The Emerging Role of Gut Microbiota in Metabolic Diseases

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ABSTRACT

The human gut microbiota, consisting of around 100 trillion microorganisms, plays an essential role in regulating metabolic balance and supporting overall health. It is well documented that dysbiosis is associated with a number of metabolic disorders including type 2 diabetes mellitus (T2DM), obesity, hypercholesterolemia, and cardiovascular diseases (CVDs). Recent studies have shown that the gut microbiome influences metabolism, immune responses, and even neuroendocrine signaling by producing metabolites like short-chain fatty acids. In obesity, the altered Firmicutes/Bacteroidetes ratio is linked to increased energy harvest from the diet. At the same time, specific bacterial taxa such as *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* exhibit anti-inflammatory properties and are inversely correlated with obesity-related inflammation. Dysbiosis in T2DM is associated with reduced levels of beneficial bacteria like *Bifidobacterium* and *Roseburia*, which are important for maintaining gut barrier integrity and regulating immune responses. Furthermore, hypercholesterolemia and CVDs have also been linked to gut microbiota composition. Specific bacterial strains, including *Lactobacillus* and *Clostridium*, are involved in bile acid metabolism, cholesterol homeostasis, and the modulation of lipid levels. This review article aims to provide an in-depth analysis of the role of gut microbiota in metabolic diseases, exploring the underlying mechanisms of microbial dysbiosis and its contribution to disease progression. Targeting microbial dysbiosis through therapeutic interventions such as probiotics, prebiotics, and dietary modifications could offer promising strategies for preventing and managing metabolic disorders, thereby improving overall health outcomes.

Keywords: Gut microbiota, Microbiome, Metabolic diseases, Diabetes, Obesity, CVDs

Introduction

The human gut microbiota comprises around 100 trillion cells, outnumbering human cells by a factor of 10.[1,2] Its density and composition increase progressively from the upper to the lower intestines, with the greatest diversity occurring in the colon.[3] The gut microbiome plays a key role in influencing several aspects of physiology, such as metabolism, immunity, and various other diseases.[4–6] It is well documented that conditions such as irritable bowel syndrome and inflammatory bowel disease (IBD) have been associated with dysbiosis in the gut microbiota.[7,8] The microbiome also contributes to visceral fat inflammation and metabolic disorders, with macrophage infiltration in adipose tissue serving as a key factor in obesity-related metabolic dysfunction.[9,10]

Interactions between the human genome and the gut microbiome can be explored through transcriptome profiling of innate and adaptive immune cells, as well as epigenetic regulation of cytokine expression.[11,12] The gut microbiota influences host gene expression, primarily through pattern recognition receptors such as Toll-like receptors (TLRs) and the MyD88 signaling pathway.[13,14] This interaction impacts innate immune responses, including the synthesis of antimicrobial peptides and mucins. Recent breakthroughs in genomics and synthetic biology present exciting opportunities for creating targeted therapies, such as probiotics and pharmabiotics, aimed at modulating the gut microbiome to enhance health outcomes.[15]

Recent studies indicate that dysbiosis in the gut microbiota may contribute to various diseases, including diabetes mellitus (DM), obesity, and multiple sclerosis. This happens due to a number of reasons such as reduction in microbial diversity and abundance, modulation of paracrine and endocrine functions, alterations in energy metabolism, effects on brain satiety centers, disruption of inflammatory pathways, and interference with essential microbial functions.[16–19] Dysbiosis, in conjunction with genetic and environmental factors, may contribute to the development of metabolic disorders.[20] Various strategies have been proposed to regulate the gut microbiota in managing various metabolic diseases, including the use of probiotics, antimicrobial agents, prebiotics, and bariatric surgery.[21] While targeting the gut microbiome and the associated metabolic pathways holds potential as a therapeutic option,[22] more comprehensive research is required to better understand the connection between gut microbiota and metabolic diseases. This review article seeks to explore and summarize the role of gut microbiota in metabolic diseases, highlighting the diverse mechanisms by which microbial dysbiosis influences disease progression and examining potential therapeutic approaches that target the microbiome for disease management.

