carry out by blood in portal vein into liver. This procedure store 95% of bile acid pool. Deoxycholic and lithocholic acids are secondary bile acids with gut microbiotas they can affect cardiovascular health (Wang & Zhao, 2018). As signalling mediators' bile acids bind to different receptors and affect metabolism of lipid profile (Pushpass et al., 2021).

Cardiometabolic risk is generated due to imbalance of bile acids (Panyod et al., 2021).

Microbiota in gut split trimethylamine containing compounds to form trimethylamine [TMA] which can further oxidized as TMAO by FMOs in the host liver. The amplest enzyme in liver is FMO3. The oxidation of TMA is catalysed by FMO1 and FMO2. To produce TMA the precursors for gut microbiota which are mostly present in animal diet include choline, Betaine, Carnitine, γ Butyrobetaine Phosphatidylcholine, TMAO Crotonobetaine, Glycerophosphocholine, (Wang & Zhao, 2018).

TMAO contribute to atherosclerotic lesion development by enhancing macrophage migration and transformation into a foam cell which can regulate metabolism of lipoprotein. Low density lipoprotein (LDL) tends to be modified oxidatively in vascular walls in atherosclerosis. Macrophages detect oxidized modified LDL (ox-LDL) via cluster of differentiation 36 (CD36) and class A1 scavenger receptors. A high-affinity macrophage scavenger receptor detects (ox LDL). By increasing the expression of CD-36 and SR-A1, TMAO helped to increase (ox-LDL) accumulation. Atherosclerotic plaque formation occurs when these macrophages can accumulate in vessel intima and penetrate through endothelial barrier. TMAO leads to endothelial dysfunction by damaging the self-repairing ability of endothelial cells. The endothelial progenitor cells(EPCs) decreases and increased inflammation impaired endothelial function or response of oxidate stress is aggravates due to increased plasma TMAO levels. (Jiang et al., 2020).

TMAO plays influential role in platelet hyperactivity and increased potential for thrombosis. Exposing platelets directly to TMAO improves their response to various agonists by increasing the release of intracellular Ca^{2+} (Yang et al., 2019). Elevated levels of TMAO increased the risk of atherosclerosis, dyslipidaemia which leads to serious cardiovascular events (Al-Rubaye, Perfetti, & Kaski, 2019).

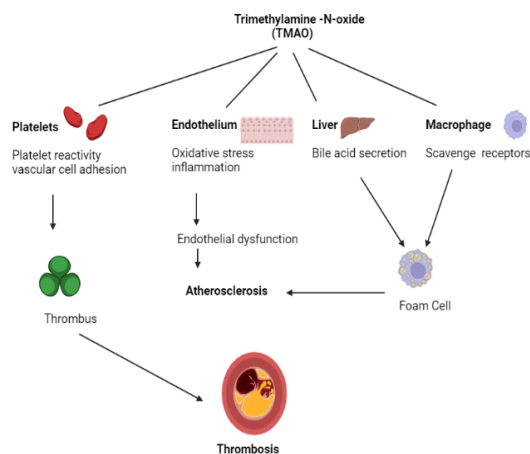


Figure 4: Prothrombotic and proatherogenic mechanisms of TMAO (Canyelles et al., 2023)

As a therapeutic strategy modulating the gut microbiome for prevention and treatment by altering the composition and function of the gut microbiome is becoming increasingly popular. These adjustments can be achieved through lifestyle changes, dietary interventions and transplantation from healthy donors (Tang, Kitai, & Hazen, 2017). Unhealthy diet developing risk of CVD by causing high level of blood cholesterol and triglyceride. Food and nutrients are important not only for human health but also for the health of the gut microbiome. Intestinal microbiota metabolites include trimethylamine (TMA), phenyl acetic acid, the lipopolysaccharide flagellin, peptidoglycan and short-chain fatty acids (SCFAs). Dietary interventions are subtle and reversible and permanent change in dietary patterns can affect structure of gut microbiota. metabolic capacity of gut microbes can be altered by long term dietary changes (Shoaie et al., 2015).

