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GUT MICROBIOME-HEART AXIS RELEVANCE ACROSS HEALTH AND PREGNANCY

A.R.
ARTIGO DE REVISÃO

RELEVÂNCIA DO EIXO MICROBIOMA INTESTINAL-CORAÇÃO NA SAÚDE E NA GRAVIDEZ

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ABSTRACT

The gut microbiome has recently been implicated in some chronic pathologies, including cardiovascular diseases, even at an early stage of cardiovascular risk factor diagnosis. Indeed, the gut microbiome may impact the regulation of cardiovascular metabolism, affecting the mother's and offspring's health during pregnancy. Diverse microbiota mechanisms have been documented in this context, including inflammatory mechanisms. This review aims to discuss the role of gut microbiome in cardiovascular diseases and the impact of diet on preventing or treating cardiovascular diseases by modulating the gut microbiome, with a special focus on pregnancy. Two databases (PubMed and ScienceDirect) were thoroughly searched between February 2024 and May 2025. According to the literature analysis conducted, alterations in the ratio of *Bacillota/Bacteroidota* and the imbalance of microbial-dependent metabolites, including short-chain fatty acids and trimethylamine N-oxide, play a crucial role in the pathogenesis of cardiovascular diseases. The Mediterranean dietary pattern is mentioned as cardioprotective, underlying its high concentration of bioactive compounds that exert antioxidant, anti-inflammatory and antithrombotic effects. Prebiotics and probiotics confer various health benefits on the host and are emerging as promising therapeutic interventions for cardiovascular diseases and preventive complications during pregnancy.

PALAVRAS-CHAVE

Cardiovascular diseases, Cardiovascular risks factors, Dysbiosis, Gut microbiome, Pregnancy

RESUMO

Recentemente, o microbioma intestinal tem sido associado a um conjunto de patologias crónicas incluindo as doenças cardiovasculares, mesmo em fases iniciais aquando do diagnóstico dos fatores de risco cardiovascular. Efetivamente, o microbioma intestinal pode ter impacto na regulação do metabolismo cardiovascular, incluindo durante a gravidez, afetando diretamente a saúde da mãe e da criança. Os mecanismos pelos quais a microbiota intervém na saúde cardiovascular são múltiplos, incluindo mecanismos inflamatórios. O objetivo desta revisão é discutir o papel do microbioma intestinal nas doenças cardiovasculares e o impacto da dieta enquanto modulador do mesmo na prevenção e tratamento destas doenças, com especial destaque para o contexto da gravidez. Duas bases de dados (*PubMed* e *ScienceDirect*) foram utilizadas para pesquisa bibliográfica entre fevereiro de 2024 e maio de 2025. De acordo com a análise da literatura, alterações no rácio *Bacillota/Bacteroidota* e o desequilíbrio nos metabolitos microbianos, incluindo ácidos gordos de cadeia curta e N-óxido de trimetilamina, têm um importante papel na patogénese das doenças cardiovasculares. A gravidez representa uma oportunidade única para prever e prevenir doenças cardiovasculares em mulheres com fatores de risco. A Dieta Mediterrânica é considerada cardioprotetora devido às altas concentrações de compostos bioativos que exercem efeitos antioxidantes, anti-inflamatórios e antitrombóticos. Os prebióticos e probióticos conferem benefícios à saúde, podendo funcionar como intervenções terapêuticas promissoras nas doenças cardiovasculares e prevenção de aparecimento de complicações durante a gravidez.

KEYWORDS

Doenças cardiovasculares, Fatores de risco cardiovascular, Disbiose, Microbioma intestinal, Gravidez

INTRODUCTION

The human microbiome is an ecological collection of microorganisms (*eukaryotes*, *archaea*, bacteria, and viruses), their associated genomes and metabolites, that interact with the host environment (1). The microbiome is located mainly in the gastrointestinal tract, specifically in the gut, where microorganisms carry out various functions that contribute to the host's health (2). Some of their functions include fermentation of indigestible dietary fibre, regulating the immune system, synthesising certain vitamins, and maintaining the intestinal epithelial mucosal barrier (3). *Bacillota* (known as *Firmicutes*) and *Bacteroidota* (known as *Bacteroidetes*) are the two dominating phyla, accounting for more than 90% of the bacterial community (4, 5). Gut dysbiosis, an imbalance in gut microbiome composition, significantly correlates with the pathogenesis