Methodology

Literature Search Strategy

A total of 210 articles were collected from a variety of relevant databases, including Web of Science, ScienceDirect, Medline, PubMed, EMBASE, Google Scholar, and BioMed Central. The search strategy employed a comprehensive approach to identify key literature on the role of microbiota in metabolic diseases. To perform the search, specific keywords such as microbiota, microbiome, and metabolic diseases were used. Different combinations of terms were also employed, to ensure comprehensive coverage of relevant studies.

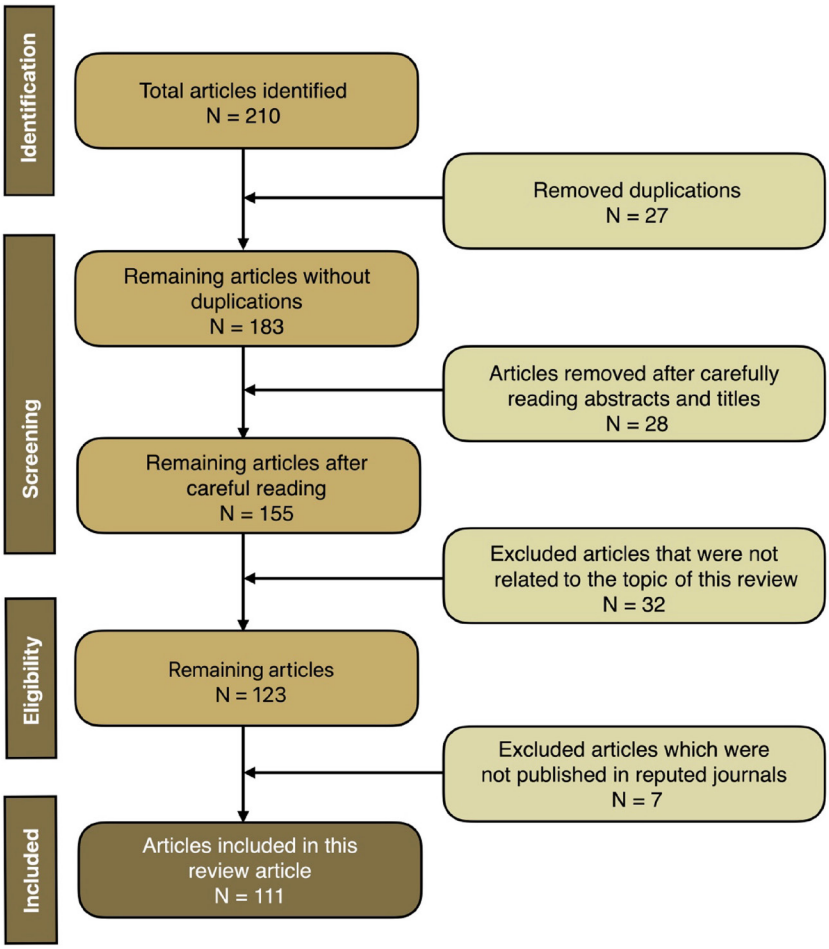

Fig 1 | A summary and flowchart of the included articles. A total of 184 articles were retrieved from multiple databases, and after careful screening, 111 articles were included in this review

The inclusion criteria consisted of original research articles, meta-analyses, and review papers that focus on the role of gut microbiota in metabolic diseases. Following a thorough screening for quality and relevance, 116 articles were retrieved and included in this review (Figure 1).

The Emerging Role of Gut Microbiota in Metabolic Diseases

The global increase in the incidence of metabolic disorders, type 2 diabetes mellitus (T2DM), obesity, cardiovascular diseases (CVDs), metabolic dysfunction-associated fatty liver disease, and various cancer types poses a significant and urgent public health challenge. Most of the metabolic disorders are triggered by external factors, such as environmental influences and lifestyle choices (Figure 2). A key aspect of this discussion is the gut microbiome, which is profoundly shaped by lifestyle-related factors such as physical activity and diet. The microbiota in the human gut is integral to key physiological processes that support metabolic balance and regulation. The subsequent topic attempts to explain how the gut microbiome plays a role in modulating metabolic diseases.

