International Journal of Innovative Technologies in Social Science

e-ISSN: 2544-9435

Scholarly Publisher
RS Global Sp. z O.O.
ISNI: 0000 0004 8495 2390

Dolna 17, Warsaw,
Poland 00-773
+48 226 0 227 03
editorial_office@rsglobal.pl

ARTICLE TITLE	THE ROLE OF GUT MICROBIOME IN PREVENTION AND DEVELOPMENT OF ATHEROSCLEROSIS
DOI	https://doi.org/10.31435/ijitss.4(48).2025.4342
RECEIVED	29 October 2025
ACCEPTED	20 December 2025
PUBLISHED	24 December 2025
LICENSE	The article is licensed under a **Creative Commons Attribution 4.0 International License.**

THE ROLE OF GUT MICROBIOME IN PREVENTION AND DEVELOPMENT OF ATHEROSCLEROSIS

Agnieszka Bajkacz *(Corresponding Author, Email: agnieszkabajkacz99@gmail.com)*
University Hospital (UH) in Wroclaw, Wrocław, Poland
ORCID ID: 0000-0002-2027-8216

Katarzyna Piotrowicz
University Clinical Hospital in Poznan, Poznań, Poland
ORCID ID: 0009-0009-3888-3885

Hubert Piotrowicz
University Clinical Hospital in Poznan, Poznań, Poland
ORCID ID: 0009-0008-2453-3561

Jacek Kurzeja
J Strus City Multispecialty Hospital, Poznań, Poland
ORCID ID: 0009-0004-4075-7208

Wojciech Kraśnik
J Strus City Multispecialty Hospital, Poznań, Poland
ORCID ID: 0009-0003-7754-2174

Olga Jankowska
J Strus City Multispecialty Hospital, Poznań, Poland
ORCID ID: 0009-0001-8047-7962

Anna Rogala
MSWiA Hospital, Poznań, Poland
ORCID ID: 0009-0005-5465-6771

Joanna Osmólska
Voivodeship Hospital in Poznan, Poznań, Poland
ORCID ID: 0000-0002-8754-7222

ABSTRACT

Introduction and Purpose. The gut microbiome has been the focus of scientific attention for many years. Modification of its composition are used in the prevention and treatment of many diseases. The aim of this review is to summarise the current knowledge about the role of the gut microbiome in cardiovascular diseases, using atherosclerosis as an example.
Materials and methods. A literature review was carried out using the professional PubMed database. Articles were searched using keywords such as: "gut microbiome", "atherosclerosis", "diet", "physical activity".
State of knowledge. The review describes the mechanism linking the gut microbiome to atherosclerosis and the differences in the composition of the gut microbiota in people with atherosclerosis risk factors compared with healthy individuals. The effect of probiotics on atherosclerotic lesions and the role of appropriate donor selection in faecal microbiota transplantation (FMT) are discussed. The review describes also how the composition of the gut microbiome affects physical performance.
Summary. The gut microbiome plays a huge role in the human body. It affects the health of the entire body including the cardiovascular system. The composition of the intestinal microbiota varies between individuals. It has been found that the microbiome of people with risk factors for atherosclerosis is dominated by pro-inflammatory bacteria. The possibility of modifying the composition of the microbiome through diet, physical activity and the use of probiotics offers hope for the contribution of the gut microbiota to the prevention and treatment of atherosclerosis.

KEYWORDS

Gut Microbiome, Atherosclerosis, Diet, Physical Activity

CITATION

Agnieszka Bajkacz, Katarzyna Piotrowicz, Hubert Piotrowicz, Jacek Kurzeja, Wojciech Kraśnik, Olga Jankowska, Anna Rogala, Joanna Osmólska. (2025) The Role of Gut Microbiome in Prevention and Development of Atherosclerosis. *International Journal of Innovative Technologies in Social Science*. 4(48). doi: 10.31435/ijitss.4(48).2025.4342

Introduction

Today, cardiovascular diseases are the leading cause of human mortality worldwide. Atherosclerosis is most responsible for their occurrence [1]. This progressive inflammatory disease involving mainly the subendothelial space (tunica intima) of medium and large arteries often leads to complications such as myocardial infarction. Risk factors for developing this condition include hypertension, obesity and hypercholesterolemia [2]. In recent years, researchers have emphasized the importance of the gut microbiome in the development of atherosclerosis. Among other things, gut bacteria affect cholesterol metabolism [1]. Diet and physical activity also affect the microbiome [3]. Modifications in the composition of the gut microbiota are also possible through the use of probiotics [4]. Bacteria of the gut microbiome with anti-inflammatory properties may play a key role in the prevention and treatment of atherosclerosis.

Purpose

The purpose of this review is to assess the impact of the gut microbiome on selected risk factors for atherosclerosis, and thus this condition. Modification of the composition of the gut microbiota is possible through diet, physical activity and the use of probiotics. The goal is also to determine whether appropriately selected bacterial strains of the intestinal microbiome can be used as a form of prevention of atherosclerosis by affecting its risk factors and participate in the treatment of this condition.

Materials And Methods

A literature review was conducted using the professional PubMed database. Articles from 2015 to 2024 were included. Search terms: “gut microbiome”, “gut microbiome and atherosclerosis”, “probiotics”, “gut microbiota transplantation (FMT) and atherosclerosis”, “hypertension”, “obesity”, ‘hypercholesterolemia’, “diet and microbiome”, “physical activity and microbiome”. The retrieved articles were analysed.