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of both intestinal disorders and extra-intestinal disorders, including cardiovascular diseases (CVDs) (6, 7). CVDs can refer to several conditions, including heart failure (HF), stroke, coronary artery disease (CAD), and peripheral artery disease (PAD) (8). Globally, CVDs are major contributors to a decreased quality of life and the principal cause of morbidity and mortality (8). The cardiovascular risk factors, such as arterial hypertension (AHT), obesity, diabetes mellitus, high low-density lipoprotein (LDL) cholesterol, smoking, physical inactivity and unhealthy diet, are the precursors of the CVDs development (8). Furthermore, changes in the ratio of *Bacillota*/*Bacteroidota* and the imbalanced levels of gut microbial metabolites, such as short-chain fatty acids (SCFAs) and trimethylamine N-oxide (TMAO), have been strongly associated with the pathogenesis of CVDs (6, 9). Despite continued research on the relationship between gut microbiome and CVDs, the exact mechanism by which the gut microbiome and its metabolites act on the pathogenesis of CVDs remains unclear.

During pregnancy, the gut microbiome may also participate in physiological activities and further regulate cardiovascular metabolism, affecting the health of both mother and offspring (10). Some factors, namely an excessive gestational weight gain and obesity, are associated with the gut microbiome of mothers, which promotes an increase in the ratio of *Bacillota/Bacteroidota* and inflammatory markers (11).

This review aims to discuss the role of gut microbiome in CVDs and the impact of diet on preventing or ameliorating these diseases by modulating the gut microbiome, with a special focus on pregnancy.

METHODOLOGY

This narrative literature review was based on a bibliographic search conducted between February 2024 and May 2025 using two databases: PubMed and ScienceDirect. The search strategy combined the search terms “gut microbiota”, “cardiovascular disease”, “cardiovascular risk factors”, “pregnancy”, “maternal health”, and “dysbiosis”, using the Boolean operators “AND” and “OR”. The following search string was applied: (“gut microbiota”) AND (“cardiovascular disease” OR “cardiovascular risk factors”) AND (“pregnancy” OR “maternal health”) AND (“dysbiosis”). Initially, this search retrieved 1315 articles from both databases, focusing on the association between the gut microbiome and cardiovascular and metabolic health. The exclusion criteria included duplicate records and articles published more than 10 years ago. The inclusion criteria comprised articles written in English or Portuguese that investigated the relationship between the gut microbiome and cardiovascular diseases, both in the general population and in pregnancy. After screening titles and abstracts according to the inclusion and exclusion criteria, a total of 84 articles were included in the final analysis.

Interaction Between Cardiovascular Risk Factors and the Gut Microbiota

Currently, the role of the gut microbiome in the development of cardiovascular risk factors has become a prominent topic of scientific literature, particularly concerning type 2 diabetes *mellitus* (T2DM), AHT, low-grade inflammation, obesity and its subsequent complications (12,13). In obese mice and humans, an increase in *Bacillota* (formerly *Firmicutes*) and a reduction in *Bacteroidota* (*Bacteroidetes*) were characteristic gut microbiota features (14). In obesity, infiltrating macrophages and leukocytes, along with the secretory profile of adipocytokines, can promote a proinflammatory state linked to obesity-related complications (15). Dysbiosis also negatively impacts insulin sensitivity and is associated with higher diabetes risk, partly due to decreased butyrate levels, a SCFA (16).

AHT and gut microbiota were associated through Mendelian randomisation, revealing both protective and harmful bacteria (17). Protective bacteria, including *Verrucomicrobia*, *Bifidobacteriales*, *Bacteroidales* S24-7 group, *Bifidobacteriaceae*, *Adlercreutzia*, *Phascolarctobacterium*, *Lachnospiraceae* NK4A136 group, and *Ruminococcus*-2, promote the production of beneficial metabolites such as SCFAs like butyrate, propionate, and acetate, which help reduce inflammation, improve gut barrier function, and regulate blood pressure. In contrast, *Alcaligenaceae*, *Anaerostipes*, *Collinsella*, and *Lachnospiraceae_UCG_010* promote inflammation and intestinal permeability, increasing AHT risk (18).

