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Mini Review

Compositional and Functional Diversity of Microbiota in Human Diseases

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Abstract

Introduction: The microbes residing in the intestines, referred to as the intestinal microbiota, play a crucial role in energy metabolism, normal body function, immune system regulation, obesity, malnutrition, neurological conditions, mood, behavior, and various diseases, particularly intestinal disorders and cancer. This mini-review summarizes the compositional and functional diversity of the microbiota in relation to human diseases.

Methods: We searched published studies across several electronic databases, including ScienceDirect, PubMed, PubMed Central (PMC), Scopus, Google Scholar, ISI Web of Science, Medlib, Magiran, the Iranian Scientific Information Database (SID), and IranMedex.

Results: The intestinal microbiota is associated with a broad range of human health conditions, including inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), obesity, diabetes, allergic disorders, colon cancer, cardiovascular disease (CVD), and type 2 diabetes (T2D). Moreover, the intestinal microbiota influences the functioning of the central nervous system through the intestinal nervous system, production of metabolites, stimulation of enteroendocrine cells, and modulation of the immune system.

Conclusion: There is a complex interplay between the gut microbiota and overall human health, with imbalances in gut microbiome composition associated with gastrointestinal disorders, metabolic diseases, neurological disorders, and immune-related disorders.

Keywords: Microbiota, Intestinal microbes, Human diseases

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Introduction

The microorganisms that coexist in the human gut are collectively known as the gut microbiota. This microbiota primarily consists of bacteria but also includes archaea and eukaryotes. Together, these microorganisms maintain a beneficial relationship with the human host. The human gut hosts a diverse array of microorganisms. The microbiota includes not only bacteria, archaea, and yeasts but also single-celled eukaryotes, parasites, and viruses, such as bacteriophages (1).

Additionally, intestinal protozoa and helminths interact with these bacterial microbes (2). Over 10^{14} microorganisms inhabit the human gastrointestinal tract, representing more than 10^{4} bacterial species (3). Research has shown that the microbiota significantly influences the development and progression of diseases in various parts of the human body (4).

Microbiota refers to the microbial community residing in a specific environment, including bacteria, archaea, viruses, and some unicellular eukaryotes. The primary groups of the human microbiota include *Actinobacteria*, *Firmicutes*, *Proteobacteria*, and *Bacteroides*. It is estimated that approximately 10^{14} microorganisms inhabit various parts of the human body, including the skin and the digestive, genital, and respiratory tracts (5).

Intestinal microbes, known as the intestinal microbiota, play a crucial role in energy production, normal physiological function, and immune system regulation. They are also involved in conditions such as obesity, malnutrition, neurological disorders, mood and behavior changes, and various diseases, particularly intestinal disorders and certain cancers. It is estimated that over 10^{14} microorganisms inhabit the human gastrointestinal tract (6), as illustrated in Figure 1.

Dysbiosis, or an imbalance in the intestinal microbiota, combined with genetic and environmental factors, can lead to various disorders, including obesity, atopic dermatitis, asthma, celiac disease, type 1 (T1D) diabetes and type 2 (T2D) diabetes, inflammatory bowel disease (IBD), irritable bowel syndrome (IBS) (Figure 2), *Clostridium difficile* infection, human immunodeficiency virus (HIV) infection, colorectal cancer, kidney stones, periodontitis, and psoriasis (5).

The intestinal microbiota is linked to a wide range of human diseases, including IBD, IBS, obesity, diabetes, allergic conditions, colon cancer, cardiovascular disease (CVD), and T2D (7) (Figure 3). Intestinal microbes are also associated with several health issues, including metabolic

