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Unlocking the secrets of the human gut microbiota: Comprehensive review on its role in different diseases

Paul JK *et al.* Role of the human gut microbiota

Abstract

The human gut microbiota, a complex and diverse community of microorganisms, plays a crucial role in maintaining overall health by influencing various physiological processes, including digestion, immune function, and disease susceptibility. The balance between beneficial and harmful bacteria is essential for health, with dysbiosis - disruption of this balance - linked to numerous conditions such as metabolic disorders, autoimmune diseases, and cancers. The review highlights key genera such as *Enterococcus*, *Ruminococcus*, *Bacteroides*, *Bifidobacterium*, *Escherichia coli*, *Akkermansia muciniphila*, *Firmicutes* (including *Clostridium* and *Lactobacillus*), and *Roseburia* due to their well-established roles in immune regulation and metabolic processes, but other bacteria, including *Clostridioides difficile*, *Salmonella*, *Helicobacter pylori*, and *Fusobacterium nucleatum*, are also implicated in dysbiosis and various diseases. Pathogenic bacteria, including *Escherichia coli* and *Bacteroides fragilis*, contribute to inflammation and cancer progression by disrupting immune responses and damaging tissues. The potential for microbiota-based therapies, such as probiotics, prebiotics, fecal microbiota transplantation, and dietary interventions, to improve health outcomes has been examined. Future research directions in the integration of multi-omics, the impact of diet and lifestyle on microbiota composition, and advancing microbiota engineering techniques have been discussed. Understanding the gut microbiota's role in health and disease is essential for formulating personalized, efficacious treatments and preventive strategies, thereby enhancing health outcomes and progressing microbiome research.

Key Words: Gut microbiota; Cancer; Diabetics; Autoimmune disease; Dysbiosis

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Core Tip: ³ The human gut microbiota, a complex and diverse community of microorganisms, plays a critical role in maintaining health by influencing digestion, immune function, and disease susceptibility. Dysbiosis, an imbalance in this microbial community, is linked to conditions like metabolic disorders, autoimmune diseases, and cancers. Key genera, including *Enterococcus*, *Ruminococcus*, and *Bacteroides*, are essential for immune regulation and metabolic health. Microbiota-based therapies, including probiotics and fecal microbiota transplantation, offer the potential for restoring balance and improving health outcomes. We herein discussed the intimate correlations between gut microbiota and human health, predominantly associated with function, regulation, and management strategies.

INTRODUCTION

The human gastrointestinal tract harbors a complex ecosystem of microorganisms, inclusively known as the gut microbiota. This microbial community, dominated by bacteria but also viruses, fungi, and archaea, profoundly influences host physiology, metabolism, and vulnerable function[1]. They play a pivotal part in maintaining gut barrier integrity and regulating vulnerable responses, impacting immune system development and function[2]. Human gastrointestinal tract harbors an essential ecosystem of bacteria that profoundly impacts health and disease susceptibility. *Enterococcus*, *Ruminococcus*, *Bacteroides*, *Bifidobacterium*, *Prevotella*, *Escherichia coli* (*E. coli*), *Akkermansia muciniphila*, *Firmicutes* (including *Clostridium* and *Lactobacillus*), and *Roseburia* are important genera that support vulnerable regulation and metabolic processes, which are essential for gut health and general well-being[3]. It is important to recognize that other bacteria, such as *Clostridioides difficile*, *Salmonella*, *Helicobacter pylori*, and *Fusobacterium nucleatum*, are also involved in various diseases. Dysbiosis of the gut microbiota is implicated in a spectrum of diseases ranging from metabolic disorders like obesity and diabetes, to autoimmune conditions and cancers, emphasizing their profound impact on overall health[4]. Certain gut bacteria, such as *E. coli*, O157 and *Bacteroides fragilis* produce toxins, *Fusobacterium nucleatum* is involved in colorectal

cancer, *Helicobacter pylori* in gastric cancer, and *Prevotella* in sedentary bowel complaint, contribute to inflammation and cancer progression by damaging skins and dismembering host vulnerable responses[5]. These bacteria demonstrate the intricate relationship between gut microbiota composition and complaint development, emphasizing the need for targeted interventions in complaint forestallment and treatment strategies[6].