The gut microbiome

The gut microbiome is now treated as an organ of the human body. Its functions are not only participation in digestion and metabolism, but also influence the immune system. The human intestinal microbiota includes 5 main types of bacteria: Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria and Cerrucomicrobia [5]. The intestinal microbiota primarily colonizes the colon, where conditions are predominantly anaerobic. Therefore, in a healthy body, the anaerobic bacteria Bacteroides and Firmicutes make up the majority. However, the composition of the gut microbiome differs in everyone. It is influenced not only by genetics, but also by antibiotic use, lifestyle, hygiene and diet [6].

Many studies have been conducted showing differences in the composition of the gut microbiome in healthy people and those with cardiovascular disease. It has been observed that the gut microbiome differs in patients with a cardiac burden.

Dysbiosis and the link between gut microbiota and cardiovascular disease

Diseases cause changes in the composition of the intestinal microbiota. This phenomenon is referred to as dysbiosis. These changes include diversity and stability. The microbiome interacts with the body through multiple metabolic pathways. It is sometimes compared to an endocrine organ [7]. The main pathway associated with atherosclerosis is the trimethylamine/ trimethylamine N-oxide (TMA/TMAO) pathway. From quaternary amines derived from the diet (mainly meat and eggs), choline, carnitine and lecithin, among others, the intestinal microbiota bacteria produce trimethylamine (TMA). It is then absorbed by the intestinal epithelium and oxidized to trimethylamine N -oxide (TMAO) [8]. Bacteria of the Clostridia and Enterobacteriaceae families are mainly responsible for this transformation. This compound exhibits pro-inflammatory properties, increasing the production of pro-inflammatory cytokines (TNF- alpha, IL-1B), and decreasing the production of anti-inflammatory factors (IL-10) [9]. It also promotes thrombotic events by increasing platelet activity [10]. TMAO is mainly excreted via the renal route [9].

The gut microbiota has been linked to the pathogenesis of many diseases including cardiovascular disease also through metabolism-independent processes. Studies have shown that heart failure causes congestion of the visceral circulation and impairs intestinal function, resulting in translocation of bacteria and the presence of their products in the circulation, thereby increasing inflammation [11].

Bacterial species

Differences were observed in the composition of the gut microbiome in patients with cardiovascular burden compared to healthy individuals.

Studies have shown that atherosclerotic plaques contain bacterial DNA. Fecal samples from people with atherosclerotic cardiovascular disease (ACVD) were analyzed and compared with fecal samples from healthy people. In the diseased individuals, a lower percentage were fermentative bacteria and a higher percentage showed inflammatory potential [12].

In patients with coronary artery disease (CAD), most often resulting from atherosclerosis, the number of Bacteroidetes (Bacteroides + Prevotella) decreased [13]. However, the proportion of Firmicutes bacteria increased relative to Bacteroidetes [14].

Animal model studies have shown an association between the composition of the gut microbiome and the severity of myocardial infarction. In rodent model studies, administration of Lactobacillus plantarum was associated with a significant reduction in infarct size and improved left ventricular function after myocardial infarction. A study in an animal model showed that administration of Lactobacillus rhamnosus attenuated left ventricular hypertrophy and heart failure after experimental myocardial infarction [15]. A study of human atherosclerotic tissue showed that the nucleic acid component of Lactobacillus rhamnosus is present in high amounts especially in stable atherosclerotic plaques [16]. These observations may suggest that the use of appropriately selected probiotics may provide additional treatment benefits in cardiac patients, such as reducing the severity of heart failure after myocardial infarction and increasing the stability of atherosclerotic plaques [15, 16].

Another studies have shown that Lactobacillus plantarum in patients with stable coronary artery disease reduces the inflammatory cytokines IL-8 and IL-12. This suggests the possibility of using this bacterium as an agent to inhibit the progression of coronary artery disease [17].

Hypertension

Hypertension is one of the main risk factors for atherosclerosis. Research suggests that the gut microbiome influences the pathogenesis of this condition mainly through short-chain fatty acids (SCFAs). Specific microorganisms that make up the microbiota produce SCFAs in the gut from dietary fiber. These acids include acetate, propionate and butyrate. Their levels in the blood and feces depend on the composition of the gut microbiota and the fiber content of the diet. Acetate and propionate are primarily absorbed through the intestines, in contrast to butyrate, which is used as an energy source [18]. Butyrate is produced by bacteria in the Ruminococcaceae and Lachnospiraceae families, as well as Anaerobutyricum hallii and Anaerostipes spp, among others. In contrast, Bifidobacterium spp. and mucin-degrading bacteria such as Akkermansia muciniphila produce acetate and propionate [19]. Higher fecal SCFA concentrations have been observed in hypertensive people. Additional studies are needed to assess whether this is due to their poorer absorption. Lower diversity of the gut microbiota in hypertensive patients has also been described. Greater diversity was associated with lower intestinal permeability [20].

Differences were found in the composition of the gut microbiome in patients with and without hypertension. The first group was found to have a lower abundance of bacteria producing short-chain fatty acids (SCFAs), such as Bifidobacterium, Enterococcus and Lactobacillus. Gram-negative bacteria that are a source of lipopolysaccharides (LPS) predominated. These compounds have pro-inflammatory properties [21]. The abundance of Klebsiella, Streptococcus and Parabacteroides increased [22].

Diet also has a huge impact on the development of hypertension. Foods high in salt affect the gut microbiome and increase blood pressure. It has been found to reduce the number of lactobacilli in the gut. Studies in a mouse model have shown that this interaction is directly related to hypertension induced by a salt-rich diet, as Lactobacillus supplementation lowers blood pressure in salt-sensitive hypertensive mice. [23]

Obesity

Another risk factor for atherosclerosis is obesity. The composition of the gut microbiome varies with body weight. Studies have shown that the population of bacteria from the genera Akkermansia, Faecalibacterium and Oscillibacter decreases in obese people [24]. On the other hand, bacteria from the Enterobacteriaceae family, which exhibit pro-inflammatory effects, are more numerous. After weight reduction, the population of these bacteria decreased significantly [25].