Gut Microbiota and DM

The gut microbiota is influenced by a number of factors, such as diet, antibiotic use, medications, and even the pH of drinking water. A high-fat diet disrupts the balance of intestinal flora, impairs gut function, and increases intestinal permeability, enabling harmful substances to pass into the bloodstream. These effects collectively lead to the development of DM.[23,24] The gut microbiota contributes to the development of T2DM, which is linked to conditions such as obesity, non-alcoholic fatty liver disease, insulin resistance, and chronic inflammation (Figure 3). T2DM patients have shown a decreased abundance of *Bifidobacterium, Faecalibacterium, Bacteroides, Akkermansia,* and *Roseburia*. The latter three inhibit inflammation by enhancing the production of chemokines and anti-inflammatory and pro-inflammatory cytokines. Moreover, decreased concentrations of butyrate-producing *Faecalibacterium* and *Roseburia intestinalis* have been reported to be associated with the dysregulation of fatty acid metabolism, creating oxidative stress and promoting cardiometabolic adverse manifestations.[25] Another study reported the positive correlation of dysbiosis in DM with bacteria belonging to the phylum Firmicutes and genera *Ruminococcus* and *Fusobacterium* that cause inflammation, which intensifies the inflammatory process.[26–28]

According to a study by Chung et al.,[29] *in vitro* cell tests have demonstrated that *Eubacterium eligens* can significantly stimulate the production of interleukin (IL)-10. The microbial anti-inflammatory molecule produced by *F. prausnitzii*, one of the most abundant bacteria in the human gut microbiota[30], has been shown to inhibit the nuclear factor-kappa B (NF-κB) pathway *in vitro*.[31–33] Another study revealed that patients with T2DM had a higher abundance of short-chain fatty acid (SCFA) producers, such as *Faecalibacterium*, *Roseburia*, *Lachnospira*, *Bacteroides*, and *Akkermansia*, in their gut microbiomes compared to healthy individuals who followed either a high-fiber diet or a control diet.[34]

Different studies elaborate that along with the immunological, sensory, neurological, and enteroendocrine systems, the gut microbiota is a component of a complex network that regulates the chemical and physical components of the intestinal barrier.[35,36] Maintaining a balanced gut microbiota ecosystem can help protect the host from infections.[37,38] Navab-Moghadam et al. demonstrated that the composition of the human gut microbiota significantly influences the risk and development of T2DM.[39] It has also been reported that a chemically enriched pathogenic bacterium in gut dysbiosis can induce insulin-dependent DM following its translocation to the pancreas.[40] Probiotics promote the growth of beneficial bacteria and safeguard the body against harmful bacteria. A previous study indicated that probiotics effectively regulate the gut microbiota and manage inflammation by enhancing intestinal permeability. Additionally, probiotics influence the secretion of pro-inflammatory mediators, reducing intestinal permeability and strengthening the immune system.[41]

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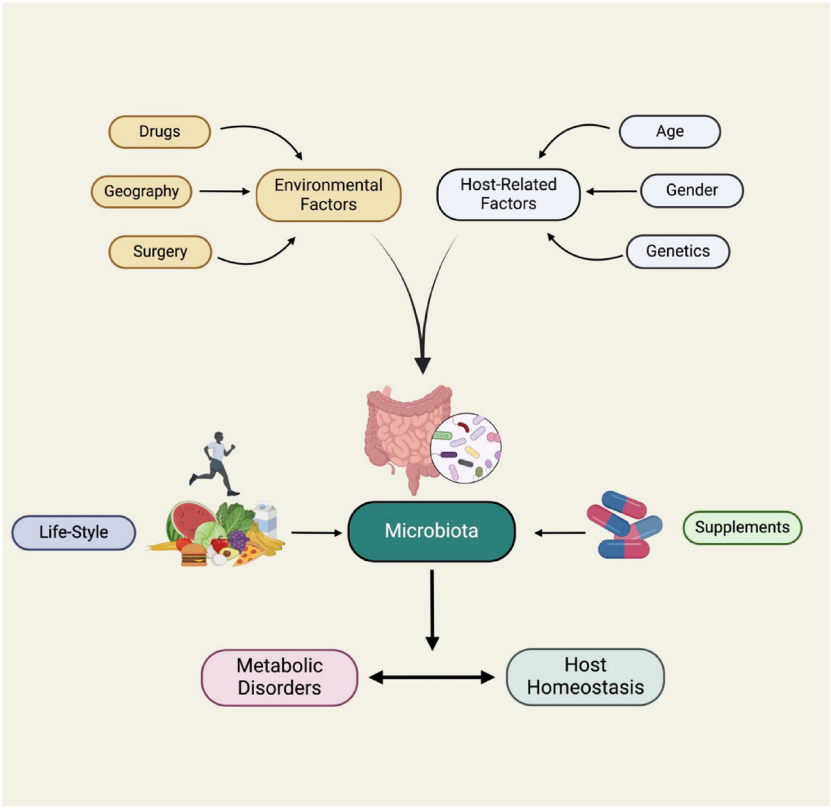