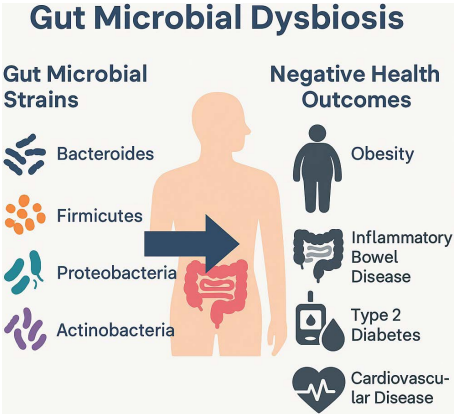


Figure 1. Gut Microbiota Dysbiosis. Created with ChatGPT.com

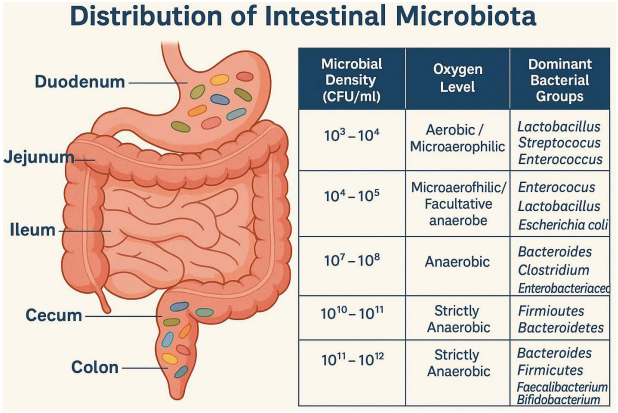


Figure 2. Distribution of Intestinal Microbiota. Created with ChatGPT.com

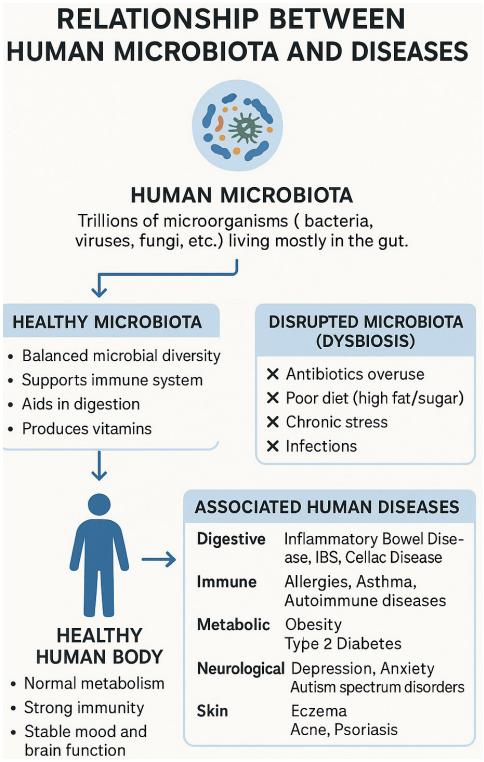


Figure 3. Relationship Between Human Microbiota and Diseases. Created with ChatGPT.com

disorders, gastrointestinal diseases, liver diseases, and allergies (3). This mini-review summarizes the available research on the compositional and functional diversity of the microbiota in relation to human diseases.

Materials and Methods

We conducted a comprehensive search of published studies on the role of the gut microbiota in obesity, neurological diseases, anxiety, depression, gastrointestinal diseases, periodontitis, and CVD in electronic databases, including ScienceDirect, PubMed, PubMed Central (PMC), Scopus, Google Scholar, ISI Web of Science, Medlib, Magiran, the Iranian Scientific Information Database (SID), and IranMedex.

Results

Microbiota and Obesity

Ruminococcus gnavus and *Clostridium sporogenes* can affect mood and appetite through the production of tryptamine (8). The rising global prevalence of obesity has become a significant public health concern due to its strong connection with metabolic disorders such as T2D, CVD, and non-alcoholic fatty liver disease. Key contributors to obesity include genetics, dietary habits, and a lack of physical activity —typically managed through caloric restriction, increased exercise, anti-obesity medications, or surgery.

Recent research has suggested that the gut microbiota may also play a role in the global obesity epidemic. An increase in *lactobacilli* and a decrease in *Roseburia* have been associated with T2D. The microbiota can influence the gut-brain axis through complex neural, immune, and hormonal pathways. Specifically, intestinal microorganisms that interact with the enteric nervous system (ENS) can affect the production of neuroactive compounds, such as gamma-aminobutyric acid (GABA) (9).

The Role of Microbiota in Neurological Diseases

The influence of the gut microbiota on neurological health is substantial. The gut microbiota modulates the central nervous system (CNS) function through the ENS by producing metabolites, stimulating enteroendocrine cells, and interacting with the immune system (10). Furthermore, the microbiota can modify behavior and may even slow the progression of several neurological disorders, including multiple sclerosis (MS), autism, Alzheimer's disease, schizophrenia, and Parkinson's disease (11).