Among other things, obesity is accompanied by an increase in serum leptin levels. This leads to resistance of the central nervous system (CNS) to this substance and its appetite suppressing effect is reduced [26]. In a human model study, administration of Lactobacillus rhamnosus was shown to have an anti-obesity effect by affecting leptin levels. The SCFAs produced by this strain, mainly acetate, propionate and butyrate, were found to reduce circulating leptin levels. Lactobacillus rhamnosus reduces the leptin resistance found in obesity [27]. In a study, supplementation with Lactobacillus rhamnosus GG (LGG) was shown to improve exogenous leptin sensitivity in obese mice given a high-fat diet [28].

Hypercholesterolaemia

The gut microbiome is involved in the metabolism of bile acids and cholesterol [29]. Bacteria can convert cholesterol into coprostanol. This compound is mainly excreted in the feces and is poorly absorbed. Bacteria of the genus Lactobacillus and Eubacterium are responsible for this conversion, but the bacterial enzymes are not fully understood. Cholesterol is mainly absorbed in the small intestine, but the production of coprostanol from cholesterol is greatest in the large intestine [30].

One of the main risk factors for cardiovascular disease is hypercholesterolemia. Studies have shown that SCFA-producing bacteria have a beneficial effect on cholesterol levels. Administration of Bifidobacterium and Lactobacillus strains to mice with hypercholesterolemia decreased the LDL fraction of cholesterol and increased the HDL fraction and propionic acid belonging to SCFAs [31].

First-line drugs for the treatment of hypercholesterolemia are statins. They lower LDL cholesterol levels. Their effectiveness is inter-individually variable. Diet and physical activity play a major role in treatment. The influence of the gut microbiome on the effectiveness of statins has been studied. Statins have been shown to reduce TMAO, which increases the risk of cardiovascular events [32]. The response to statin treatment has been studied in relation to the composition of the gut microbiome. It was shown that statin-sensitive patients had a higher proportion of bacteria from the genera Lactobacillus, Eubacterium, Faecalibacterium and Bifidobacterium, and fewer bacteria from the genus Clostridium compared to the statin-resistant group. The bacterial diversity of the microbiome was higher in the statin-responsive group [33]. The statin-resistant group showed higher TMAO [34].

The composition of the gut microbiome in statin-treated and healthy patients was also compared. The former group showed increased abundance of Faecalibacterium prausnitzii and Akkermansia muciniphila, which exhibit anti-inflammatory effects, and lower abundance of Bifidobacterium bifidum, a bacterium associated with bile acids [35].

Physical activity

Physical activity is a recognized factor in reducing the risk of cardiovascular disease. A study of a group of people without cardiovascular disease found that low, moderate and high intensity physical activity reduces the risk of atherosclerosis in the coronary and carotid arteries compared to a sedentary lifestyle. Low-intensity physical activity does this to a lesser extent than moderate and heavy exercise [36]. Other researchers have found that the effect of physical activity on the body depends on gender. Regular aerobic activity compared to a sedentary lifestyle resulted in a 36% reduction in cardiovascular mortality in women and a 14% reduction in men [37].

Physical activity is a key element in the treatment of obesity, one of the risk factors for atherosclerosis. It not only allows weight reduction, but also has a beneficial effect on the diameter of arteries. The type of physical activity is important. We studied how high-intensity interval training (HIIT) and moderate-intensity continuous training (MICT) affect blood vessels in obese adults with a previously sedentary lifestyle. HIIT was assessed to dilate arterial endothelium in a flow-dependent manner, while MICT increased resting arterial diameter after 8 weeks. Measurements were made using the brachial artery as an example [38].

Many studies have shown that aerobic exercise lowers blood pressure in people with hypertension. Moderate-intensity exercise shows the same hypotensive effect as more intense exercise. Intensity was determined by maximal oxygen consumption. Lower energy expenditure and shorter training time in the form of more intense (>70% of maximal oxygen uptake) intermittent aerobic and anaerobic exercise have also been shown to effectively lower blood pressure in hypertensive patients [39].

Physical activity also affects the microbiome. Studies have shown that athletes have a greater diversity of gut microbiota bacteria compared to people with sedentary lifestyles [40]. More types of health-positive bacteria, such as Akkermansia, Veillonella, Prevotella, were detected in physically active individuals [41]. However, the diets of physically active and inactive people differed significantly, so it is impossible to determine conclusively whether the changes in the composition of the microbiome were due to the exercise used, since diet also has a huge impact on the microbiome. Other studies have shown that the composition of the gut microbiome can affect the physical fitness of the host. More fecal SCFAs have been observed in physically active individuals who exercise regularly [42]. These compounds are involved in glucose, cholesterol and lipid metabolism, and are used as an energy source [43]. It has also been discovered that lactate produced by skeletal muscle during anaerobic exercise is a substrate for, among others, the species Veillonella atypica, which produces propionate belonging to SCFAs. In an animal model, this strain has been shown to improve running performance due to the energy derived from propionate. This compound was formed from the conversion of lactate produced during exercise [44].

Diet

Diet plays a significant role in the prevention and treatment of atherosclerosis and cardiovascular disease. It has a huge impact on the gut microbiome and changes in its composition.

Certain nutrients help multiply beneficial gut bacteria. These include omega 3 polyunsaturated fatty acids, green tea, vegetables, fruits and extra virgin olive oil [25].