Fig 2 | A depiction of how environmental and host-related factors contribute to an imbalance in the gut microbiota, leading to a disrupted homeostasis. This dysbiosis subsequently results in the development of various metabolic disorders

Microbiological metabolites such as succinate, indole, imidazole, SCFAs, and branched-chain amino acids (BCAAs) are generated during anaerobic fermentation in the gut and play a crucial role in microbe-to-host signaling pathways.[42] Microbial taxa such as *Akkermansia*, *Eubacterium*, *Bacteroides*, *Coprococcus*, *Prevotella*, *Streptococcus*, *Ruminococcus*, *Faecalibacterium*, and *Fusobacterium* are the primary producers of these metabolites.[43,44] The Bacteroidetes phylum predominantly produces acetate and propionate, whereas the Firmicutes phylum primarily generates butyrate. When patients take metformin, their gut microbiota composition rapidly shifts, leading to enhanced microbial diversity and improved intestinal function.[45]

Numerous studies have demonstrated that changes in the gut flora can control how BCAAs are metabolized, which can accelerate the onset of DM. The primary species associated with the link between insulin resistance and the synthesis of BCAAs are *Bacteroides* and members of the *Prevotellaceae* family. *Prevotellaceae* enhanced glucose intolerance, produced insulin resistance, and raised blood levels of BCAAs in mice.[46] Recent studies have significantly expanded our understanding of human microbiome diseases, such as DM, obesity, and other metabolic disorders. While diet can modify the composition of the gut microbiota, its impact on metabolism remains unclear.

Gut Microbiota and Hypercholesterolemia

Hypercholesterolemia, or high blood cholesterol, has long been linked to CVDs. Atherosclerosis can result from plaques caused by cholesterol accumulation in the arterial wall.[47] Cholesterol homeostasis in the human body is a complex process involving three key pathways: intestinal absorption, liver-based conversion into bile acids, and *de novo* cholesterol synthesis. These mechanisms work together to regulate cholesterol levels and maintain metabolic balance.[48–50] Certain bacterial products have been shown to influence lipid metabolism; for example, exopolysaccharides produced by *Agaricus brasiliensis* exhibit cholesterol-lowering properties in mice.[51] Moreover, the gut microbiota interacts with dietary lipids, generating bioactive compounds that modulate plasma lipoprotein levels. One such compound, conjugated linoleic acid, has demonstrated the ability to reduce cholesterol, triglycerides, and lipoproteins in both *in vivo* and *in vitro* experiments.[52]

A study reported that primary bile acids are deconjugated to create secondary ones by *Lactobacillus*, *Clostridium*, *Listeria*, *Bifidobacterium*, and some *Bacteroides* species. Additionally, gut dysbiosis can result in decreased levels of secondary bile acids, which can then cause an abnormal buildup of primary bile acids along with downregulation of the FXR–TGR5 pathway. This mechanism produces bile acids and leads to elevated cholesterol levels. The transformation of cholesterol into coprostanol, facilitated by specific bacterial strains primarily belonging to the genera *Eubacterium* and *Lactobacillus*, is another connection between the gut microbiota and lipid metabolism.[53–56]

Gut Microbiota and Obesity

The gut microbiota plays a critical role in regulating host metabolism and has been increasingly recognized as a key factor in the development of obesity.[57] An imbalance in the gut microbiota, known as dysbiosis, has been linked to altered energy homeostasis, increased fat storage, and low-grade systemic inflammation, all of which contribute to obesity (Figure 4).[58,59] Turnbaugh et al. demonstrated that obese mice had a considerably higher Firmicutes/Bacteroidetes ratio and that their microbiota had a stronger ability to get energy from their diet.[60] Another study reported similar findings in humans, showing that the gut microbiota of obese children had a higher proportion of Firmicutes and a lower proportion of Bacteroidetes.[61]

