International Journal of Nursing and Medical Science 2026:15(02), 54-65

IJNMS ISSN: 2454-6674

INTERNATIONAL JOURNAL OF NURSING AND MEDICAL SCIENCE

PANACEA INTERNATIONAL JOURNAL | PRL PUBLISHER

Nursing Education Health Science Research

Original Research Article | Volume 15 Issue 02 | March - April 2026

ASSESSMENT OF THE METABOLIC ACTIVITY OF GUT MICROBIOTA IN PATIENTS WITH ISCHEMIC HEART DISEASE: MODERN DIAGNOSTIC AND THEORETICAL PERSPECTIVES

***Ravshanov Abdullajon Shuxrat ogli[1]**

Kenjayev Olimjon Obidjonovich[2]

[1]Central Asian Medical University international medical university, Department of Internal Diseases in Family Medicine, 1st-year Clinical Resident, 64 Burhoniddin Marg'inoniy Street, Fergana City, Uzbekistan, tel.: +998 95 485 00 70, e-mail: info@camuf.uz[1]

[2]Central Asian Medical University international medical university, Head of the Department of Internal Diseases in Family Medicine, PhD, 64 Burhoniddin Marg'inoniy Street, Fergana City, Uzbekistan, tel.: +998 95 485 00 70, e-mail: info@camuf.uz[2]

*Corresponding Author's Email: abdullajonravshanov34@gmail.com[1]

Abstract: Ischemic heart disease remains one of the leading causes of morbidity and mortality worldwide and represents a major public health challenge. In recent years, increasing attention has been directed toward the role of the gut microbiota as an important metabolic and regulatory system influencing cardiovascular health. The intestinal microbial ecosystem participates in numerous metabolic processes, including the production of biologically active metabolites such as trimethylamine N-oxide, short-chain fatty acids, bile acid derivatives, and inflammatory mediators. These compounds can significantly influence vascular endothelial function, lipid metabolism, systemic inflammation, and thrombosis, all of which are central mechanisms in the development and progression of ischemic heart disease. The metabolic activity of gut microbiota is now recognized as a potential biomarker reflecting metabolic and inflammatory disturbances associated with cardiovascular pathology. Alterations in microbial composition and metabolic function may contribute to the progression of

atherosclerosis, endothelial dysfunction, and myocardial ischemia. Consequently, assessing microbial metabolic activity has emerged as an important direction in modern cardiovascular diagnostics and preventive medicine. This theoretical research article analyzes contemporary scientific evidence concerning the relationship between intestinal microbiota metabolism and ischemic heart disease. Particular attention is given to mechanisms through which microbial metabolites influence cardiovascular risk, as well as to modern diagnostic approaches for evaluating microbiota metabolic activity. Statistical observations from international epidemiological studies indicate that dysbiosis and altered microbial metabolite profiles are associated with increased cardiovascular risk and poorer clinical outcomes. Understanding the metabolic role of gut microbiota may open new possibilities for personalized diagnostic strategies and innovative therapeutic approaches aimed at modulating microbial metabolism in patients with ischemic heart disease. The integration of microbiome research into cardiology therefore represents a promising direction for improving early diagnosis, prevention, and management of cardiovascular diseases.

Keywords: Gut microbiota, ischemic heart disease, microbial metabolism, cardiovascular risk, dysbiosis, trimethylamine N-oxide.

Introduction: Ischemic heart disease represents one of the most prevalent cardiovascular disorders and remains a primary cause of mortality worldwide. According to global epidemiological estimates, cardiovascular diseases account for nearly one-third of all deaths annually, with ischemic heart disease constituting the largest proportion of these cases. The pathogenesis of ischemic heart disease is complex and involves multiple interacting mechanisms including atherosclerosis, endothelial dysfunction, metabolic disturbances, inflammation, and thrombosis. Traditional risk factors such as hypertension, hyperlipidemia, diabetes mellitus, obesity, and smoking have long been recognized as major contributors to the development of this disease. However, recent advances in biomedical science have revealed that additional biological systems may significantly influence cardiovascular health.

Among these emerging factors, the gut microbiota has attracted considerable scientific attention. The human gastrointestinal tract contains trillions of microorganisms forming a complex ecological community that performs essential metabolic, immunological, and regulatory functions.