The brain-gut axis represents the connection between the CNS and the gastrointestinal tract. A healthy gut microbiota may help alleviate neurological disorders such as autism, Parkinson's, and Alzheimer's by leveraging the brain-gut axis (12). Additionally, various neurological conditions, including MS, anxiety, autism, Parkinson's, and stroke, are associated with the behavior of microglia and the gut microbiota (13).

Moreover, the intestinal microbiota may play a significant role in improving MS by modulating immune responses (14). Gut microbiota can also contribute to the development of various autoimmune and neurological conditions, including MS, Alzheimer's disease, anxiety, depression, Parkinson's disease, and autism. Additionally,

the microbiota influences microglial function (15). Consequently, altered interactions between the microbiota, the intestines, and the brain may potentially lead to specific brain disorders (16), such as autism spectrum disorder, Parkinson's disease, MS, and mood disorders.

MS is a chronic, inflammatory, degenerative condition characterized by the demyelination of the CNS. As an autoimmune disorder, it is a leading cause of disability among younger adults, with initial clinical symptoms typically appearing between the ages of 20 and 40. This disease has a global prevalence, affecting approximately 2.5 million people. Several studies suggest that patients with MS experience intestinal dysbiosis, characterized by a microbial composition that differs significantly from that of healthy individuals. Furthermore, the microbiota can modulate astrocyte function (17) by regulating astrocyte activity through metabolic byproducts (18).

Research indicates that the microbiota of individuals with MS differs significantly from that of healthy individuals. Patients with MS often exhibit lower levels of *Butyricimonas*, *Lactobacillus*, and *Parabacteroides* (e.g., *Parabacteroides distasonis*) compared with healthy individuals. In contrast, MS patients tend to show higher levels of *Akkermansia muciniphila*, *Methanobrevibacter*, and *Acinetobacter calcoaceticus* than their healthy counterparts (19-21). Moreover, the gut microbiota is involved in myelin sheath synthesis in the brain's frontal lobe (22). Intestinal bacteria that stimulate Th17 cells promote the production of IL-17A and increase IL-6 synthesis, which leads to inflammation in the CNS and contributes to the development of autoimmune diseases such as MS (23).

The gut microbiota plays a significant role in influencing various aspects of human behaviors by producing metabolites and promoting the release of specific hormones. This biochemical activity affects key brain regions, including the hypothalamus, amygdala, and hippocampus. One important component, tryptophan, which is produced by gut bacteria, contributes significantly to serotonin production. This process can enhance social behaviors and help reduce stress, anxiety, and depression. Additionally, tryptophan, which influences satiety, may therefore play a role in obesity. Dysbiosis, or imbalance in the microbiota, can result from excessive antibiotic use or psychological disorders, and can have a profound impact on brain function and behavior. The gut microbiota regulates brain activity and behavior through its metabolites and interactions with the immune system. Moreover, it affects brain development and behavior through communication along the host-intestinal axis (24). Intestinal microbes also contribute to the regulation of subconscious behaviors (25) and influence the secretion of key neurotransmitters that operate along the gut-brain axis (26).

Furthermore, the gut microbiota can elevate oxytocin levels, a hormone that promotes social interactions, supports emotional regulation, and reduces anxiety and stress. Although the precise molecular mechanisms by which gut microbiota influence oxytocin production are not fully understood (27), research has shown that *Lactobacillus johnsonii* can increase oxytocin levels (28). Similarly, *Lactobacillus reuteri* can increase the number of oxytocin-producing cells (29).

The Relationship Between Microbiota and Anxiety and Depression

The intestinal microbiota can significantly influence depressive-like behaviors by modifying host metabolism (9). In animal models of depression and chronic stress, alterations in intestinal microbiota composition, combined with emotional or physical stressors, may affect visceral regulation and emotional responses by disrupting the brain-gut axis, which includes the CNS (30).