Probiotics are live microorganisms that are ingested in sufficient amounts to exert a beneficial effect on the host. Bacterial probiotics refer to Gram positive bacteria are Lactobacillus and Bifid and Escherichia coli Nissl 1917 strain is Gram negative bacteria. According to some studies probiotics show beneficial metabolic effect by improving the risk of CVD (Pushpass et al., 2021). The role of prebiotics in cardiovascular disease prevention via gut microbiome includes regulating gut microbiome balance and strengthening the gut

barrier. Supplementation with dietary fiber polysaccharide-rich lingonberries reduces triglyceridemic and atherosclerosis, improves gut microbiome composition and improves SCFA profile (Shoaie et al., 2015). Anthocyanin's have been found to improve visual function in the brain, with beneficial effect on cardiovascular disease and cancer prevention. Beneficial effect of anthocyanins on cardiovascular system acting as antiplatelet agents in atherosclerosis and other cardiovascular disease enhancing vascular relaxation, including nitric oxide formation in blood vessels (Tsuda, 2012).

Discussion

According to recent studies by Wang and Tang et al Trimethylamine N-oxide (TMAO), a molecule produced by the gut microbiota, was found to be predictive of existing cardiovascular diseases (CVDs) and future cardiovascular events in clinical cohorts (Helanza et al., 2017). The hypothesis that the interaction between microbes and the host contributes to atherosclerotic cardiovascular disease (CVD) has been strongly supported by recent research (Liu et al., 2019). Additionally, dietary TMAO may worsen poor glucose tolerance, block hepatic insulin signaling, and increase adipose tissue inflammation, according to findings from recent research in mice fed a high-fat diet. With several recently identified connections to chronic cardiometabolic illnesses, the extent of biological processes impacted by both TMAO and the TMAO generation pathway is only now beginning to be understood (Tang et al., 2014).

Conclusion

According to recent research, the gut microbiota and its metabolites particularly TMAO have a significant impact on the development and course of CVD. New approaches to treating CVD are offered by treatments that target the gut microbiota and metabolites, such as probiotics and prebiotics and anthocyanins. But current study in this area is only the beginning. To fully comprehend the chemical and genetic pathways of the gut, much more work needs to be done.

Abbreviations

CVD	Cardiovascular Disease
WHO	World Health Organization
SCFAs	Short-chain Fatty Acids
TMA	Trimethylamine
TMAO	Trimethylamine n-oxide
FMOs	Flavin-Containing Monooxygenases
FMO1	Flavin-Containing Monooxygenase 1
FMO2	Flavin-Containing Monooxygenase 2
FMO3	Flavin-Containing Monooxygenase 3
LDL	Low-Density Lipoprotein
ox-LDL	Oxidized Low-Density Lipoprotein
CD36	Cluster of Differentiation 36
SR-A1	Scavenger Receptor Class A Member 1
EPCs	Endothelial Progenitor Cells