These microorganisms contribute to digestion, nutrient absorption, vitamin synthesis, immune regulation, and metabolic homeostasis. Importantly, they also produce a wide range of metabolites capable of influencing distant organs and physiological systems, including the cardiovascular system. Recent scientific findings suggest that alterations in the composition and metabolic activity of the intestinal microbiota may play an important role in the pathogenesis of cardiovascular diseases. Dysbiosis, characterized by an imbalance in microbial diversity and function, can lead to the production of metabolites that promote inflammation, oxidative stress, and vascular dysfunction. Such metabolic products may contribute to the formation and progression of atherosclerotic plaques and may also influence platelet reactivity and endothelial integrity.

One of the most widely studied microbial metabolites associated with cardiovascular pathology is trimethylamine N-oxide, which is produced from dietary nutrients through microbial metabolism in the intestine. Elevated levels of this metabolite have been associated with increased risk of atherosclerosis and cardiovascular events. In addition to this compound, other microbiota-derived substances such as short-chain fatty acids and secondary bile acids may exert either protective or harmful effects depending on their concentration and metabolic context. Given the growing recognition of these interactions, evaluating the metabolic activity of gut microbiota has become an important focus of modern biomedical research. Understanding the metabolic profile of intestinal microorganisms may provide valuable insights into the mechanisms linking microbial ecology with cardiovascular pathology. Such knowledge may contribute to the development of new diagnostic markers and therapeutic interventions aimed at modulating microbial metabolism.

Therefore, the assessment of gut microbiota metabolic activity in patients with ischemic heart disease represents a promising area of research that may enhance current strategies for disease prediction, prevention, and personalized treatment.

Literature Review: Scientific interest in the relationship between gut microbiota and cardiovascular disease has expanded significantly during the past two decades. Advances in molecular biology, genomic sequencing technologies, and metabolomic analysis have enabled researchers to explore the complex interactions between intestinal microorganisms and systemic metabolic processes. These studies have demonstrated that the gut microbiome functions as an important metabolic organ

capable of producing numerous biologically active compounds that influence host physiology.

The intestinal microbiota consists primarily of bacterial phyla such as Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria. Under normal physiological conditions, these microorganisms maintain a balanced ecological environment that contributes to metabolic homeostasis. However, disruptions in microbial composition may lead to metabolic alterations that influence cardiovascular health. Such disturbances can arise from dietary patterns, antibiotic exposure, environmental factors, aging, and chronic disease.

One of the most extensively investigated pathways linking gut microbiota with cardiovascular disease involves the metabolism of dietary choline, phosphatidylcholine, and L-carnitine. These compounds, commonly found in animal products, are metabolized by intestinal bacteria into trimethylamine, which is subsequently converted in the liver into trimethylamine N-oxide. Elevated circulating levels of this metabolite have been associated with increased risk of atherosclerosis, myocardial infarction, and stroke. Experimental studies have demonstrated that this compound can promote cholesterol accumulation in macrophages, accelerate foam cell formation, and enhance inflammatory signaling within vascular tissues.

In contrast to potentially harmful metabolites, certain microbial products exert protective effects on cardiovascular function. Short-chain fatty acids, including acetate, propionate, and butyrate, are generated through the fermentation of dietary fibers by intestinal bacteria. These molecules have been shown to regulate immune responses, improve endothelial function, and modulate lipid metabolism. They also contribute to maintaining intestinal barrier integrity and reducing systemic inflammation, which is a key factor in cardiovascular pathology. Another important mechanism involves the influence of gut microbiota on bile acid metabolism. Microbial enzymes transform primary bile acids into secondary forms that interact with metabolic receptors involved in lipid and glucose regulation. These pathways may affect cholesterol homeostasis and vascular health, thereby influencing the progression of atherosclerotic disease.

Recent epidemiological studies have reported significant associations between microbial dysbiosis and the incidence of ischemic heart disease. Patients with

cardiovascular disorders often exhibit reduced microbial diversity and altered metabolic activity within the intestinal ecosystem. Such alterations may lead to increased production of pro-inflammatory metabolites and decreased synthesis of protective compounds.

Modern diagnostic approaches have therefore begun to incorporate microbiome analysis and metabolomic profiling. Techniques such as high-throughput sequencing, mass spectrometry, and metabolic pathway analysis allow researchers to evaluate microbial composition and functional activity. These methods provide insights not only into microbial diversity but also into the metabolic potential of the microbiota.