Germ-free (GF) mice, which lack intestinal microbiota, have demonstrated reduced depression-like behaviors. For instance, GF mice show a notable decrease in sedentary time during the forced swimming test, a commonly used indicator of depression, compared with specific-pathogen-free (SPF) mice. This underscores the relationship between the brain-gut microbiota axis and depression-like behavior (9). Particular species, such as *Lactobacillus* and *Bifidobacterium*, can enhance stress resilience, reduce anxiety, and alleviate depression by inhibiting pro-inflammatory mediators within the immune system (31).

GF rats exhibit atypical stress responses, altered social interaction patterns, and variations in exploratory behavior and cognitive function (9). One study reported that adult GF mice exhibited a heightened stress response compared to SPF mice. Although GF mice showed no differences in baseline stress hormone levels, they demonstrated elevated adrenergic plasma and corticosterone levels following exposure to stress. Notably, colonization of the gut microbiota during adolescence normalized the stress axis, whereas colonization in early adulthood (around 8 weeks of age) resulted in a persistently altered stress response (32).

Additionally, research by Li et al demonstrated that treatment with the probiotic *Bifidobacterium infantis* normalizes stress-related behaviors without significantly reducing corticosterone levels. These findings suggest that microbial components significantly influence resistance to environmental stress (33). Moreover, the gut microbiota may help reduce depression, anxiety, and other psychosocial disorders through mechanisms involving tryptophan metabolism (34).

The gut microbiota also plays an important role in learning and memory by affecting the brain's hippocampus. Antibiotic use can alter approximately 30% of the gut microbiota (35,36). The use of antibiotics and antimicrobial agents can lead to dysbiosis of intestinal microbiota, which can subsequently affect behavior by increasing anxiety and stress levels. Misuse of antibiotics, which disrupts the balance of intestinal microbiota, may negatively impact brain function and behavior, including mood regulation (37).

A decrease in microbial diversity in individuals with major depressive disorder (MDD) correlates with changes in the relative frequency of phyla such as *Firmicutes*,

Actinobacteria, and *Bacteroidetes* (9). The general brain-gut-microbiota (BGM) axis comprises the CNS, the nervous system, and the endocrine system, including the sympathetic and parasympathetic nervous systems (PSNS), the ENS, and the gut microbiota. Intestinal bacteria play a vital role in host metabolism. The presence of microbes in the gut is essential for the proper development of the stress response, as their colonization contributes to the normal maturation of the pituitary-adrenal-hypothalamic axis (26).

The gut microbiota is also believed to influence the CNS via interactions with the ENS. Recent studies have highlighted the significance of the gut–brain axis. The intestinal microbiota has been linked to several conditions, including IBS, anxiety, stress, depression, behavioral changes, and psychosomatic disorders (38). Stress can alter the composition of the intestinal microbiota, thereby increasing intestinal permeability (7). Most research investigating the role of microbiota in brain function has been conducted using animal models (39), and these studies have shown that depression can alter the composition of the gut microbiota (7).

In mouse models, treatment with *B. infantis* has been shown to reduce the incidence of depression (40). Research further indicates that individuals with depression often exhibit increased levels of *Alistipes* and *Enterobacteriaceae*, while levels of *Ruminococcus* and *Faecalibacterium* decrease. Additionally, individuals experiencing stress generally display lower levels of *Lactobacillus* (41). One mouse study demonstrated that social disruption stress reduced levels of certain bacterial groups while increasing *Clostridia*, leading to inflammatory changes in cytokine profiles produced by the gut microbiota (7). A decrease in *Bacteroidetes* in the stool of patients with depression further supports the well-established connection between gut and brain microbiota, stress, and depression (42). Factors such as poor nutrition, excessive antibiotic use, and the presence of stress, anxiety, and depression can disrupt the balance of gut microbiota (dysbiosis), which significantly contributes to the progression of nervous system disorders (43).

The Role of Microbiota in Gastrointestinal Diseases

The gut microbiota plays a crucial role in the development of IBD (44). The gut microbiota, or gut microbial ecosystem, consists of various endemic species that permanently inhabit the gastrointestinal tract, as well as microorganisms that temporarily reside there. Together, these microbial communities, along with their genes and metabolites, make up the microbiome (45). Additionally, intestinal microbiota influence both mucosal and extracellular immune responses beyond just the gastrointestinal tract. Notably, *Methanobrevibacter* is found to be more prevalent in individuals with constipation and IBS (46-48).