In a study of the Ukrainian population, the ratio of Bacteroidetes to Firmicutes increased in correlation with rising body mass index (BMI).[62] Contradictory to previously mentioned findings, Zhang et al. reported no difference between normal and obese individuals.[63] Recently, the family *Christensenellaceae* has been linked to weight loss, with studies showing an inverse correlation between the relative abundance of this family and the host's BMI.[64–66]

Furthermore, it was revealed that the abundances of *Lactobacillus reuteri* and *Lactobacillus gasseri* were significantly connected with obesity. Additionally, it

demonstrated a strain-dependent impact on the BMI when *Bifidobacterium* was administered in animal models of diet-induced obesity.[67] Million et al. identified an elevated Firmicutes/Bacteroidetes ratio as a potential biomarker for obesity.[68] Specifically, *L. reuteri* has been associated with obesity, whereas *Methanobrevibacter smithii* and *Bifidobacterium animalis* have been linked to normal weight. Additionally, in morbidly obese individuals, the relative abundance of Firmicutes has been positively correlated with brown adipocyte markers, indicating a potential role in energy regulation.[69]

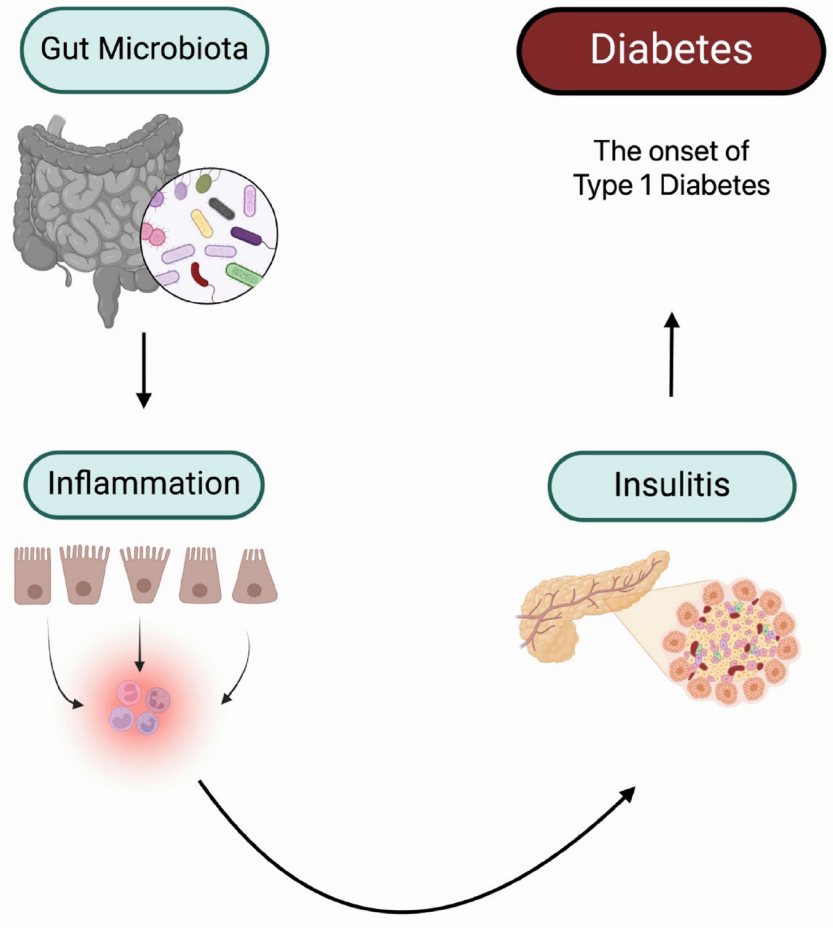

Fig 3 | An illustration of the connection between the gut microbiota and the onset of type 1 diabetes. Disruptions in the gut microbiota lead to inflammation, which can trigger insulitis—an autoimmune response targeting pancreatic islets. This inflammatory cascade contributes to the development of type 1 diabetes