Three types of diets are mainly mentioned in the prevention of cardiovascular disease: the Mediterranean diet, the DASH (Dietary Approaches to Stop Hypertension) diet and the plant-based diet [45].

The Mediterranean diet is rich in prebiotics, thus stabilizing the intestinal microflora. It increases the diversity of the gut microbiome, as does a diet low in carbohydrates and fat. It has been observed that following a Mediterranean diet increases the number of SCFA-producing species such as Clostridium leptum and Eubacterium rectale. The proportion of Bifidobacteria, Bacteroides, Faecalibacterium prausnitzii species also increases, while the number of Firmicutes and Blautia bacteria is reduced. These changes have a beneficial effect on the host organism [46].

The effects on the gut microbiome of the low-calorie DASH diet and the low-carb diet were compared. The former group showed a large decrease in TMAO and lipopolysaccharides compared to the low-calorie diet group [47].

There are known differences in the composition of the gut microbiota in people who follow a vegan diet compared to meat eaters. Following a vegan diet results in an increase in the number of Bifidobacterium and Lactobacillus bacteria due to the high amount of polyphenols. These bacteria exhibit anti-inflammatory effects. Prevotella, Bacteroides and Clostridium bacteria are also on the rise. These bacteria convert fiber to SCFAs [48].

Probiotics, prebiotics and synbiotics

Probiotics, prebiotics and synbiotics are also used to modify the composition of the intestinal microbiota. Probiotics are supplements containing live organisms that favorably influence the composition of the intestinal microbiota [4]. Their natural sources include cucumbers and sauerkraut. Prebiotics are substrates used by these bacteria. The most common are inulin and oligofructose found in garlic and chicory, among others, as well as lactulose, fructooligosaccharides and galactooligosaccharides [49]. Studies in an animal model have shown that the use of prebiotics improves glucose tolerance and insulin resistance, among other effects [50]. Synbiotics are a combination of a probiotic and a prebiotic [51].

Most probiotics contain SCFA-producing bacteria, such as Bifidobacterium and Lactobacillus [52]. These are the best studied strains of probiotic bacteria. Among other things, their effects on lowering cholesterol have been studied. Meta-analyses have shown that supplementation with Bifidobacterium lactis, Lactobacillus acidophilus and Lactobacillus plantarum reduce total cholesterol [53]. The greatest reduction in LDL cholesterol was achieved in patients supplementing Lactobacillus plantarum and Lactobacillus reuteri [54].

A well-known mixture of probiotic bacteria is VSL-3. It contains eight strains: Bifidobacterium breve, Bifidobacterium longum, Bifidobacterium infantis, Lactobacillus acidophilus, Lactobacillus plantarum, Lactobacillus paracasei, Lactobacillus bulgaricus and Streptococcus thermophilus [55]. Studies have shown that it attenuates pro-inflammatory effects. In mice fed a fat-rich diet, VSL-3 supplementation reduced fat deposition in the aorta and resulted in a reduction in atherosclerotic lesion area similar to telmisartan. However, the combination of VSL-3 and telmisartan did not increase atherosclerotic lesion reduction [56].

Faecal microbiota transplantation (FMT)

Fecal microbiota transplantation (FMT) is mainly associated with the treatment of recurrent Clostridium difficile infections. However, FMT is also known to be used in the treatment of chronic conditions. The super donor effect has been described. It relies on the fact that the success of the treatment depends on the composition of the donor's stool, demonstrating the importance of its proper selection for a given condition. The donor microbiome colonizes the recipient's body and multiplies. When properly selected, there should be a noticeable improvement in clinical symptoms [57]. The disadvantage of this treatment modality is the possibility of viral transplantation [58].

The role of FMT in the treatment of obesity, one of the risk factors for atherosclerosis, has been studied. Transplanting microbiota from a lean donor for a patient with metabolic syndrome resulted in an increase in insulin sensitivity in the recipient [59]. Studies have shown that FMT from a properly selected donor can increase the diversity of the microbiome [49].

The use of FMT in the treatment of cardiovascular disease requires a careful analysis of the balance of benefits and losses and a very thorough donor screening [60].

Summary

The gut microbiome is of great interest to researchers. Its role is not limited to the digestive system. The gut microbiota and its metabolites affect a number of other systems, including the cardiovascular system. The most common cause of cardiovascular disease is atherosclerosis. Specific species that make up the gut microbiome play an important role in the pathogenesis of this condition by, among other things, producing TMAO. The composition of the gut microbiome differs in people who have risk factors for atherosclerosis, such as hypertension, obesity, or hypercholesterolemia compared to healthy individuals. Bacterial species that produce short-chain fatty acids (SCFAs) play an important role. Adequate diet and physical activity are of great importance in the prevention and treatment of atherosclerosis by, among other things, inducing changes in the composition of the gut microbiome. Analysis of the microbiome can be used to predict a patient's response to statins. However, more detailed research in this area is needed.

Probiotics can be used in the prevention and treatment of atherosclerosis, but it is necessary to select them appropriately in terms of composition. Knowledge of efficacy varies from strain to strain, making it very difficult to compare and identify a specific probiotic. The use of fecal microbiota transplantation (FMT) in the treatment of cardiovascular disease requires additional research. A thorough study of donors is important. At present, more detailed research is needed to identify specific bacterial strains that can be used in the prevention and treatment of atherosclerosis. This is difficult due to their different mechanisms of action. Further analysis of differences in the composition of the gut microbiome in people with atherosclerosis or its risk factors may provide additional information on the role of the microbiome in the prevention and development of cardiovascular disease, and enable appropriate regulation of the composition of the gut microbiome.