The composition and diversity of the gut microbiota are influenced by various factors such as diet, life, genetics, and environmental exposures[7]. The link between gut microbiota dysbiosis and complaint development has prompted ferocious exploration into understanding of microbial species and their relations with the host. Understanding the gut microbiota's role in health and disease is an area of intense scientific interest, with implications for developing novel therapeutic strategies[8]. Researchers are investigating how alterations in the gut microbiota contribute to these conditions and exploring ways to restore a healthy microbial balance[9]. The gut microbiota interacts with the host immune system, influencing immune development and responses. They can also produce metabolites that can affect host physiology, highlighting the intricate crosstalk between the gut microbiota and the host[10].

To delve deeper into the composition and function of the gut microbiota, advanced sequencing technologies and computational tools are paving a better understanding[11]. As the field of gut microbiota research continues to evolve, there is a growing interest in developing microbiota-based therapies, such as probiotics, prebiotics, fecal microbiota transplantation (FMT), and microbiota engineering[12]. These approaches hold promise to prevent and treat diseases by modulating gut microbiota. However, challenges remain in understanding the complex interactions between the gut microbiota and the host, as well as in developing safe and effective microbiota-based interventions[13]. The influence of gut bacteria on carcinogenesis is of particular interest, both within the gastrointestinal tract and on distant organs. Studies have linked microbial signatures associated with increased cancer threat, mechanisms by which gut bacteria modulate inflammation, and vulnerable responses[14]. This

comprehensive review aims to explore the current understanding of human gut microbiota in association with disease and cancer development. It summarizes crucial findings from epidemiological studies, mechanistic exploration, and clinical observations to interpret the complex interplay between microbial communities and host health. By addressing gaps in knowledge and proposing unborn exploration, this review seeks to contribute to the broader trouble of employing microbiota-based therapies for disease prevention and treatment.

GUT BACTERIAL DIVERSITY

The human gut microbiota consists of different bacteria essential for digestion, metabolism, and immune function. Beneficial bacteria like *Bifidobacterium* and *Lactobacillus* aid in carbohydrate breakdown, vitamin production, and immune support[15]. *Bifidobacterium*, for instance, plays a crucial role in digesting dietary fiber and producing short-chain fatty acids (SCFAs) like acetate, which provide energy to gut cells and help maintain a healthy gut environment[16]. *Lactobacillus* is known for its ability to ferment lactose into lactic acid, aiding in lactose digestion and preventing the growth of harmful pathogens by lowering the pH of the gut[17]. *Lactobacillus* species also produce antimicrobial substances such as bacteriocins, which inhibit the growth of harmful bacteria, contributing to a balanced gut microbiome. Moreover, these bacteria are involved in the production of bioactive peptides that can modulate the immune system and reduce inflammation[18]. *Akkermansia muciniphila* maintains gut barrier integrity by degrading mucin, the main component of mucus, which fortifies the gut lining and prevents pathogens from invading the gut wall. This bacterium has been linked to metabolic health, with studies showing its association with reduced inflammation, improved glucose metabolism, and protection against obesity and diabetes. *Akkermansia's* ability to interact with the host's immune system and promote the production of anti-inflammatory molecules highlights its therapeutic potential[19]. *Faecalibacterium prausnitzii* produces anti-inflammatory butyrate, a SCFA that nourishes colon cells, reduces inflammation, and enhances gut barrier function, playing a

significant role in preventing conditions like inflammatory bowel disease (IBD). This bacterium is one of the most abundant and important in the human gut, contributing to overall gut health by modulating immune responses and promoting a balanced inflammatory environment. Low levels of *Faecalibacterium prausnitzii* have been associated with various inflammatory conditions, making it a key target for probiotic and dietary interventions[20].