Lipopolysaccharide (LPS), a component of the outer membrane of gram-negative bacteria, plays a central role in the pathogenesis of cardiovascular diseases, particularly in AHT, through its ability to induce systemic inflammation and endothelial dysfunction (19, 20). Increased intestinal permeability allows LPS to enter the bloodstream, triggering inflammation and endothelial damage. It contributes to the development of AHT by causing endothelial dysfunction, reducing the production of vasodilators like nitric oxide (NO), and increasing vascular resistance (20). Similarly, zonulin, a protein regulating intestinal permeability, plays a crucial role in cardiovascular diseases (21) and several metabolic disorders, including obesity, AHT and other cardiovascular conditions (22, 23). Elevated zonulin levels disrupt the tight junctions between intestinal epithelial cells, promoting intestinal hyperpermeability (22, 23). Zonulin-related disruption of the gut barrier also alters the gut microbiome, increasing the number of pathogenic bacteria and promoting further production of harmful metabolites and inflammatory molecules (22). Kim and colleagues provided the first evidence that increased intestinal permeability in hypertensive patients was associated with increased LPS and zonulin circulating levels (24). Yan *et al*. demonstrated specific microbial alterations, with a reduced microbial diversity linked to increased disease risk (25).

The increased serum cholesterol levels have been reported as a cardiovascular risk factor due to the association with atherosclerosis, CAD and PAD (26). Gut microbiota can alter blood lipid composition, particularly cholesterol, through their role in bile acid metabolism and the generation of microbial products (27). For example, *Lactobacillus reuteri* is associated with higher high-density lipoprotein (HDL) cholesterol, while *Eggerthella* is linked to lower HDL levels (28). These findings underscore the gut microbiome's role in regulating cardiovascular risk factors, including cholesterol metabolism, and its potential in influencing the progression of CVDs.

Gut Microbiota Composition in Cardiovascular Diseases

Considering the described associations between the gut microbiome and some cardiovascular risk factors, it is understood that a dysbiosis gut is involved in the aetiology of CVDs. The reduced cardiac output is associated with changes in the intestine's structure and function, leading to intestinal wall oedema and intestinal ischaemia (29). As previously mentioned, serum LPS is associated with cardiovascular events, insulin resistance, glycaemic control and abdominal obesity (30). Increased intestinal permeability allows LPS from gut bacteria to enter the bloodstream, triggering systemic inflammation and contributing to conditions like atherosclerosis, AHT, CAD and HF (29, 31, 32).

Walker and colleagues reported that gut microbial diversity was reduced during 10 years of follow-up in participants with cardiovascular risk factors. Specifically, *Ruminococcaceae*, *Clostridiales* and *Lachnospiraceae* were significantly associated with cardiovascular risk factors, including diabetes and metabolic syndrome (31).

More recently, studies have been conducted to identify the presence of a significant correlation between gut microbiome composition and CAD. Among them, Toya *et al.* analysed faecal samples from advanced CAD patients and controls matched for age, gender, race, and body mass index (33). Using the 16S ribosomal RNA (rRNA), the authors found that the ratio of *Bacillota*/*Bacteroidota* did not significantly differ between the two groups. However, *Ruminococcus gnavus*, which is linked to inflammation, was found to be more abundant in CAD patients, while butyrate-producing bacteria, such as *Lachnospiraceae* group NK4B4 and *Ruminococcus gauvreauii*, were less abundant (33). Zheng *et al.* also identified an association between gut microbial dysbiosis and CAD by sequencing 16S rRNA of faecal samples from CAD patients and healthy controls (34). They found that *Chryseobacterium*, *Butyricimonas*, and *Megasphaera* were more abundant in CAD patients. At the same time, beneficial SCFA producers like *Anaerostipes* and *Blautia* were less prevalent (34).
Similarly, in PAD, there was an increased abundance of *Lachnospiraceae* and *Ruminococcaceae* compared to healthy individuals (35).
Patients with stroke and transient ischaemic attack had more opportunistic pathogens, such as *Enterobacter*, Megasphaera, *Oscillibacter* and fewer commensal or health-associated genera, including *Bacteroides*, *Prevotella*, and *Faecalibacterium* (32).
In HF, patients' gut microbiota was characterised by an increased abundance of *Bacteroidota* and a decreased abundance of *Bacillota*. In a Mendelian randomisation analysis, Tian and colleagues found that *Bacteroides dorei* was associated with increased levels of apolipoprotein B, suggesting an elevated risk for HF (36).
These studies highlight how shifts in gut microbiota composition are associated with various cardiovascular conditions, influencing disease development through inflammation, metabolic changes, and microbial metabolites.