A significant connection has been established between gut microbiota and its potential impacts on the immune system and colon cancer. Intestinal infections caused by bacteria or viruses may also contribute to the development of gastrointestinal cancers. Disruption of immune homeostasis by harmful flora can lead to inflammation and neoplastic changes within the intestinal mucosa. The gut microbiota appears to play a role in colorectal cancer development by promoting chronic inflammation and producing reactive metabolites and carcinogens. Moreover, fecal microbiota profiles in individuals with IBD differ from those in healthy individuals; specifically, as the number of mucosal-adhesion bacteria increases, fecal microbiota diversity decreases (49).

Additionally, intestinal microbiota play a significant role in regulating obesity through interactions with the nervous system (21). According to the World Health Organization (WHO), approximately 3.4 million adults die each year from complications related to overweight or obesity. The involvement of gut microbiota in the development of obesity and subsequent insulin resistance has been widely proposed. Research in both humans and mice indicates a correlation between obesity and changes in microbiota composition. The gut microbiota is also directly linked to the sensation of satiety; it promotes satiety by fermenting complex carbohydrates into short-chain fatty acids. These short-chain fatty acids can decrease appetite by altering levels of glutamate, glutamine, GABA, and neuropeptides (50).

Research has shown that gut microbiota composition differs across various diseases. In allergic conditions, levels of *Lactobacillus*, *Bifidobacterium adolescentis*, *Clostridium difficile*, and *Helicobacter pylori* are reduced. In autism, *Bacteroides* and *Proteobacteria* are elevated, while *Actinobacteria* and *Firmicutes* are decreased. In obesity, reductions in *Lactobacillus* and *Firmicutes* have been reported alongside higher levels of *Bacteroides*. In T2D, increased levels of *Firmicutes*, *Betaproteobacteria*, and *Clostridium* are observed, accompanied by reduced levels of *Bacteroides*.

In celiac disease, *Bacteroides vulgatus* levels increase, while *Escherichia coli* and *Clostridium coccoides* decrease. In nonalcoholic fatty liver disease (NAFLD), *Bacteroides* levels decrease, whereas *Veillonella* and P*orphyromonas* increase. In cirrhosis, the abundance of *Streptococcus*, *Enterobacteriaceae*, and *Veillonella* increases, while levels of *Bacteroides*, *Firmicutes*, and *Bifidobacterium* decrease.

In patients with alcoholism, *Bacteroides* levels decrease, while *Prevotella* levels increase. In alcoholic liver disease, populations of *Enterobacteriaceae* rise, and in cirrhosis accompanied by encephalopathy, *Porphyromonas* and *Alcaligenes* become more abundant (3).

The Role of Microbiota in Cardiovascular Disease

The role of microbiota in CVD is significant, as CVD remains a leading cause of mortality worldwide. Preliminary research suggests that microbes may contribute to the development of CVD. Studies indicate a connection between atherosclerosis and infectious agents, as well as a relationship between poor dental health and CVD.

An analysis comparing the fecal microbiomes of patients with atherosclerosis and healthy controls revealed significant alterations in both composition and function. These changes included a reduction in specific beneficial

microbial genes and an increase in genes associated with inflammation. Notably, the abundance of genes involved in β-carotene synthesis—an anti-inflammatory pathway—was elevated alongside higher levels of genes related to peptidoglycan biosynthesis, a known pro-inflammatory factor. These alterations were observed in the gut microbiomes of patients with atherosclerosis (45).

Atherosclerosis is characterized by cholesterol accumulation and macrophage recruitment within arterial walls, leading to the formation of atherosclerotic plaques. This condition can eventually lead to clinically serious events, such as myocardial infarction and stroke. Additionally, bacterial species such as *Chryseomonas*, *Veillonella*, and *Streptococcus* have been identified in both the oral cavity and dental plaque (Figure 4).

Recent studies have shown that patients with atherosclerosis exhibit higher levels of *Collinsella* and lower levels of *Eubacterium* and *Roseburia* in their microbiota compared with healthy individuals (49). In addition to influencing visceral pain, the gut microbiota can also modulate pain related to environmental factors through immune system pathways.