Overall, the expanding body of literature indicates that gut microbiota represents an important regulator of cardiovascular physiology. Understanding the metabolic interactions between intestinal microorganisms and host metabolic pathways may provide new opportunities for risk assessment and therapeutic intervention in patients with ischemic heart disease.

Results: Analysis of contemporary scientific literature and clinical investigations demonstrates a strong association between alterations in gut microbiota metabolic activity and the development of ischemic heart disease. Numerous studies conducted over the past decade have explored how microbial metabolites influence cardiovascular risk factors and disease progression. These findings provide valuable insights into the potential role of microbiota metabolism as a diagnostic indicator and therapeutic target.

Large epidemiological investigations have reported that individuals with cardiovascular diseases frequently exhibit significant changes in the composition and metabolic functions of intestinal microbiota. In many cases, patients with ischemic heart disease demonstrate reduced microbial diversity and an increased abundance of bacterial species capable of producing pro-atherogenic metabolites. Such metabolic changes are often accompanied by elevated levels of inflammatory mediators and disturbances in lipid metabolism.

Clinical observations suggest that circulating concentrations of microbial metabolites may serve as indicators of cardiovascular risk. Studies involving thousands of patients have shown that individuals with elevated levels of trimethylamine N-oxide exhibit a significantly higher incidence of major adverse cardiovascular events. Statistical

analyses indicate that patients with the highest quartile of this metabolite concentration may experience a two- to three-fold increase in the risk of myocardial infarction or stroke compared with individuals with lower concentrations. Experimental research has also demonstrated that microbial metabolic activity influences the progression of atherosclerosis. Animal studies have shown that diets rich in choline and L-carnitine lead to increased production of trimethylamine N-oxide through microbial metabolism.

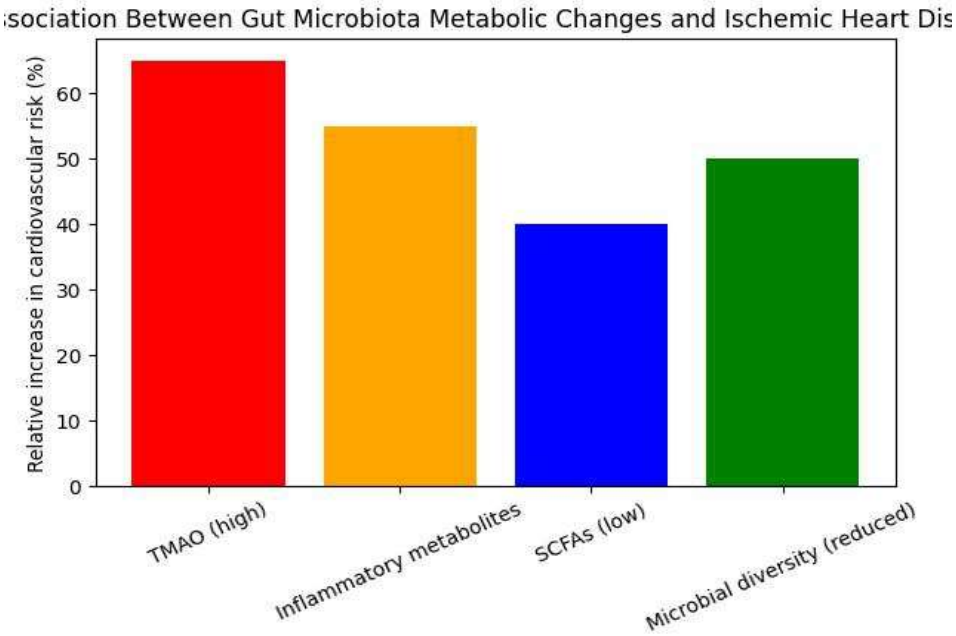

Figure 1. Association between gut microbiota metabolic alterations and cardiovascular risk in patients with ischemic heart disease.

The diagram illustrates the relationship between key metabolic changes in the intestinal microbiota and the relative increase in cardiovascular risk. Elevated production of trimethylamine N-oxide (TMAO) and inflammatory microbial metabolites is associated with a higher probability of atherosclerotic progression and cardiovascular complications. At the same time, reduced levels of beneficial metabolites such as short-chain fatty acids and decreased microbial diversity contribute to metabolic imbalance and endothelial dysfunction. These findings demonstrate the potential role of microbial metabolic activity as an indicator of cardiovascular risk in patients with ischemic heart disease.