Microbial Metabolites and Their Impact on Cardiovascular Health

Microbial metabolites, such as TMAO, SCFAs, and bile acids, significantly influence cardiovascular health by affecting inflammation, lipid metabolism, and endothelial function (37). TMAO is a pro-inflammatory and pro-atherosclerotic metabolite produced from the metabolism of dietary precursors like choline, carnitine, and phosphatidylcholine, resulting in the metabolite trimethylamine (TMA) in the gut, which is absorbed into the portal circulatory system (37). In the liver, TMA is oxidised into TMAO by hepatic flavin monooxygenases and is excreted primarily by the kidneys (37). It is involved in foam cell formation, maturation, and secretion of inflammatory cytokines and adhesion molecules that result in vascular inflammation (38). In a meta-analysis study, the authors found that increased levels of TMAO were associated with increased risk of major cardiovascular events (62%), such as heart attack and stroke, and death from all causes (63%) (9). Stroke patients have a significant correlation between the TMAO serum level and the first haemorrhagic stroke (38). Moreover, marked overexpression of TMA-producing intestinal microbial enzymes was observed in patients with CAD compared with healthy controls (29).
Another critical group of metabolites associated with CVDs are SCFAs. Gut bacteria produce SCFAs through the fermentation of dietary fibre and resistant starches. Acetate, propionate, and butyrate are the main end-products of prebiotic fermentation. SCFAs have been recognised as anti-inflammatory metabolites, increasing the expression of anti-inflammatory factors and improving the intestinal barrier. These effects are essential to maintain a healthy cardiovascular system (39, 40). Furthermore, bacteria in the gut produce secondary bile acids, which appear to bind to and activate several host nuclear receptors to a greater extent than host primary bile acids and seem to impact CVDs (41). A systematic review of the association between secondary bile acids and CVD risk reported inconsistent results among studies. No significant results were shown for total CVDs, whereas increased levels of glycocholenate sulphate were associated with an increased risk of atrial fibrillation (40).

Interaction Between the Gut Microbiome and Cardiovascular Health in Pregnancy

During pregnancy, a woman's body undergoes several physiological changes to ensure optimal foetal growth and development (42). These changes include increased cardiac output and stroke volume, accompanied by a reduction in systemic vascular resistance (43). These adaptations lead to anatomical and functional cardiac alterations, such as left ventricular hypertrophy and impaired relaxation. After delivery, some studies have shown that in the absence of cardiovascular complications during pregnancy, the heart fully recovers in a process known as cardiac reverse remodelling (RR) (43-45). However, comorbidities, such as AHT, obesity, and diabetes, influence cardiac remodelling and RR during pregnancy and postpartum, respectively, impacting future maternal cardiovascular risk and mortality (46).
The gut microbiome also plays a role in pregnancy, participating in physiological processes and regulating cardiovascular metabolism, which affects the health of both the mother and the offspring (11). Certain factors, such as excessive gestational weight gain and obesity, are associated with changes in the maternal gut microbiome (10). An increased *Bacillota*/*Bacteroidota* ratio and an inflammatory state on the intestinal mucosal surface have been observed (10). This results in elevated levels of pro-inflammatory cytokines and leukocytes throughout pregnancy, even though the placenta produces anti-inflammatory substances to protect the foetus (10).
Alongside microbial modifications, pregnancy represents a period of systemic low-grade inflammation (42), with the gut mucosa experiencing elevated inflammatory responses with high levels of pro-inflammatory cytokines as the pregnancy advances (11). Increased zonulin levels are considered a marker of intestinal hyperpermeability, and it is associated with some pregnancy complications (47). However, there is insufficient information about the involvement of zonulin in pregnancy complications. Zonulin levels were significantly higher in the participants with pregnancy-induced hypertension when compared to the normal pregnant controls (47). Serum zonulin levels were also associated with higher odds of gestational diabetes *mellitus* (GDM) (48, 49). A leaky gut, characterized by a reduced barrier function with increased intestinal permeability and higher levels of circulating zonulin (50), shifts the maternal inflammatory state leading to deleterious effects such as foetal growth restriction and preeclampsia (51). Furthermore, higher levels of TMAO, a pro-inflammatory and pro-atherosclerotic metabolite, in later pregnancy could be associated with an increased risk of cardiometabolic disorders such as GDM or impaired RR (52, 53). TMAO levels were significantly higher in women with preeclampsia than in those with normal pregnancies (52). A recent study reported that left ventricular end-diastolic volume and left ventricular end-systolic volume values of patients with gestational hypertension were elevated and were related to serum TMAO (54). Two studies have reported that higher plasma TMAO in the second or third trimester of pregnancy was also associated with the increased odds of GDM in pregnant women (55, 56).