The interaction between the gut microbiota and the hypothalamus influences pain-sensing systems. The impact of gut microbiota on pain regulation has been assessed using colorectal stress testing. Administration of antibiotics alongside a *Lactobacillus* suspension during colorectal stress testing reduced tenderness and discomfort in the colons of mice (38). Additionally, the gut microbiota can produce intestinal hormones or peptides, such as orexin, galanin, ghrelin, gastrin, and leptin (37). GABA is recognized as a key inhibitor of neurotransmitters in the human brain, contributing to the regulation of neurodegeneration-related processes, pain, blood pressure, heart rate, anxiety, and depression.

The Role of Microbiota in Periodontitis

In other research, metagenomic and metatranscriptomic analyses were conducted to compare the oral microbiomes of healthy individuals and patients with periodontitis. The findings revealed discrepancies between gene frequency and gene expression. Research indicates that various bacteria, such as *Bacteroides* and *Aggregatibacter actinomycetemcomitans*, can modulate gene expression in response to disease without significant changes in their genomic content. Additionally, *Lactococcus lactis* has been associated with periodontitis and may be metabolically inactive (45).

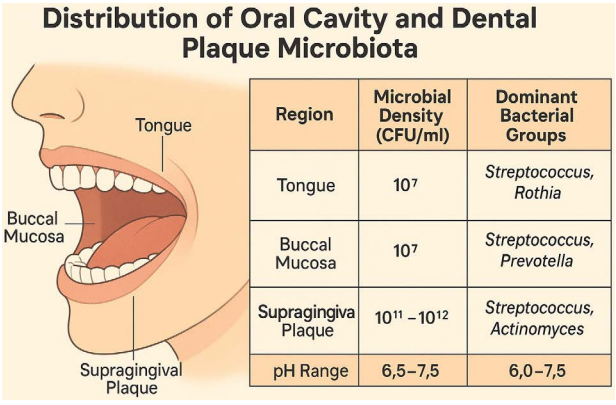
Microbiota and Women's Health

The gut microbiota is essential for maintaining women's reproductive health, with over 20 *Lactobacillus* species identified in many healthy women. The dominant vaginal *Lactobacillus* species include *L. crispatus*, *L. iners*, *L. jensenii*, and *L. gasseri*. The diversity of other bacteria in the vagina is significantly lower than that of *Lactobacillus*. Additionally, several additional microorganisms, such as *Staphylococcus*, *Ureaplasma*, *Corynebacterium*, *Streptococcus*, *Peptostreptococcus*, *Gardnerella*, *Prevotella*, *Clostridium*, *Bacteroides*, *Listeria monocytogenes*, *Enterococcus*, *Escherichia*, *Veillonella*, and *Bifidobacterium*, may also be present in smaller quantities in the vagina.

The vaginal microbiota plays a crucial role in protecting against viral infections through several mechanisms. *Lactobacillus* species produce antimicrobial metabolites, which may provide direct protection against viral infections in the vagina. In a healthy vaginal environment, the microbiota acts as one of the body's natural defense mechanisms against pathogenic invasions (39).

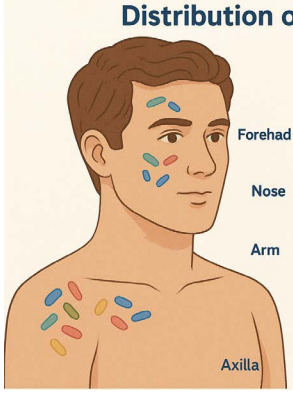
Microbiota and Allergic Diseases

The skin microbiota consists of microorganisms, including bacteria, viruses, archaea, and fungi, that colonize the skin surface (45), as illustrated in Figure 5. Several studies have investigated the composition of the intestinal microbiota in individuals with allergic conditions such as eczema, food allergies, wheezing, allergic rhinitis, asthma, and sensitization. Asthma, characterized by chronic airway inflammation, involves contraction of airway smooth muscle, increased mucus production, eosinophilia, and elevated levels of helper 2 (Th2) cytokines. The gut microbiota can influence the underlying pathophysiological processes involved in asthma. Epidemiological studies examining the relationship between intestinal bacteria and allergy-related conditions have revealed a higher prevalence of *Clostridium* spp and a lower prevalence of