Association of Gut Microbiota with Chronic Heart Failure and Atrial Fibrillation

The gut microbiota has emerged as an important factor in the development and progression of chronic heart failure (CHF) and atrial fibrillation (AF). Dysbiosis, or an imbalance in the gut microbial community, has been linked to increased systemic inflammation, which plays a central role in the pathophysiology of both CHF and AF.[70,71] Patients having arterial hypertension have a less diverse gut microbiota.[72–75] The gut microbiota of smokers differs from that of non-smokers and is similar to the gut microbiota of patients with inflammatory bowel illnesses. Smokers have been found to have higher relative abundances of *Actinobacteria and Cyanobacteria* than non-smokers. The impact of quitting smoking on the gut microbiota is poorly understood; however, it appears to primarily result in a decrease in Bacteroidetes and an increase in Firmicutes. It is yet unclear, nevertheless, whether these modifications may affect cardiovascular risk.[76]

Providencia rettgeri, Clostridium asparagiforme, Clostridium sporogenes, Anaerococcus hydrogenalis, Edwardsiella tarda, and *Proteus penneri* are just a few of the bacterial species linked to trimethylamine N-oxide (TMAO) production that are abundant in the microbiomes of chronic heart failure patients compared to healthy controls.[77] The impaired function of the intestinal barrier provides more proof that the gut microbiota directly influences the mechanisms underlying congestive heart failure (CHF). Gut wall permeability has been positively correlated with illness severity.[78,79] The gut microbial profile is linked with AF as it was shown that patients have a significantly high ratio of Firmicutes to Bacteroidetes, the gut microbial overgrowth of harmful bacteria (including *Escherichia coli, Streptococcus, and Enterococcus*), and a lower abundance of commensals (like *Faecalibacterium* and *Prevotella*). Metabolite changes often accompany these microbial shifts, with clinical evidence specifically linking elevated levels of TMAO to an increased risk of AF. Higher TMAO levels, a by-product of gut microbial metabolism, have been associated with enhanced thrombogenesis, inflammation, and cardiovascular risk, all of

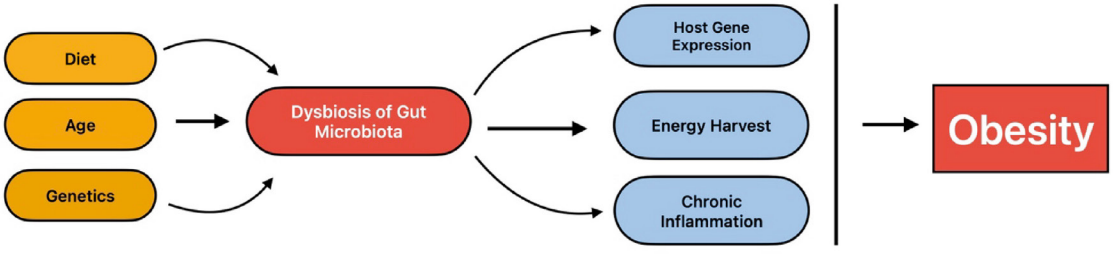

Fig 4 | An illustration of how certain diets induce dysbiosis in the gut microbiota, transforming normal microbiota into obese microbiota. This shift contributes to the development of obesity by altering host gene expression, affecting energy extraction from food, and causing chronic inflammation

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which contribute to the development and recurrence of AF.[80] Recent observational studies have characterized the gut microbial profiles of patients with AF, revealing significant imbalances. These profiles show a markedly high Firmicutes/Bacteroidetes ratio, an overgrowth of harmful bacteria such as *E. coli*, *Streptococcus*, and *Enterococcus*, and a reduced abundance of beneficial commensal bacteria, including *Faecalibacterium* and *Prevotella*. These microbial shifts contribute to increased inflammation and may play a role in the pathogenesis of AF.[81, 82]

Previous research has also shown that the overactivation of the atrial NLRP3 inflammasome in conjunction with elevated serum concentrations of lipopolysaccharide (LPS) and glucose contributed to the onset of AF. This increased inflammatory signaling in cardiomyocytes leads to significant structural and functional changes, including atrial fibrosis and alterations in the action potential duration that promote reentry circuits. These changes are characterized by a shortened atrial action potential and an increased frequency of spontaneous diastolic calcium releases from the sarcoplasmic reticulum, which are pivotal in defining the characteristics of the condition.[83,84]