Author's Contribution

Conceptualization, Agnieszka Bajkacz and Katarzyna Piotrowicz; Resources, Jacek Kurzeja, Hubert Piotrowicz, Olga Jankowska and Wojciech Kraśnik; Writing – Original Draft Preparation, Agnieszka Bajkacz and Katarzyna Piotrowicz; Writing - Review and Editing, Jacek Kurzeja, Anna Rogala, Joanna Osmólska, Olga Jankowska, Wojciech Kraśnik, Agnieszka Bajkacz, Katarzyna Piotrowicz and Hubert Piotrowicz; Visualization, Joanna Osmólska, Anna Rogala, Olga Jankowska and Wojciech Kraśnik; Supervision, Jacek Kurzeja.

All authors have read and agreed with the published version of the manuscript.

Funding Statement

This research received no financial support.

Institutional Review Board Statement

Not applicable.

Informed Consent Statement

Not applicable.

Data Availability Statement

Not applicable.

Conflict of Interest Statement

The authors declare no conflict of interest.

REFERENCES

1. Zhai T, Wang P, Hu X, Zheng L. Probiotics Bring New Hope for Atherosclerosis Prevention and Treatment. Oxid Med Cell Longev. 2022 Sep 24;2022:3900835. doi: 10.1155/2022/3900835.
2. Fan J, Watanabe T. Atherosclerosis: Known and unknown. Pathol Int. 2022 Mar;72(3):151-160. doi: 10.1111/pin.13202. Epub 2022 Jan 25.
3. Sanchez-Rodriguez E, Egea-Zorrilla A, Plaza-Díaz J, Aragón-Vela J, Muñoz-Quezada S, Tercedor-Sánchez L, Abadia-Molina F. The Gut Microbiota and Its Implication in the Development of Atherosclerosis and Related Cardiovascular Diseases. Nutrients. 2020 Feb 26;12(3):605. doi: 10.3390/nu12030605.
4. Kim SK, Guevarra RB, Kim YT, Kwon J, Kim H, Cho JH, Kim HB, Lee JH. Role of Probiotics in Human Gut Microbiome-Associated Diseases. J Microbiol Biotechnol. 2019 Sep 28;29(9):1335-1340. doi: 10.4014/jmb.1906.06064.
5. Tang WH, Kitai T, Hazen SL. Gut Microbiota in Cardiovascular Health and Disease. Circ Res. 2017 Mar 31;120(7):1183-1196. doi: 10.1161/CIRCRESAHA.117.309715.
6. Tamburini S, Shen N, Wu HC, Clemente JC. The microbiome in early life: implications for health outcomes. Nat Med. 2016 Jul 7;22(7):713-22. doi: 10.1038/nm.4142.
7. Tang WHW, Li DY, Hazen SL. Dietary metabolism, the gut microbiome, and heart failure. Nat Rev Cardiol. 2019 Mar;16(3):137-154. doi: 10.1038/s41569-018-0108-7.
8. Stubbs JR, House JA, Ocque AJ, Zhang S, Johnson C, Kimber C, Schmidt K, Gupta A, Wetmore JB, Nolin TD, Spertus JA, Yu AS. Serum Trimethylamine-N-Oxide is Elevated in CKD and Correlates with Coronary Atherosclerosis Burden. J Am Soc Nephrol. 2016 Jan;27(1):305-13. doi: 10.1681/ASN.2014111063.
9. Chen K, Zheng X, Feng M, Li D, Zhang H. Gut Microbiota-Dependent Metabolite Trimethylamine N-Oxide Contributes to Cardiac Dysfunction in Western Diet-Induced Obese Mice. Front Physiol. 2017 Mar 21;8:139. doi: 10.3389/fphys.2017.00139.
10. Zhu W, Gregory JC, Org E, Buffa JA, Gupta N, Wang Z, Li L, Fu X, Wu Y, Mehrabian M, Sartor RB, McIntyre TM, Silverstein RL, Tang WHW, DiDonato JA, Brown JM, Lusis AJ, Hazen SL. Gut Microbial Metabolite TMAO Enhances Platelet Hyperreactivity and Thrombosis Risk. Cell. 2016 Mar 24;165(1):111-124. doi: 10.1016/j.cell.2016.02.011.
11. Tang WH, Kitai T, Hazen SL. Gut Microbiota in Cardiovascular Health and Disease. Circ Res. 2017 Mar 31;120(7):1183-1196. doi: 10.1161/CIRCRESAHA.117.309715.
12. Jie Z, Xia H, Zhong SL, Feng Q, Li S, Liang S, Zhong H, Liu Z, Gao Y, Zhao H, Zhang D, Su Z, Fang Z, Lan Z, Li J, Xiao L, Li J, Li R, Li X, Li F, Ren H, Huang Y, Peng Y, Li G, Wen B, Dong B, Chen JY, Geng QS, Zhang ZW, Yang H, Wang J, Wang J, Zhang X, Madsen L, Brix S, Ning G, Xu X, Liu X, Hou Y, Jia H, He K, Kristiansen K. The gut microbiome in atherosclerotic cardiovascular disease. Nat Commun. 2017 Oct 10;8(1):845. doi: 10.1038/s41467-017-00900-1.
13. Emoto T, Yamashita T, Sasaki N, Hirota Y, Hayashi T, So A, Kasahara K, Yodoi K, Matsumoto T, Mizoguchi T, Ogawa W, Hirata K. Analysis of Gut Microbiota in Coronary Artery Disease Patients: a Possible Link between Gut Microbiota and Coronary Artery Disease. J Atheroscler Thromb. 2016 Aug 1;23(8):908-21. doi: 10.5551/jat.32672.