REFERENCES

- Allais, L., Kerckhof, F. M., Verschuere, S., Bracke, K. R., De Smet, R., Laukens, D., Brusselle, G. G. (2016). Chronic cigarette smoke exposure induces microbial and inflammatory shifts and mucin changes in the murine gut. *Environmental microbiology*, 18(5), 1352-1363.
- Al-Rubaye, H., et al. (2019). "The role of microbiota in cardiovascular risk: focus on trimethylamine oxide." *Current Problems in Cardiology* 44(6): 182-196.
- Canfora, E. E., and Blaak, E. E. . (2017). A Diet-Derived Key Metabolite in Energy Metabolism: Good or Bad in Context of Obesity and Glucose Homeostasis. *The Gut Microbiota (Microbiome) in Cardiovascular Disease and Its Therapeutic Regulation*, 22.
- Canyelles, M., et al. (2023). "Gut Microbiota-Derived TMAO: A Causal Factor Promoting Atherosclerotic Cardiovascular Disease?" *International Journal of Molecular Sciences* 24(3): 1940.
- Cao, Y., Aquino-Martinez, R., Hutchison, E., Allayee, H., Lusi, A. J., & Rey, F. E. (2022). Role of gut microbe-derived metabolites in cardiometabolic diseases: Systems based approach. *Molecular Metabolism*, 101557.
- Ghosh, T. S., Rampelli, S., Jeffery, I. B., Santoro, A., Neto, M., Capri, M., Turrone, S. (2020). Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. *Gut*, 69(7), 1218-1228.
- Hajigha, M. N., Taghizadeh, S., Asgharzadeh, M., Dao, S., Ganbarov, K., Köse, Ş., & Kafil, H. S. (2022). Gut microbiota and human body interactions; its impact on health: a review. *Current pharmaceutical biotechnology*, 23(1), 4-14.
- Hasan, N., & Yang, H. (2019). Factors affecting the composition of the gut microbiota, and its modulation. *PeerJ*, 7, e7502.
- Heianza, Y., Ma, W., Manson, J. E., Rexrode, K. M., & Qi, L. (2017). Gut microbiota metabolites and risk of major adverse cardiovascular disease events and death: a systematic review and meta-analysis of prospective studies. *Journal of the American Heart Association*, 6(7), e004947.
- Holmes, A. J., Chew, Y. V., Colakoglu, F., Cliff, J. B., Klaassens, E., Read, M. N., Ruohonen, K. (2017). Diet-microbiome interactions in health are controlled by intestinal nitrogen source constraints. *Cell Metabolism*, 25(1), 140-151.
- Jardon, K. M., Canfora, E. E., Goossens, G. H., & Blaak, E. E. (2022). Dietary macronutrients and the gut microbiome: a precision nutrition approach to improve cardiometabolic health. *Gut*, 71(6), 1214-1226.
- Jiang, R. D., Liu, M. Q., Chen, Y., Shan, C., Zhou, Y. W., Shen, X. R., ... & Shi, Z. L. (2020). Pathogenesis of SARS-CoV-2 in transgenic mice expressing human angiotensin-converting enzyme 2. *Cell*, 182(1), 50-58.

- Korzonek-Szlacheta, I., Hudzik, B., Nowak, J., Szkodziniski, J., Nowak, J., Gąsior, M., & Zubelewicz-Szkodziniska, B. (2018). Mean platelet volume is associated with serum 25-hydroxyvitamin D concentrations in patients with stable coronary artery disease. *Heart and Vessels*, 33, 1275-1281.
- Lichota, A., Gwozdziniski, K., & Szewczyk, E. M. (2020). Microbial modulation of coagulation disorders in venous thromboembolism. *Journal of Inflammation Research*, 387-400.
- Liu, H., Chen, X., Hu, X., Niu, H., Tian, R., Wang, H., & Zhang, C. (2019). Alterations in the gut microbiome and metabolism with coronary artery disease severity. *Microbiome*, 7(1), 68.
- Marzullo, P., Renzo, L., Pugliese, G., De Siena, M., Barrea, L., Muscogiuri, G., et al. (2020). From Obesity Through Gut Microbiota to Cardiovascular Diseases. *Frontiers in Cellular and Infection Microbiology*, 22.
- Novakovic, M., Rout, A., Kingsley, T., Kirchoff, R., Singh, A., Verma, V., & Chaudhary, R. (2020). Role of gut microbiota in cardiovascular diseases. *World journal of cardiology*, 12(4), 110.
- Panyod, S., Wu, W. K., Chen, C. C., Wu, M. S., Ho, C. T., & Sheen, L. Y. (2023). Modulation of gut microbiota by foods and herbs to prevent cardiovascular diseases. *Journal of Traditional and Complementary Medicine*, 13(2), 107-118.
- Pushpass, R. A. G., Alzoufairi, S., Jackson, K. G., & Lovegrove, J. A. (2022). Circulating bile acids as a link between the gut microbiota and cardiovascular health: impact of prebiotics, probiotics and polyphenol-rich foods. *Nutrition Research Reviews*, 35(2), 161-180.
- Rahman, M., Islam, F., Or-Rashid, M., Mamun, A. A., Rahaman, M., Islam, M., Mimi, A. A. (2022). The gut microbiota (microbiome) in cardiovascular disease and its therapeutic regulation. *Frontiers in Cellular and Infection Microbiology*, 713.
- Rothschild, D., Weissbrod, O., Barkan, E., Kurilshikov, A., Korem, T., Zeevi, D., & Segal, E. (2018). Environment dominates over host genetics in shaping human gut microbiota. *Nature*, 555(7695), 210-215.
- Sattar, N., Gill, J. M., & Alazawi, W. (2020). Improving prevention strategies for cardiometabolic disease. *Nature Medicine*, 26(3), 320-325.
- Schiattarella, G. G., Sannino, A., Esposito, G., & Perrino, C. (2019). Diagnostics and therapeutic implications of gut microbiota alterations in cardiometabolic diseases. *Trends in cardiovascular medicine*, 29(3), 141-147.
- Schwartz, A., Taras, D., Schäfer, K., Beijer, S., Bos, N. A., Donus, C., & Hardt, P. D. (2010). Microbiota and SCFA in lean and overweight healthy subjects. *Obesity*, 18(1), 190-195.
- Shoaie, S., Ghaffari, P., Kovatcheva-Datchary, P., Mardinoglu, A., Sen, P., Pujos-Guillot, E., & Nielsen, J. (2015). Quantifying diet-induced metabolic changes of the human gut microbiome. *Cell metabolism*, 22(2), 320-331.
- Tang, W. W., & Hazen, S. L. (2014). The contributory role of gut microbiota in cardiovascular disease. *The Journal of clinical investigation*, 124(10), 4204-4211.
- Tang, W. W., & Hazen, S. L. (2017). The gut microbiome and its role in cardiovascular diseases. *Circulation*, 135(11), 1008-1010.
- Tang, W. W., Bäckhed, F., Landmesser, U., & Hazen, S. L. (2019). Intestinal microbiota in cardiovascular health and disease: JACC state-of-the-art review. *Journal of the American College of Cardiology*, 73(16), 2089-2105.
- Tang, W. W., Kitai, T., & Hazen, S. L. (2017). Gut microbiota in cardiovascular health and disease. *Circulation research*, 120(7), 1183-1196.