In contrast, harmful bacteria such as pathogenic *E. coli* and *Clostridium difficile* produce toxins causing gut damage and severe illnesses like diarrhea. Pathogenic *E. coli* strains can produce *Shiga* toxin, leading to bloody diarrhea and potentially life-threatening hemolytic uremic syndrome[21]. *Clostridium difficile*, often triggered by antibiotic use, can cause severe colitis and life-threatening diarrhea through the production of potent toxins that damage the intestinal lining[22]. *Salmonella* causes foodborne illnesses, characterized by symptoms such as diarrhea, fever, and abdominal cramps, by invading intestinal cells and triggering an inflammatory response[23]. *Fusobacterium nucleatum* contributes to colorectal cancer by promoting inflammation and tumor growth. This bacterium adheres to and invades epithelial cells, facilitating a pro-inflammatory environment and providing a conducive setting for cancer development[24]. *Helicobacter pylori* increases gastric cancer risk through chronic inflammation and the production of cytotoxins that damage stomach lining cells, leading to ulcers and malignancies[25]. *Bacteroides fragilis* produces a toxin that disrupts the tight junctions between epithelial cells, leading to chronic inflammation and an increased risk of tumor formation[26]. These diverse bacterial communities with their harmful activities, highlight the intricate role of gut microbiota in maintaining health. Understanding these interactions further underscores the potential of targeted microbiome therapies to enhance beneficial bacteria and mitigate the effects of harmful ones, contributing to improved health outcomes (Figure 1).

GUT MICROBIOTA LINKED TO DIFFERENT DISEASES

Human gut microbiota, a complex community of trillions of microorganisms residing in our intestines, has garnered significant attention for its profound impact on various aspects of health and disease. This intricate microbial ecosystem influences a range of physiological processes, from digestion and metabolism to immune system function and even brain health. Recent research has elucidated the role of gut microbiota in numerous diseases, highlighting its potential as a therapeutic target and its significance in maintaining overall health (Figure 2).

Microbiota and mental health: Exploring the gut-brain axis

One of the most fascinating areas of research is ¹the gut-brain axis, which refers to the bidirectional communication between the gut microbiota and the brain. This connection is mediated through ⁶neural, endocrine, and immune pathways. Studies have shown that alterations in gut microbiota composition can influence brain function and behavior, potentially contributing to mental health disorders such as depression, anxiety, and autism spectrum disorders[27]. Certain gut bacteria can produce neurotransmitters like serotonin and γ -aminobutyric acid, which are crucial for regulating mood and anxiety levels[28]. Moreover, microbial metabolites such as SCFAs can affect the brain by modulating inflammation and the integrity of the blood-brain barrier[29]. These findings underscore the therapeutic potential of targeting gut microbiota to alleviate symptoms of mental health disorders. This evolving understanding suggests that probiotic and prebiotic treatments, alongside dietary modifications, could offer new avenues for managing and treating mental health conditions, thus integrating mental health care with dietary and microbiota-based strategies (Table 1)[32-44]. Associations between gut microbiota composition and emotion-related brain functions suggest potential links to anxiety and depression, with regions such as the insula and amygdala - key players in emotional processing - frequently connected to microbial diversity[30]. A recent review underscores a significant association between gut microbiota and brain connectivity, with specific

genera such as *Bacteroides*, *Prevotella*, and *Ruminococcus* consistently linked to brain networks like the default mode network and frontoparietal network[31].

Microbiota linked to autoimmune and inflammatory diseases

⁴ The gut microbiota plays a critical role in the development and modulation of the immune system. Dysbiosis, or an imbalance in the gut microbial community, has been implicated in various autoimmune diseases, where the body's immune system mistakenly attacks its own tissues²[45]. Conditions like rheumatoid arthritis, multiple sclerosis, and IBD have been linked to alterations in gut microbiota[46]. Studies have shown that certain pathogenic bacteria can trigger inflammatory responses, while beneficial microbes can help to maintain immune tolerance[47]. This delicate balance is essential for preventing autoimmune reactions. Understanding the specific microbial changes associated with these diseases can lead to new strategies for prevention and treatment[48]. This line of research opens promising avenues for using microbiota modulation as a form of immunotherapy, offering hope for better management of autoimmune diseases through non-invasive and dietary-based approaches (Table 2)[49-61].