Region	Microbial Density (CFU/ml)	Dominant Bacterial Groups
Tongue	10^7	*Streptococcus, Rothia*
Buccal Mucosa	10^7	*Streptococcus, Prevotella*
Supragingiva Plaque	10^{11} –10^{12}	*Streptococcus, Actinomyces*
pH Range	6,5–7,5	6,0–7,5

Figure 4. Distribution of Oral Cavity and Dental Plaque Microbiota. Created with ChatGPT.com



Microbial Density (CFU/cm²)	Oxygen Level	Dominant Bacterial Groups
10^3–10^6	Anaerobic	*Cutibocterium Staphylococcus*
10^3–10^6	Aeroobic	*Cutabacterium Staphylococcus*
10^1–10^4	Aerobic	*Staphylococcus Streptococcus Corynebacterium*
10^5–10^7	Anaerobic	*Staphylococcus Corynebacterium Anaerococcus*
10^5–10^7	Anaerobic	*Staphylococcus Anaerococcus*

Figure 5. Distribution of Skin Microbiota. Created with ChatGPT.com

Bifidobacterium in children with asthma (18).

Microbiota and Urologic Diseases

The connection between dysbiosis and urological disorders has not been extensively studied. Most observational and cohort studies have primarily focused on individuals with *Veillonella*, *Streptococcus*, and *Bacteroides*. In patients with prostate cancer, higher abundance of *Faecalibacterium*, lactobacilli, and *Acinetobacter* has been reported. Additionally, the prevalence of anti-inflammatory bacteria, such as *Streptococcus anginosus*, *Actinobaculum schaalii*, and *Propionibacterium lymphophilum*, has been reported to be higher in patients than in healthy individuals (4). Figure 6 illustrates changes in gut microbiota across various diseases, and Table 1 summarizes the increase (↑) or decrease (↓) of specific microbiota bacteria in different disease categories.

Discussion

The human microbiota constitutes a complex and dynamic ecosystem that plays a vital role in maintaining metabolic and immune homeostasis. Disruption of this balance, known as dysbiosis, has been linked to the development and progression of various disorders, including metabolic, inflammatory, neurological, and even malignant diseases.

Recent advances in sequencing technologies have significantly enhanced our understanding of microbial composition and its functional roles in health and disease. However, distinguishing causal relationships from correlations remains a significant challenge, as microbial alterations can both contribute to and result from disease processes. Microbial metabolites, such as short-chain fatty acids and bile acids, are important mediators that regulate immune responses and metabolic pathways. These compounds can serve as functional biomarkers of dysbiosis and represent potential therapeutic targets.

Overall, a better understanding of the compositional

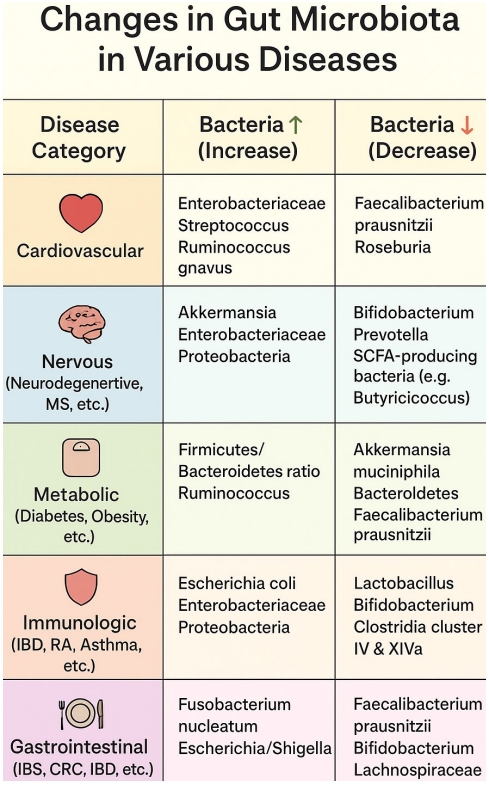


Figure 6. Changes in Gut Microbiota in Various Diseases. Created with ChatGPT.com

Table 1. The Increase or Decrease of Microbiota Bacteria in Different Disease Categories