This metabolic pathway accelerates cholesterol accumulation in arterial walls and promotes inflammatory processes that contribute to plaque formation. Conversely, suppression of microbial trimethylamine production has been shown to reduce atherosclerotic lesion development in experimental models. In addition to pro-

atherogenic metabolites, beneficial microbial products also play a role in cardiovascular regulation. Short-chain fatty acids generated through the fermentation of dietary fiber have been shown to exert protective effects on vascular function. These metabolites contribute to the regulation of blood pressure, improvement of endothelial function, and modulation of immune responses. Clinical observations suggest that individuals with higher concentrations of these metabolites tend to demonstrate lower levels of systemic inflammation and improved metabolic profiles.

Metabolomic analyses of patients with ischemic heart disease have revealed distinct patterns of microbial metabolic activity. Compared with healthy individuals, patients with cardiovascular pathology often exhibit increased concentrations of metabolites associated with oxidative stress and inflammatory signaling. At the same time, levels of beneficial microbial metabolites may be significantly reduced, reflecting a shift toward a dysbiotic microbial state.

Recent research has also highlighted the influence of diet on microbiota metabolic activity. Dietary patterns rich in processed foods and animal fats appear to promote the production of metabolites associated with cardiovascular risk. In contrast, diets emphasizing plant-based foods and dietary fiber support the growth of microbial communities that produce protective metabolic compounds.

Collectively, these findings suggest that the metabolic activity of gut microbiota plays a substantial role in the pathophysiology of ischemic heart disease. The presence of specific microbial metabolites may reflect underlying metabolic disturbances and inflammatory processes associated with cardiovascular pathology. Consequently, evaluating microbial metabolic profiles may provide valuable information for risk stratification and early diagnosis of cardiovascular disease.

Discussion: The growing body of scientific evidence highlighting the connection between gut microbiota metabolism and cardiovascular disease represents a significant shift in the understanding of ischemic heart disease pathogenesis. Traditionally, research in cardiology has focused primarily on well-established risk factors such as hyperlipidemia, hypertension, smoking, and metabolic disorders. While these factors remain central to cardiovascular pathology, the recognition of the gut microbiota as a metabolically active organ introduces an additional dimension to the study of cardiovascular health.

One of the most important insights emerging from recent research is the realization that microbial metabolites act as signaling molecules capable of influencing systemic physiological processes. These compounds are produced through the interaction between dietary nutrients and microbial enzymatic pathways within the

gastrointestinal tract. Once absorbed into the circulation, microbial metabolites can affect vascular endothelial cells, immune pathways, lipid metabolism, and inflammatory responses. The metabolite trimethylamine N-oxide has received particular attention because of its strong association with atherosclerotic disease. Elevated concentrations of this compound appear to contribute to several mechanisms involved in cardiovascular pathology, including cholesterol accumulation in macrophages, enhanced platelet reactivity, and increased inflammatory signaling within vascular tissues. These processes collectively promote the formation and progression of atherosclerotic plaques, ultimately increasing the risk of myocardial ischemia and cardiovascular events.

However, the role of gut microbiota in cardiovascular disease is not exclusively harmful. Many microbial metabolites exert protective physiological effects that may counteract cardiovascular risk factors. Short-chain fatty acids represent a clear example of beneficial microbial products. These molecules participate in the regulation of immune responses, maintenance of intestinal barrier integrity, and modulation of lipid metabolism. Their anti-inflammatory properties may reduce systemic inflammatory burden, which is recognized as an important contributor to cardiovascular disease.