Thrombosis and Gut Microbiota

Recent research has revealed a complex relationship between the gut microbiota and thrombosis, highlighting how the microbiome influences hemostasis through various mechanisms. Dysbiosis can lead to increased inflammation, elevating pro-thrombotic markers and promoting platelet activation.[85] TMAO promotes atherosclerosis by stimulating vascular inflammation, endothelial cell dysfunction, foam cell generation, and increased platelet activity.[86–88] Increased levels of TMAO resulting from the intake of choline supplements in mice have provided a better explanation for shortening the duration it takes for blood flow to stop after $FeCl_3$ injury in animal models of thrombosis.[89] Besides, there were a few other notable facets regarding the period until blood flow cessation, as it was unaffected by choline administration in germ-free animals with no intestinal microbiota population. This signified that the blood-borne components linked to TMAO gradually formed without involvement from the gut microbes. When the phyla Firmicutes and Proteobacteria expanded in a diet high in choline, it induced dysbiosis. Transplanting this restructured microbiome makeup into germ-free mice amplified both their innate predisposition for thrombosis *in vivo*, as quantified via the $FeCl_3$ carotid artery damage model, and platelet reactivity *ex vivo*, as measured through platelet aggregometry. TMAO did not stimulate platelets directly but heightened the calcium release and activation response to platelet stimuli, demonstrating a TMAO-dependent enhancement, as noted by Zhu et al. in 2016. Unfortunately, additional research is required to completely understand TMAO's role in thrombosis, as other studies have demonstrated that it is linked negatively with atherosclerotic lesion size.[90] As a result, these findings are inconsistent. The size of aortic lesions was not impacted by choline supplementation and did not correlate with TMAO levels.[91] However, choline administration did raise TMAO levels. While Wang et al.[92] depleted the gut microbiota using antibiotics and initiated choline supplementation at just 4 weeks, Jonsson et al.[93] employed germ-free mice as microbiota-depleted controls, starting choline supplementation at a later age of 8 weeks, when atherosclerosis had likely already developed in the mice.

Immune System, Polycystic Ovary Syndrome, and Gut Microbiota

According to previous studies, the immune system develops antigen-specific tolerance to microorganisms and microbial products, which is the basis for immunological tolerance to the commensal microbiota during the early phase of life.[94–96] According to a study, IL-10 knockout mice with early-life antibiotic-induced dysbiosis were more susceptible to spontaneous colitis if the immune system was unable to develop tolerance to critical components of the gut microbiota.[97] Goblet cell-associated antigen passages also form in the colon during the early stages of development, facilitating the transport of various bacterial antigens from the lumen to the lamina propria. Factors such as antibiotic exposure, cesarean sections, formula feeding, and diet can alter the early-life microbiome, potentially limiting its diversity and maturation. This disruption may hinder the immune system's ability to establish immunity to essential commensal microbiota and increase the long-term risk of complex immune disorders, including IBD.[98] One study found that patients exhibited an overrepresentation of the phyla Actinobacteria and Proteobacteria, along with an underrepresentation of the phylum Euryarchaeota. Additionally, individuals with glycogen storage diseases had a microbiome predominantly dominated by *Escherichia/Shigella*, displaying limited diversity.[99]

Research has shown that *Bacteroides ovatus* can digest inulin extracellularly, incurring a cost to itself while simultaneously benefiting other species that derive advantages from this process.[100] This kind of cooperation is especially noticeable in the outer mucus layer, where bacteria that break down mucin supply mono- or oligosaccharides to bacteria that lack specific mucolytic activity.[101] For instance, only bacterial species expressing GH33 sialidases can cleave sialic acid from mucins. Many bacteria, including pathogens like *Salmonella typhimurium* and *Clostridium difficile*, lack sialidase but have a "nan cluster" that is involved in the metabolism of sialic acid; as a result, they depend on other gut microbiota members to supply them with this carbon source.[102–104] Furthermore, inflammatory bowel disorders are characterized by an abundance of sialylated short mucin glycoprotein chains. This abundance may provide these specific bacteria with increased competition for nutrients compared to other bacterial types within the intestinal mucosal environment.[105] In this context, a lack of *F. prausnitzii* may predict the onset of Crohn's disease in patients.[106] Furthermore, animals previously treated with *F. prausnitzii*

in vivo demonstrated recovery from colitis in a mouse model, attributed to the blockade of NF-κB signaling in intestinal epithelial cells by an anti-inflammatory protein produced by *F. prausnitzii*.[107] Previous studies have shown that 56% of women of reproductive age suffer from different forms of polycystic ovary syndrome (PCOS).[108] Furthermore, research has revealed that the human gut contains trillions of microorganisms that significantly influence biological processes.[109] Studies have also indicated a relationship between the gut microflora and hyperandrogenism.[110]