Strategies to Modulate the Gut Microbiome

Diet

Diet has multiple effects on the gut microbiota, being able to modify its composition and function. According to the Framingham Offspring Study, after 18 years of follow-up, consuming additional daily servings of ultra-processed foods was associated with an increased risk of CVDs (7%) (57). Moreover, red meat, eggs, fish, and high-fat dairy products are abundant in TMA nutritional precursors, such as choline, phosphatidylcholine, and carnitine-trimethylamine (37). Long-term adherence to a Mediterranean diet (MED) promotes a higher relative abundance of fibre-metabolising bacterial species than other pathogens, mainly associated with a Western-type diet (58). A systematic review found a significant reduction in cardiovascular mortality in patients with higher MED adherence scores compared to those with lower adherence. Also, patients who followed the MED showed a considerable risk reduction in the composite outcome of myocardial infarction, revascularisation, stroke, peripheral artery disease, and cardiovascular death (59). MED is cardioprotective because its high concentration of bioactive compounds such as unsaturated fatty acids, polyphenols, fibre, phytosterols, vitamins and minerals exert antioxidant, anti-inflammatory and antithrombotic effects, contributing to the delay of CVD development. MED is often described as a rich source of n-3 polyunsaturated fatty acids (PUFA) derived from fish, seafood and nuts (60). The abundance of several SCFAs-producing bacteria is increased by n-3 PUFA, decreasing the TMAO production (61).

The MED is optimal to ensure an adequate supply of nutrients during pregnancy. It provides energy and nutrients required to allow adequate foetal growth and development, protecting against the development of obstetric pathologies, including childbirth complications and infections. The MED can also prevent some maternal complications such as diabetes, sleep quality and overweight or obesity (62). Olive oil consumption can reduce adverse maternal and foetal effects, GDM, preeclampsia, cardiovascular risk, and gestational weight gain (63).

Prebiotics

Prebiotics are non-digestible plant carbohydrates, such as disaccharides, oligosaccharides [galactooligosaccharides (GOS), fructooligosaccharides (FOS), lactulose, and inulin], polysaccharides and dietary fibres, that promote beneficial gut bacteria, such as *Lactobacillus* and *Bifidobacterium* (64). They improve cardiovascular health by altering the gut environment, enhancing gut permeability, lowering total and LDL cholesterol and the incidence of CVD risk factors (65). An example of fibre is beta-glucan from oats, which the Food and Drug Administration recommends consuming more than 3 g daily to ameliorate lipid profile (66). Prebiotics, including soluble and insoluble fibre and resistant starch, support gut microbiota diversity, which may reduce allergic symptoms in neonates (67). A study showed that 14.2 g/day of GOS and FOS during pregnancy increased the abundance of commensal *Bifidobacteria* and the developing infant gut microbiome, reducing *Negativicutes* (68).