14. Vourakis M, Mayer G, Rousseau G. The Role of Gut Microbiota on Cholesterol Metabolism in Atherosclerosis. Int J Mol Sci. 2021 Jul 28;22(15):8074. doi: 10.3390/ijms22158074.
15. Lam V, Su J, Hsu A, Gross GJ, Salzman NH, Baker JE. Intestinal Microbial Metabolites Are Linked to Severity of Myocardial Infarction in Rats. PLoS One. 2016 Aug 9;11(8):e0160840. doi: 10.1371/journal.pone.0160840.
16. Mitra S, Drautz-Moses DI, Alhede M, Maw MT, Liu Y, Purbojati RW, Yap ZH, Kushwaha KK, Gheorghe AG, Bjarnsholt T, Hansen GM, Sillesen HH, Hougen HP, Hansen PR, Yang L, Tolker-Nielsen T, Schuster SC, Givskov M. In silico analyses of metagenomes from human atherosclerotic plaque samples. Microbiome. 2015 Sep 3;3:38. doi: 10.1186/s40168-015-0100-y.
17. Malik M, Suboc TM, Tyagi S, Salzman N, Wang J, Ying R, Tanner MJ, Kakarla M, Baker JE, Widlansky ME. Lactobacillus plantarum 299v Supplementation Improves Vascular Endothelial Function and Reduces Inflammatory Biomarkers in Men With Stable Coronary Artery Disease. Circ Res. 2018 Oct 12;123(9):1091-1102. doi: 10.1161/CIRCRESAHA.118.313565.
18. Boets E, Gomand SV, Deroover L, Preston T, Vermeulen K, De Preter V, Hamer HM, Van den Mooter G, De Vuyst L, Courtin CM, Annaert P, Delcour JA, Verbeke KA. Systemic availability and metabolism of colonic-derived short-chain fatty acids in healthy subjects: a stable isotope study. J Physiol. 2017 Jan 15;595(2):541-555. doi: 10.1113/JP272613.
19. Parada Venegas D, De la Fuente MK, Landskron G, González MJ, Quera R, Dijkstra G, Harmsen HJM, Faber KN, Hermoso MA. Short Chain Fatty Acids (SCFAs)-Mediated Gut Epithelial and Immune Regulation and Its Relevance for Inflammatory Bowel Diseases. Front Immunol. 2019 Mar 11;10:277. doi: 10.3389/fimmu.2019.00277. Erratum in: Front Immunol. 2019 Jun 28;10:1486. doi: 10.3389/fimmu.2019.01486.
20. de la Cuesta-Zuluaga J, Mueller NT, Álvarez-Quintero R, Velásquez-Mejía EP, Sierra JA, Corrales-Agudelo V, Carmona JA, Abad JM, Escobar JS. Higher Fecal Short-Chain Fatty Acid Levels Are Associated with Gut Microbiome Dysbiosis, Obesity, Hypertension and Cardiometabolic Disease Risk Factors. Nutrients. 2018 Dec 27;11(1):51. doi: 10.3390/nu11010051.
21. Verhaar BJH, Prodan A, Nieuwdorp M, Muller M. Gut Microbiota in Hypertension and Atherosclerosis: A Review. Nutrients. 2020 Sep 29;12(10):2982. doi: 10.3390/nu12102982.
22. Yan Q, Gu Y, Li X, Yang W, Jia L, Chen C, Han X, Huang Y, Zhao L, Li P, Fang Z, Zhou J, Guan X, Ding Y, Wang S, Khan M, Xin Y, Li S, Ma Y. Alterations of the Gut Microbiome in Hypertension. Front Cell Infect Microbiol. 2017 Aug 24;7:381. doi: 10.3389/fcimb.2017.00381.
23. Wilck N, Matus MG, Kearney SM, Olesen SW, Forslund K, Bartolomaeus H, Haase S, Mähler A, Balogh A, Markó L, Vvedenskaya O, Kleiner FH, Tsvetkov D, Klug L, Costea PI, Sunagawa S, Maier L, Rakova N, Schatz V, Neubert P, Frätzer C, Krannich A, Gollasch M, Grohme DA, Côrte-Real BF, Gerlach RG, Basic M, Typas A, Wu C, Titze JM, Jantsch J, Boschmann M, Dechend R, Kleinewietfeld M, Kempa S, Bork P, Linker RA, Alm EJ, Müller DN. Salt-responsive gut commensal modulates T_H17 axis and disease. Nature. 2017 Nov 30;551(7682):585-589. doi: 10.1038/nature24628.
24. Thingholm LB, Rühlemann MC, Koch M, Fuqua B, Laucke G, Boehm R, Bang C, Franzosa EA, Hübenthal M, Rahnavard A, Frost F, Lloyd-Price J, Schirmer M, Lusis AJ, Vulpe CD, Lerch MM, Homuth G, Kacprowski T, Schmidt CO, Nöthlings U, Karlsen TH, Lieb W, Laudes M, Franke A, Huttenhower C. Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. Cell Host Microbe. 2019 Aug 14;26(2):252-264.e10. doi: 10.1016/j.chom.2019.07.004.
25. Lau LHS, Wong SH. Microbiota, Obesity and NAFLD. Adv Exp Med Biol. 2018;1061:111-125. doi: 10.1007/978-981-10-8684-7_9.
26. Liu H, Du T, Li C, Yang G. STAT3 phosphorylation in central leptin resistance. Nutr Metab (Lond). 2021 Apr 13;18(1):39. doi: 10.1186/s12986-021-00569-w.
27. Ahmed H, Leyrolle Q, Koistinen V, Kärkkäinen O, Layé S, Delzenne N, Hanhineva K. Microbiota-derived metabolites as drivers of gut-brain communication. Gut Microbes. 2022 Jan-Dec;14(1):2102878. doi: 10.1080/19490976.2022.2102878.
28. Cheng YC, Liu JR. Effect of *Lactobacillus rhamnosus* GG on Energy Metabolism, Leptin Resistance, and Gut Microbiota in Mice with Diet-Induced Obesity. Nutrients. 2020 Aug 24;12(9):2557. doi: 10.3390/nu12092557.
29. Kriaa A, Bourgin M, Potiron A, Mkaouar H, Jablaoui A, Gérard P, Maguin E, Rhimi M. Microbial impact on cholesterol and bile acid metabolism: current status and future prospects. J Lipid Res. 2019 Feb;60(2):323-332. doi: 10.1194/jlr.R088989.
30. Tang WH, Kitai T, Hazen SL. Gut Microbiota in Cardiovascular Health and Disease. Circ Res. 2017 Mar 31;120(7):1183-1196. doi: 10.1161/CIRCRESAHA.117.309715.
31. Villette R, Kc P, Beliard S, Salas Tapia MF, Rainteau D, Guerin M, Lesnik P. Unraveling Host-Gut Microbiota Dialogue and Its Impact on Cholesterol Levels. Front Pharmacol. 2020 Apr 3;11:278. doi: 10.3389/fphar.2020.00278.
32. Li DY, Li XS, Chaikijurajai T, Li L, Wang Z, Hazen SL, Tang WHW. Relation of Statin Use to Gut Microbial Trimethylamine N-Oxide and Cardiovascular Risk. Am J Cardiol. 2022 Sep 1;178:26-34. doi: 10.1016/j.amjcard.2022.05.010.