Numerous studies indicate that a compromised intestinal lining can lead to increased absorption of LPS. When the integrity of the mucosa is disrupted, LPS can enter the bloodstream and cause endotoxemia. TLR4 recognizes and binds LPS via an LPS-binding protein, CD14, and myeloid differentiation factor 2. According to a recent study, LPS can trigger the expression of signaling molecules and inflammatory cytokines. This inflammatory reaction is prompted by the upregulation of pro-inflammatory factors such as IL-6 and IL-6, which can launch the inflammatory response. As outlined by Dahan et al., insulin resistance is believed to underlie the metabolic abnormalities seen in PCOS patients, exacerbating their chronic inflammatory state.[111] According to another study, mice in two groups (high-fat diet group and control group) were given diets that were rich in fat and normal, respectively. Mice given a high-fat diet for 4 weeks developed obesity and insulin resistance. Also, mice in the high-fat diet group had blood concentrations of LPS two to three times greater than those in the control group. LPS was injected subcutaneously into mice in the control group that were given a regular diet. After 4 weeks, the control group's mice developed insulin resistance and obesity.[112]

Association of Gut Microbiota with Hyperuricemia and Obstructive Sleep Apnea-Hypopnea Syndrome

According to Xu et al.,[113] there was a notable decrease in the frequency of Firmicutes between wild-type mice and a hyperuricemia mouse model at the phylum level. Bacteroides occurred more frequently at the same time. In hyperuricemic mice, there was an increase in the relative abundance of *Prevotellaceae, Rikenellaceae, Bacteroidaceae,* and *Bacteroidales*. At the genus level, the hyperuricemia group showed a higher or lower frequency of specific bacterial communities, such as *Lactobacillus, Clostridium, Ruminococcaceae, Clostridium*, and others. According to Guo et al., there are significant differences in the organismal and functional architecture of the gut microbiota between gout patients and healthy individuals. *F. prausnitzii* and *Bifidobacterium pseudocatenulatum* reduced, but *Bacteroides caccae* and *Bacteroides xylanisolvens* increased in the gut microbiota of gout patients.[114]

Obstructive sleep apnea-hypopnea syndrome (OSAHS), a sleep disorder, includes irregular sleep patterns and abrupt apnea that occur during sleep. Previous studies have reported that gut flora alteration contributes to the development of OSAHS. In a previous study, 10 mice were exposed to chronic intermittent hypoxia for 6 weeks, while another 10 mice were maintained under normal oxygen levels. Fecal samples were collected, and the findings showed that mice subjected to intermittent hypoxia had a higher abundance of Firmicutes compared to the control group, whereas the abundance of Bacteroidetes and Proteobacteria was lower.[115] Ko et al. collected fecal samples from 20 controls and 93 patients with OSAHS to analyze their microbiome composition. The findings revealed that microbiome alterations in OSAHS patients were associated with an increase in pathogens and a reduction in SCFA-producing bacteria, along with elevated IL-6 levels. Additionally, *Ruminococcus* was identified as the most significant risk factor for the development of OSAHS.[116]

Conclusion

Dysbiosis within the gut microbiota has been closely linked to the development of various metabolic disorders, including obesity, T2DM, hypercholesterolemia, CVDs, and PCOS. The complex interactions between the gut microbiota and host metabolism—primarily mediated by microbial metabolites such as SCFAs, anti-inflammatory microbial molecules, and bile acids—highlight the promise of microbiome-targeted therapies. Current evidence suggests that restoring microbial balance through probiotics, prebiotics, dietary interventions, and novel therapeutic agents holds promise for managing and even preventing these metabolic diseases. However, the complexity of microbial ecosystems and their interactions with host factors such as genetics, diet, and environmental influences make it difficult to develop standardized treatments.

Future Prospects

Future research should aim to explore the complexities of gut microbiota–host interactions at a deeper level, particularly the role of specific bacterial strains and their metabolites in regulating metabolic processes. Advances in next-generation sequencing, metagenomics, and metabolomics will enable a more precise characterization of the microbiome and its functional capabilities. Furthermore, gaining insights into the variations in gut microbiota composition among individuals could pave the way for personalized treatments tailored to each patient's distinct microbial makeup.

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