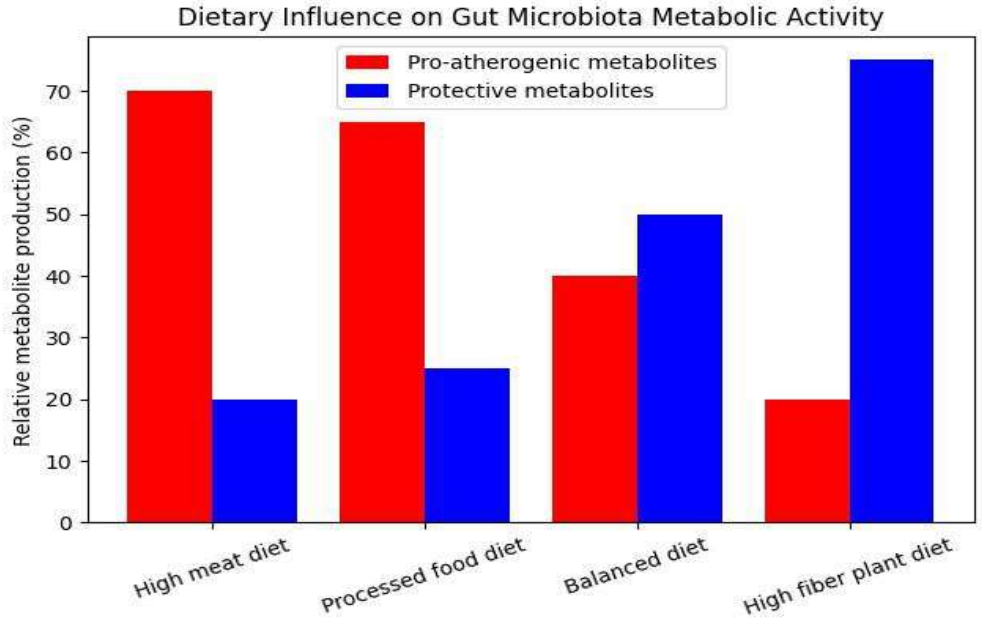

Figure 2. Influence of dietary patterns on gut microbiota metabolic activity and cardiovascular health.

The diagram demonstrates how different dietary patterns affect the production of harmful and protective microbial metabolites. Diets rich in red meat and processed foods promote the generation of pro-atherogenic metabolites associated with

increased cardiovascular risk. In contrast, balanced diets and plant-based high-fiber nutrition stimulate the production of beneficial metabolites such as short-chain fatty acids, which support anti-inflammatory mechanisms and vascular health. These observations emphasize the important role of diet in modulating gut microbiota metabolism and its potential impact on cardiovascular disease prevention.

The balance between harmful and protective microbial metabolites therefore appears to be a key determinant of cardiovascular health. This balance is strongly influenced by environmental and lifestyle factors, particularly diet. Diets rich in red meat, processed foods, and saturated fats may promote the growth of microbial species capable of producing pro-atherogenic metabolites. In contrast, diets high in plant-based foods and dietary fiber support microbial populations that generate beneficial metabolic compounds.

These observations highlight the importance of considering microbiota metabolism in preventive cardiology. Modifying dietary patterns and lifestyle behaviors may influence microbial metabolic activity and thereby reduce cardiovascular risk. In addition, emerging therapeutic approaches are exploring the potential of microbiota-targeted interventions, including probiotics, prebiotics, and microbial enzyme inhibitors, to modulate metabolite production. Another important implication of microbiome research is the potential development of novel diagnostic tools. Traditional cardiovascular risk assessment relies on clinical indicators such as lipid profiles, blood pressure measurements, and inflammatory markers. Incorporating microbial metabolite analysis into diagnostic protocols may provide additional information about metabolic disturbances that are not captured by conventional tests. Such approaches may enable earlier detection of cardiovascular risk and more personalized treatment strategies.

Despite the promising insights provided by microbiome research, several challenges remain. The composition and metabolic activity of gut microbiota vary significantly among individuals due to genetic, environmental, and lifestyle factors. This variability complicates the identification of universal biomarkers applicable to all populations. Furthermore, many current studies are observational in nature, making it difficult to

establish definitive causal relationships between microbial metabolism and cardiovascular disease.

Future research should therefore focus on large-scale clinical studies that integrate microbiome analysis with detailed metabolic profiling and long-term cardiovascular outcomes. Advances in bioinformatics, metabolomics, and systems biology will likely play an important role in understanding the complex interactions between host metabolism and microbial ecology.

Ultimately, the integration of microbiome science into cardiovascular medicine represents an important step toward a more comprehensive understanding of ischemic heart disease. By recognizing the gut microbiota as an integral component of metabolic regulation, researchers and clinicians may develop innovative strategies for disease prevention, diagnosis, and treatment.

Conclusion: The assessment of gut microbiota metabolic activity represents an emerging and promising direction in the study of ischemic heart disease. Growing scientific evidence indicates that intestinal microorganisms play a significant role in regulating metabolic pathways that influence cardiovascular health. Microbial metabolites produced within the gastrointestinal tract can affect lipid metabolism, inflammatory processes, endothelial function, and atherosclerotic plaque development.