Probiotics

Probiotics are live microorganisms that provide health benefits when consumed in adequate amounts (69). They improve the *Bacillota*/*Bacteroidota* ratio and gut microbiota diversity, while reducing chronic inflammation, endotoxemia, and the risk of CVDs (70). For example, supplementation with *Lactobacillus* ameliorates CVDs by inducing changes in gut microbiota-derived circulating metabolites, reducing TMAO and LPS serum concentration (71). According to Ahmadian *et al*., probiotic supplementation with *Lactobacillus acidophilus*, *Lactobacillus* plantarum, *Lactobacillus fermentum* and *Lactobacillus gasseri* for 6 weeks led to a significant improvement in major CVD-related parameters in populations with T2DM (72). Moreover, *Bifidobacteria* can also prevent cardiac damage, promote the maintenance of the intestinal barrier, and have antioxidant and immunomodulatory effects (73). Lastly, kefir, a natural probiotic, helps lower blood pressure and protect against vascular dysfunction and cardiovascular damage (74).

Probiotic and prebiotic supplementation have potential health benefits, including preventing adverse pregnancy outcomes. The incidence of adverse effects in pregnant women and their infants associated with probiotic/prebiotic/symbiotic intake remains unclear. Prebiotic supplementation, such as FOS, GOS and inulin, during pregnancy can positively influence maternal and infant health. It can potentially prevent adverse outcomes like preterm birth, GDM, and infections by improving gut microbiota, enhancing immune function, and reducing inflammation (75). Probiotic supplementation with *Lactobacillus rhamnosus* and *Lactobacillus reuteri* is considered safe for use during pregnancy and lactation, with adverse effects being rare and typically limited to mild changes in stool consistency. These effects did not pose significant risks to either mothers or infants (76). Probiotics, including these strains and *Bifidobacterium* species, support immune function, prevent infections, and improve gut health (77). Additionally, probiotic/symbiotic interventions improved glucose, lipid metabolism, and anti-inflammatory responses in GDM patients, but had no notable effects on women with hypertensive disorders and GDM (78,79). Probiotics have been proposed as a potential preventive measure for preterm birth, with the idea that they could protect against conditions leading to preterm labour. This may occur by promoting the movement and elimination of harmful pathogens, increasing anti-inflammatory cytokines, and lowering vaginal pH to create an environment conducive to beneficial bacteria (80). More research is needed to determine the most effective prebiotic and probiotic types and their long-term safety.

Faecal Microbiota Transplantation

Faecal microbiota transplantation (FMT) involves transferring a faecal solution from a healthy donor to the recipient's intestinal tract (81). Since gut microbiome dysbiosis is linked to CVD, restoring it could benefit the treatment of diseases. Indeed, FMT was proven to alleviate myocarditis in experimental autoimmune myocarditis mouse models by improving the *Bacillota*/*Bacteroidota* ratio and reducing inflammation (81). A recent clinical study on FMT for primary hypertension showed positive results, with reduced blood pressure (82). FMT is also used to improve gut microbiota in infants, particularly after caesarean delivery, by using the mother's microbiota, where a faecal suspension previously screened and processed under sterile conditions is mixed with the mother's breast milk and administered orally to the newborn (83). Also, a single FMT treatment has been successfully used in pregnant women with recurrent *Clostridium* infection (84).

However, the complex preparation of FMT remains a limitation, and more research is needed to explore its full potential for CVD and pregnancy-related conditions.

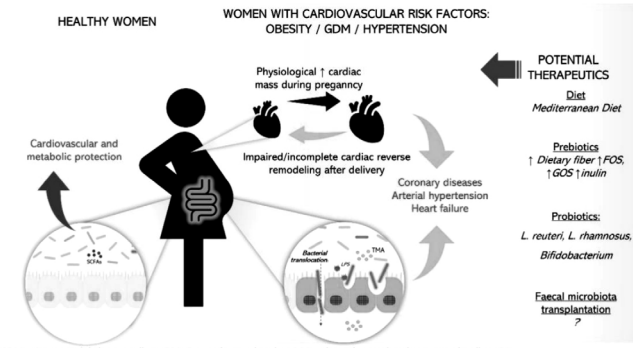
DISCUSSION OF THE RESULTS

The current body of evidence supports an association between the gut microbiome and CVDs, particularly through mechanisms involving inflammation, metabolic regulation, and intestinal permeability. Microbial metabolites such as TMAO and SCFAs have been consistently implicated in cardiometabolic processes. Additionally, emerging research highlights the relevance of the gut microbiome in pregnancy, suggesting