Diseases	Changes in Gut Microbiota
Anorexia	↓*Ruminococcus gnavus* ↓*Clostridium sporogenes*
Multiple Sclerosis	↓*Butyricimonas*, ↓*Lactobacillus* ↓*Parabacteroides* ↑*Akkermansia muciniphila* ↑*Methanobrevibacter* ↑*Acinetobacter calcoaceticus*
Stress	↑*Lactobacillus* ↑*Bifidobacterium* ↓ *Lactobacillus*
Major Depressive Disorder	↓*Firmicutes* ↓*Actinobacteria* ↓*Bacteroidetes*
Depression	↑*Alistipes* ↑*Enterobacteriaceae* ↓*Ruminococcus* ↓*Faecalibacterium* ↓*Bifidobacterium infantis*
Constipation and Irritable Bowel Syndrome	↑*Methanobrevibacter*
Allergies	↓*Lactobacillus*, ↓*Bifidobacterium adolescentis* ↓*Clostridium difficile* ↓*Helicobacter pylori*.
Autism	↑*Bacteroides* ↑*Proteobacteria* ↓*Actinobacteria* ↓ *Firmicutes*
Obesity	↓*Lactobacillus* ↓*Firmicutes*
Type 2 Diabetes	↑*Firmicutes* ↑*Betaproteobacteria* ↑*Clostridium* ↓*Bacteroides*
Celiac Disease	↑*Bacteroides vulgatus* ↓*Escherichia coli* ↓*Clostridium coccoides*
Nonalcoholic Fatty Liver Disease	↑*Veillonella* ↑*Porphyromonas* ↓*Bacteroides*
Cirrhosis	↑*Streptococcus* species ↑*Enterobacteriaceae* ↑*Veillonella* ↓*Bacteroides* ↓ *Firmicutes* ↓*Bifidobacterium*
Alcoholism	↑*Prevotella* ↓*Bacteroides*
Alcoholic Liver Disease	↑*Enterobacteriaceae*
Atherosclerosis	↑*Collinsella* ↓*Eubacterium* ↓*Roseburia*
Asthmatic Children	↑*Clostridium* species ↓*Bifidobacterium*
Prostate Cancer	↑*Faecalibacterium* ↑*Lactobacilli* ↑*Acinetobacter*

Note. ↑: Increase; ↓: Decrease

and functional diversity of the microbiota may pave the way for the development of targeted and personalized therapeutic approaches to improve human health and disease management (45, 49).

Conclusion

This mini-review focused on the s compositional and functional diversity of microbiota in human diseases. Numerous studies have confirmed alterations in microbiota in human diseases. The gut microbiota axis plays a key role in host-microbe interactions and functions through neural, endocrine, humoral, immunological, and metabolic pathways. Factors such as environment, lifestyle, diet, antibiotic use, age, and other host-related factors can affect the equilibrium of the gut microbiota and influence human health. Disruption of the symbiotic relationship between the host and gut microbiota, as well as alterations in the diversity, composition, and metabolic activity of human gut microbiota, have been linked to various health issues, including anxiety, depression, hypertension, CVD, obesity, diabetes, IBD, and colorectal cancer. Considering the intricate relationship between gut microbiota and human health, imbalances in the gut microbiome composition are associated with gastrointestinal disorders, metabolic diseases such as obesity and T2D, neurological conditions such as Alzheimer's and Parkinson's, and immune-related disorders (e.g., allergies and autoimmune diseases). However, the mechanisms underlying the beneficial or detrimental effects of gut microbiota remain largely unclear. Therefore, more extensive clinical studies are needed to better understand the complex and multifaceted role of microbiota in human diseases.

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Authors' Contribution

Data Curation: Majid Validi, Mansoor Khaledi
Investigation: Majid Validi, Mansoor Khaledi
Methodology: Majid Validi
Project Administration: Majid Validi
Resources: Majid Validi, Mansoor Khaledi
Software: Majid Validi
Supervision: Majid Validi
Validation: Majid Validi
Visualization: Majid Validi
Writing–Original Draft: Majid Validi, Mansoor Khaledi
Writing–Review & Editing: Majid Validi, Mansoor Khaledi

Competing Interests

The authors declare that they have no conflict of interests.

Ethical Approval

Not applicable.

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