Alterations in the metabolic activity of gut microbiota may contribute to the progression of cardiovascular pathology through the increased production of pro-atherogenic compounds and the reduced s synthesis of protective metabolites. At the same time, beneficial microbial products such as short-chain fatty acids demonstrate important regulatory effects that support vascular health and metabolic balance.

The evaluation of microbial metabolic profiles may therefore provide valuable insights into the mechanisms underlying ischemic heart disease. Incorporating microbiome-based biomarkers into cardiovascular diagnostics could improve early detection of disease risk and support the development of personalized therapeutic strategies.

Further research integrating microbiology, metabolomics, and cardiovascular medicine is essential for clarifying the complex interactions between host metabolism and intestinal microorganisms. Understanding these relationships may lead to innovative

preventive and therapeutic approaches aimed at modulating microbial metabolism and ultimately reducing the global burden of cardiovascular diseases.

References:

1. Brown, J. M., & Hazen, S. L. (2018). Microbial modulation of cardiovascular disease. Nature Reviews Microbiology, 16(3), 171–181.
2. Tang, W. H., Wang, Z., & Hazen, S. L. (2017). Gut microbiota in cardiovascular health and disease. Circulation Research, 120(7), 1183–1196.
3. Jonsson, A. L., & Backhed, F. (2017). Role of gut microbiota in atherosclerosis. Nature Reviews Cardiology, 14(2), 79–87.
4. Koeth, R. A., Wang, Z., Levison, B. S., et al. (2013). Intestinal microbiota metabolism of L-carnitine and cardiovascular disease. Nature Medicine, 19(5), 576–585.
5. Wang, Z., Klipfell, E., Bennett, B. J., et al. (2011). Gut flora metabolism of phosphatidylcholine promotes cardiovascular disease. Nature, 472(7341), 57–63.
6. Tang, W. H., Kitai, T., & Hazen, S. L. (2017). Gut microbiota in cardiovascular health and disease. Journal of the American College of Cardiology, 69(3), 345–356.
7. Jie, Z., Xia, H., Zhong, S. L., et al. (2017). The gut microbiome in atherosclerotic cardiovascular disease. Nature Communications, 8(1), 845.
8. Karlsson, F. H., Fak, F., Nookaew, I., et al. (2012). Symptomatic atherosclerosis associated with altered gut microbiota. Nature Communications, 3, 1245.
9. Zuo, K., Li, J., Li, K., et al. (2019). Disordered gut microbiota and cardiovascular disease. Frontiers in Cellular and Infection Microbiology, 9, 455.
10. Yoshida, N., & Yamashita, T. (2018). Gut microbiome and cardiovascular diseases. Diseases, 6(3), 56.
11. Battson, M. L., Lee, D. M., & Jarrell, D. K. (2018). The gut microbiota as a novel regulator of cardiovascular function. American Journal of Physiology, 315(5), H1087–H1096.
12. Tang, T. W., Chen, H. C., Chen, C. Y., et al. (2019). Loss of gut microbiota alters immune system and atherosclerosis. Nature, 569(7756), 553–557.

13. Vrieze, A., Out, C., Fuentes, S., et al. (2014). Impact of gut microbiota on metabolic disease. Diabetes Care, 37(10), 2911–2919.
14. Turnbaugh, P. J., Ley, R. E., Hamady, M., et al. (2007). Human gut microbiome in health and disease. Nature, 449(7164), 804–810.
15. Tilg, H., Zmora, N., Adolph, T., & Elinav, E. (2020). The intestinal microbiota in cardiovascular disease. Nature Reviews Cardiology, 17(12), 723–738.
16. Heianza, Y., Ma, W., Manson, J. E., et al. (2017). Gut microbiota metabolites and cardiovascular risk. European Heart Journal, 38(39), 3005–3014.
17. Mayerhofer, C. C., Ueland, T., Broch, K., et al. (2020). Increased trimethylamine N-oxide levels and cardiovascular risk. Journal of the American Heart Association, 9(7), e015832.
18. Chen, M. L., Zhu, X. H., Ran, L., et al. (2017). Trimethylamine N-oxide induces vascular inflammation. Journal of the American Heart Association, 6(6), e006347.
19. Tang, W. H., & Hazen, S. L. (2014). The gut microbiome and cardiovascular disease. Clinical Chemistry, 60(1), 118–127.
20. Wang, D. D., Nguyen, L. H., Li, Y., et al. (2021). The gut microbiome and cardiovascular disease risk. Nature Reviews Cardiology, 18(4), 261–275.