33. Sun B, Li L, Zhou X. Comparative analysis of the gut microbiota in distinct statin response patients in East China. J Microbiol. 2018 Dec;56(12):886-892. doi: 10.1007/s12275-018-8152-x.
34. Kummen M, Solberg OG, Storm-Larsen C, Holm K, Ragnarsson A, Trøseid M, Vestad B, Skårdal R, Yndestad A, Ueland T, Svardal A, Berge RK, Seljeflot I, Gullestad L, Karlsen TH, Aaberge L, Aukrust P, Hov JR. Rosuvastatin alters the genetic composition of the human gut microbiome. Sci Rep. 2020 Mar 25;10(1):5397. doi: 10.1038/s41598-020-62261-y.
35. Khan TJ, Ahmed YM, Zamzami MA, Siddiqui AM, Khan I, Baothman OAS, Mehanna MG, Kuerban A, Kaleemuddin M, Yasir M. Atorvastatin Treatment Modulates the Gut Microbiota of the Hypercholesterolemic Patients. OMICS. 2018 Feb;22(2):154-163. doi: 10.1089/omi.2017.0130.
36. Ekblom-Bak E, Börjesson M, Ekblom Ö, Angerås O, Bergman F, Berntsson C, Carlhäll CJ, Engström G, Engvall J, Fagman E, Flinck A, Johansson P, Jujic A, Kero T, Lind L, Mannila M, Ostenfeld E, Persson A, Persson J, Persson M, Redfors B, Sandberg C, Wennberg P, Öhlin J, Östgren CJ, Jernberg T. Accelerometer derived physical activity and subclinical coronary and carotid atherosclerosis: cross-sectional analyses in 22 703 middle-aged men and women in the SCAPIS study. BMJ Open. 2023 Nov 23;13(11):e073380. doi: 10.1136/bmjopen-2023-073380.
37. Ji H, Gulati M, Huang TY, Kwan AC, Ouyang D, Ebinger JE, Casaletto K, Moreau KL, Skali H, Cheng S. Sex Differences in Association of Physical Activity With All-Cause and Cardiovascular Mortality. J Am Coll Cardiol. 2024 Feb 27;83(8):783-793. doi: 10.1016/j.jacc.2023.12.019.
38. Sawyer BJ, Tucker WJ, Bhammar DM, Ryder JR, Sweazea KL, Gaesser GA. Effects of high-intensity interval training and moderate-intensity continuous training on endothelial function and cardiometabolic risk markers in obese adults. J Appl Physiol (1985). 2016 Jul 1;121(1):279-88. doi: 10.1152/japplphysiol.00024.2016.
39. Boutcher YN, Boutcher SH. Exercise intensity and hypertension: what's new? J Hum Hypertens. 2017 Mar;31(3):157-164. doi: 10.1038/jhh.2016.62.
40. Marttinen M, Ala-Jaakkola R, Laitila A, Lehtinen MJ. Gut Microbiota, Probiotics and Physical Performance in Athletes and Physically Active Individuals. Nutrients. 2020 Sep 25;12(10):2936. doi: 10.3390/nu12102936.
41. Petersen LM, Bautista EJ, Nguyen H, Hanson BM, Chen L, Lek SH, Sodergren E, Weinstock GM. Community characteristics of the gut microbiomes of competitive cyclists. Microbiome. 2017 Aug 10;5(1):98. doi: 10.1186/s40168-017-0320-4.
42. Barton W, Penney NC, Cronin O, Garcia-Perez I, Molloy MG, Holmes E, Shanahan F, Cotter PD, O'Sullivan O. The microbiome of professional athletes differs from that of more sedentary subjects in composition and particularly at the functional metabolic level. Gut. 2018 Apr;67(4):625-633. doi: 10.1136/gutjnl-2016-313627.
43. LeBlanc JG, Chain F, Martín R, Bermúdez-Humarán LG, Courau S, Langella P. Beneficial effects on host energy metabolism of short-chain fatty acids and vitamins produced by commensal and probiotic bacteria. Microb Cell Fact. 2017 May 8;16(1):79. doi: 10.1186/s12934-017-0691-z.
44. Scheiman J, Luber JM, Chavkin TA, MacDonald T, Tung A, Pham LD, Wibowo MC, Wurth RC, Punthambaker S, Tierney BT, Yang Z, Hattab MW, Avila-Pacheco J, Clish CB, Lessard S, Church GM, Kostic AD. Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. Nat Med. 2019 Jul;25(7):1104-1109. doi: 10.1038/s41591-019-0485-4.
45. Diab A, Dastmalchi LN, Gulati M, Michos ED. A Heart-Healthy Diet for Cardiovascular Disease Prevention: Where Are We Now? Vasc Health Risk Manag. 2023 Apr 21;19:237-253. doi: 10.2147/VHRM.S379874.
46. Abrignani V, Salvo A, Pacinella G, Tuttolomondo A. The Mediterranean Diet, Its Microbiome Connections, and Cardiovascular Health: A Narrative Review. Int J Mol Sci. 2024 Apr 30;25(9):4942. doi: 10.3390/ijms25094942.
47. Diao Z, Molludi J, Latef Fateh H, Moradi S. Comparison of the low-calorie DASH diet and a low-calorie diet on serum TMAO concentrations and gut microbiota composition of adults with overweight/obesity: a randomized control trial. Int J Food Sci Nutr. 2024 Mar;75(2):207-220. doi: 10.1080/09637486.2023.2294685.
48. Tomova A, Bukovsky I, Rembert E, Yonas W, Alwarith J, Barnard ND, Kahleova H. The Effects of Vegetarian and Vegan Diets on Gut Microbiota. Front Nutr. 2019 Apr 17;6:47. doi: 10.3389/fnut.2019.00047.
49. Geng J, Ni Q, Sun W, Li L, Feng X. The links between gut microbiota and obesity and obesity related diseases. Biomed Pharmacother. 2022 Mar;147:112678. doi: 10.1016/j.biopha.2022.112678.
50. Gérard P. Gut microbiota and obesity. Cell Mol Life Sci. 2016 Jan;73(1):147-62. doi: 10.1007/s00018-015-2061-5.
51. Farias D.P., Araújo F.F., Neri-Numa I.A., Pastore G.M. Prebiotics: Trends in food, health and technological applications. Trends Food Sci. Technol. 2019;93:23–35. doi: 10.1016/j.tifs.2019.09.004.
52. Zhao, W., Liu, Y., Latta, M., Ma, W., Wu, Z., & Chen, P. (2019). Probiotics database: a potential source of fermented foods. *International Journal of Food Properties*, *22*(1), 198–217. https://doi.org/10.1080/10942912.2019.1579737.
53. Wang L, Guo MJ, Gao Q, Yang JF, Yang L, Pang XL, Jiang XJ. The effects of probiotics on total cholesterol: A meta-analysis of randomized controlled trials. Medicine (Baltimore). 2018 Feb;97(5):e9679. doi: 10.1097/MD.0000000000009679.
54. Wu Y, Zhang Q, Ren Y, Ruan Z. Effect of probiotic Lactobacillus on lipid profile: A systematic review and meta-analysis of randomized, controlled trials. PLoS One. 2017 Jun 8;12(6):e0178868. doi: 10.1371/journal.pone.0178868.