Gut microbiota linked to diabetes

Type 2 diabetes (T2D) is another condition where gut microbiota has been shown to play a significant role. Individuals with T2D often exhibit distinct gut microbiota profiles compared to healthy individuals[62]. Dysbiosis in T2D is characterized by a reduced diversity of gut bacteria and an increase in opportunistic pathogens[63]. These microbial changes can influence glucose metabolism, insulin resistance, and chronic inflammation, all of which are key factors in the development and progression of diabetes[64]. Certain gut bacteria can affect the production of SCFAs, which in turn influence insulin sensitivity[65]. Moreover, the gut microbiota can interact with dietary components to modulate the host's metabolic response. These insights highlight the potential of manipulating gut microbiota through diet, probiotics, or other interventions

as an approach to diabetes management[66]. Future therapeutic strategies could involve personalized nutrition plans and microbiota-based treatments to improve insulin sensitivity and metabolic health, providing a more tailored approach to diabetes management (Table 3)[67-82].

Role of gut microbiota in cancer progression

The role of gut microbiota in cancer progression is a dynamic and multifaceted area of exploration that continues to evolve. Dysbiosis is implicated in various conditions, including metabolic diseases like obesity and diabetes, where altered microbial metabolism affects host energy balance and systemic inflammation[83]. Specific microbial taxa and their metabolites have been linked to cancer initiation and progression, especially in colorectal cancer, through mechanisms involving inflammation, genotoxicity, and modulation of tumor microenvironments[84]. Certain bacterial species have been found to promote colorectal cancer by producing toxins that damage DNA or by inducing chronic inflammation[85]. Conversely, other microbes may have protective effects by enhancing immune surveillance and inhibiting tumor growth. Gut microbiota can affect the efficacy and toxicity of cancer treatments, such as chemotherapy and immunotherapy[86]. Personalized modulation of the gut microbiome could therefore represent a promising strategy for improving cancer treatment outcomes and reducing side effects[87]. This underscores the potential of integrating microbiota analysis into oncological care, paving the way for precision medicine approaches that consider the individual's microbial composition in developing treatment protocols (Table 4)[88-104].

Role of gut microbiota in chronic kidney disease

The gut microbiota plays a crucial role in the development and progression of chronic kidney disease (CKD). It comprises trillions of microorganisms that influence various physiological processes, including metabolism, immune function, and inflammation[105]. In CKD, the composition and diversity of gut microbiota are often

altered, leading to dysbiosis, which exacerbates the disease[106]. This dysbiosis can result in the overproduction of uremic toxins, which accumulate in the blood due to impaired renal function and contribute to inflammation and further kidney damage[107]. Additionally, changes in diet and medication use in CKD patients can further impact the gut microbiome, highlighting the potential for dietary interventions and probiotics to restore microbial balance and potentially slow CKD progression[108]. Understanding the complex interactions between the gut microbiota and CKD could lead to novel therapeutic approaches for managing the disease and improving patient outcomes (Figure 3).

A recent paper explores the relationship between gut microbiota and CKD, revealing a significant reduction in microbial diversity in CKD patients compared to healthy individuals[109]. This reduction is linked with inflammation and metabolic alterations typical of CKD. The study highlights specific bacterial genera, such as *Bacteroides* and *Prevotella*, that are associated with inflammatory markers and metabolic imbalances. It emphasizes the role of dietary intake in influencing gut microbiota composition and suggests that nutritional interventions could modulate gut microbiota to potentially alleviate CKD symptoms. The findings propose that targeting gut microbiota through dietary modifications or probiotic treatments could be a promising therapeutic strategy for managing CKD, advocating for further research to understand the underlying mechanisms and develop effective interventions.

Another study has found significant alterations in gut microbiota composition and diversity in CKD patients compared to healthy controls, with an increase in *Proteobacteria* and a decrease in synergies, especially in advanced stages[110]. Specific bacterial genera, such as *Escherichia-Shigella*, were identified as potential biomarkers for distinguishing CKD patients from healthy individuals. Functional analysis indicated enriched metabolic pathways related to fatty acid and inositol phosphate in CKD, while amino acid and oxidative phosphorylation pathways were more active in healthy controls. These microbiota changes could aid in early CKD diagnosis and monitoring[111].

There is a consistent alteration in the gut microbiota composition in patients with CKD, marked by a decrease in beneficial bacteria like *Bifidobacterium* and *Lactobacillus* and an increase in potentially harmful bacteria such as *Enterobacteriaceae* and *Enterococcus*[112]. Dysbiosis in CKD patients is associated with increased production of uremic toxins, such as indoxyl sulfate and p-cresyl sulfate, which are linked to the progression of kidney disease and cardiovascular complications. Dietary interventions, probiotics, and prebiotics show potential in modulating gut microbiota composition, reducing uremic toxins, and improving CKD outcomes, although more clinical trials are needed to confirm these effects[113].