a potential role in maternal cardiovascular adaptations. Despite these advances, several limitations must be acknowledged: (i) most studies investigating the gut microbiome and CVDs are observational, which precludes causal inference; (ii) sample sizes are often small, and there is substantial heterogeneity in study populations, including differences in age, comorbidities, dietary habits, and medication use; (iii) moreover, methodological variability in microbiome analysis techniques, such as 16S rRNA sequencing versus metagenomics, limits comparability across studies; (iv) dietary intake, a major modulator of the gut microbiome, is not consistently controlled for, representing a significant confounding factor. Given these limitations, the findings across studies are not always consistent, making it difficult to draw robust conclusions. For instance, although alterations in the *Bacillota*/*Bacteroidota* ratio are frequently reported in obesity and cardiometabolic conditions, this association is not universally observed and may lack specificity as a biomarker of dysbiosis. Similarly, while elevated TMAO levels are associated with increased cardiovascular risk, the extent to which this relationship reflects causality or dietary patterns remains unclear. There is also a lack of longitudinal studies exploring how microbiome alterations across pregnancy influence long-term maternal cardiovascular risk and offspring health. Furthermore, although modulation of the gut microbiome through diet, probiotics, and prebiotics shows promise, current evidence is insufficient to support routine clinical application in the prevention or treatment of CVDs. The heterogeneity of findings and the absence of standardized therapeutic approaches limit translation into clinical practice. Future research should focus on well-designed longitudinal and interventional studies to clarify causal relationships and define evidence-based recommendations. The complex interaction between gut microbiota, cardiovascular health, and pregnancy-related adaptations is summarised in Figure 1, which illustrates the differences between healthy pregnancies and those complicated by cardiovascular risk factors.

Figure 1

Association between gut microbiota and cardiovascular health during pregnancy



GDM – Gestational diabetes *mellitus*; FOS- Fructooligosaccharides; GOS- galactooligosaccharides; *L. Lactobacillus*; LPS – Lipopolysaccharide; SCFAs – Short chain fatty acids; TMA – Trimethylamine

Gut microbiota and cardiovascular health during pregnancy: comparison between healthy women and those with cardiovascular risk factors. A balanced gut microbiota contributes to cardiovascular and metabolic protection in healthy pregnancies. In contrast, women with risk factors such as obesity, gestational diabetes mellitus (GDM), or arterial hypertension exhibit gut dysbiosis, which may lead to bacterial translocation, increased production of harmful metabolites (e.g., TMA, LPS), and impaired cardiac remodelling postpartum. This contributes to long-term cardiovascular outcomes such as coronary disease, arterial hypertension, and heart failure. Potential therapeutic strategies include dietary interventions (e.g., Mediterranean diet), prebiotics, probiotics, and possibly faecal microbiota transplantation.

CONCLUSIONS

The gut microbiome has emerged as a relevant factor in cardiovascular health, with growing evidence linking microbial composition and metabolites to the development of cardiovascular diseases. During pregnancy, these interactions may play an important role in maternal adaptations and influence both short- and long-term health outcomes for the mother and offspring. However, current evidence is largely observational and characterised by methodological heterogeneity, limiting the establishment of causal relationships and clinical applicability. While dietary interventions and microbiome-targeted strategies such as prebiotics and probiotics show potential, further robust and longitudinal studies are required, particularly in pregnant populations. A deeper understanding of the gut-heart axis may contribute to the development of innovative preventive and therapeutic approaches, but its integration into clinical practice remains premature.

CONFLICTS OF INTEREST

None of the authors reported a conflict of interest.

AUTHORS' CONTRIBUTION

MA: Study design, literature search, screening and analysis of the selected articles, manuscript drafting; JM: Study design, analysis of the selected articles, manuscript review and critical appraisal of the work; AF: Study design, manuscript review and critical appraisal of the work; IM: Study design, manuscript review and critical appraisal of the work.

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