55. El Hage R, Al-Arawe N, Hinterseher I. The Role of the Gut Microbiome and Trimethylamine Oxide in Atherosclerosis and Age-Related Disease. Int J Mol Sci. 2023 Jan 25;24(3):2399. doi: 10.3390/ijms24032399.
56. Chan YK, El-Nezami H, Chen Y, Kinnunen K, Kirjavainen PV. Probiotic mixture VSL#3 reduce high fat diet induced vascular inflammation and atherosclerosis in ApoE(-/-) mice. AMB Express. 2016 Dec;6(1):61. doi: 10.1186/s13568-016-0229-5.
57. Wilson BC, Vatanen T, Cutfield WS, O'Sullivan JM. The Super-Donor Phenomenon in Fecal Microbiota Transplantation. Front Cell Infect Microbiol. 2019 Jan 21;9:2. doi: 10.3389/fcimb.2019.00002.
58. Chehoud C, Dryga A, Hwang Y, Nagy-Szakal D, Hollister EB, Luna RA, Versalovic J, Kellermayer R, Bushman FD. Transfer of Viral Communities between Human Individuals during Fecal Microbiota Transplantation. mBio. 2016 Mar 29;7(2):e00322. doi: 10.1128/mBio.00322-16.
59. Kootte RS, Levin E, Salojärvi J, Smits LP, Hartstra AV, Udayappan SD, Hermes G, Bouter KE, Koopen AM, Holst JJ, Knop FK, Blaak EE, Zhao J, Smidt H, Harms AC, Hankemeijer T, Bergman JJGHM, Romijn HA, Schaap FG, Olde Damink SWM, Ackermans MT, Dallinga-Thie GM, Zoetendal E, de Vos WM, Serlie MJ, Stroes ESG, Groen AK, Nieuwdorp M. Improvement of Insulin Sensitivity after Lean Donor Feces in Metabolic Syndrome Is Driven by Baseline Intestinal Microbiota Composition. Cell Metab. 2017 Oct 3;26(4):611-619.e6. doi: 10.1016/j.cmet.2017.09.008.
60. Chen AT, Zhang J, Zhang Y. Gut microbiota in heart failure and related interventions. Imeta. 2023 Jul 10;2(3):e125. doi: 10.1002/imt2.125.