- Tomasova, L., Grman, M., Ondrias, K., & Ufnal, M. (2021). The impact of gut microbiota metabolites on cellular bioenergetics and cardiometabolic health. *Nutrition & metabolism*, 18(1), 72.
- Tsuda, T. (2012). Dietary anthocyanin-rich plants: biochemical basis and recent progress in health benefits studies. *Molecular nutrition & food research*, 56(1), 159-170.
- Wang, Z., & Zhao, Y. (2018). Gut microbiota derived metabolites in cardiovascular health and disease. *Protein & cell*, 9(5), 416-431.
- Witkowski, M., Weeks, T. L., & Hazen, S. L. (2020). Gut microbiota and cardiovascular disease. *Circulation research*, 127(4), 553-570.
- Xu, H., Wang, X., Feng, W., Liu, Q., Zhou, S., Liu, Q., & Cai, L. (2020). The gut microbiota and its interactions with cardiovascular disease. *Microbial biotechnology*, 13(3), 637-656.
- Xu, Q., Wang, W., Li, Y., Cui, J., Zhu, M., Liu, Y., & Liu, Y. (2025). The oral-gut microbiota axis: a link in cardiometabolic diseases. *npj Biofilms and Microbiomes*, 11(1), 11.
- Yang, K., Du, C., Wang, X., Li, F., Xu, Y., Wang, S., & Zhao, J. (2017). Indoxyl sulfate induces platelet hyperactivity and contributes to chronic kidney disease-associated thrombosis in mice. *Blood, The Journal of the American Society of Hematology*, 129(19), 2667-2679.
- Yang, S., Li, X., Yang, F., Zhao, R., Pan, X., Liang, J., Xing, Y. (2019). Gut microbiota-dependent marker TMAO in promoting cardiovascular disease: inflammation mechanism, clinical prognostic, and potential as a therapeutic target. *Frontiers in pharmacology*, 10, 1360.
- Yukgehnaish, K., Kumar, P., Sivachandran, P., Marimuthu, K., Arshad, A., Paray, B. A., & Arockiaraj, J. (2020). Gut microbiota metagenomics in aquaculture: Factors influencing gut microbiome and its physiological role in fish. *Reviews in Aquaculture*, 12(3), 1903-1927.