A recent systematic review paper indicates that patients with CKD exhibit distinct changes in their gut microbiota composition, characterized by a decrease in beneficial bacteria such as *Bifidobacterium* and *Lactobacillus*, and an increase in pathogenic bacteria like *Enterobacteriaceae* and *E. coli*. These alterations are associated with CKD progression and systemic inflammation, suggesting a potential link between gut microbiota dysbiosis and CKD pathophysiology. Additionally, interventions targeting gut microbiota, such as probiotics and prebiotics, have shown promise in modulating these microbial imbalances and improving CKD outcomes[114]. However, the findings across studies are often inconsistent and lack replication, with variations in methodologies and target populations complicating the ability to draw definitive conclusions about microbiota-connectivity associations across different diseases.

This underscores the complexity of gut-brain interactions and the need for more standardized research approaches to better understand these relationships[115]. Another recent original study identified significant differences in gut microbiota diversity and composition between stage 4 and 5 CKD patients and healthy controls[116]. Patients with stage 4 and 5 CKD exhibited lower species richness and diversity, with a notable reduction in beneficial bacteria such as *Faecalibacterium* and *Roseburia* and an increase in potential pathogens like *Escherichia-Shigella*. Alpha and beta diversity analyses confirmed these disparities, highlighting a strong correlation between gut microbiota alterations and CKD severity.

Linear discriminant analysis effect size analysis revealed distinct microbial and metabolic pathway profiles between the two groups, suggesting that these microbial changes could have functional implications in CKD progression[17]. A study in end-stage renal disease patients from southern China found a reduction in total gut bacteria. Beneficial butyrate-producing bacteria (*Roseburia*, *Faecalibacterium*, and *Prevotella*) were reduced in end-stage renal disease patients, while *Bacteroides* were more prevalent. These changes were associated with increased inflammation and worsened renal function, as indicated by markers like cystatin C and estimated glomerular filtration rate, suggesting that gut microbiota alterations may play a role in CKD progression[116].

CLINICAL IMPLICATIONS AND THERAPEUTIC STRATEGIES

Therapeutic strategies targeting the gut microbiota encompass a range of approaches aimed at restoring microbial balance and improving host health. Probiotics, live microorganisms that benefit health by colonizing the gut, are widely used to restore diversity post-antibiotic therapy and support gut health. Prebiotics, non-digestible fibers that promote beneficial bacteria growth, play a crucial role in reducing inflammation, particularly in conditions like IBD. FMT is highly effective in treating *Clostridium difficile* infections by restoring microbial diversity. Dietary modifications, such as high-fiber or Mediterranean diets, manage symptoms in conditions like irritable bowel syndrome. Postbiotics, metabolites produced by probiotics, are studied for their therapeutic potential in metabolic disorders. Antibiotics are used cautiously to avoid disrupting beneficial microbes. Phage therapy targets harmful bacteria, offering an alternative to antibiotics (Figure 4). Microbial ecosystem therapeutics engineer microbial communities to enhance gut health and treat inflammatory diseases, highlighting personalized microbiota-based therapies in disease prevention and treatment (Table 5)[117-136].

IMPACT OF ANTIBIOTICS AND OTHER MEDICATIONS ON GUT MICROBIOTA

Antibiotics and other medications can significantly impact the composition and function of gut microbiota, leading to various health consequences. The use of antibiotics, while essential for treating bacterial infections, often results in the disruption of the gut microbiome's balance, causing a reduction in microbial diversity and the proliferation of resistant strains[137]. This disruption can have short-term and long-term effects on health, including increased susceptibility to infections, antibiotic-associated diarrhea, and the potential for developing chronic conditions such as IBD and obesity[138].

Other medications, such as non-steroidal anti-inflammatory drugs (NSAIDs), proton pump inhibitors (PPIs), and antipsychotics, also influence gut microbiota. NSAIDs, for example, can cause intestinal inflammation and mucosal damage, which in turn alters the gut microbiota composition[139]. PPIs, commonly used to treat acid reflux, have been shown to decrease microbial diversity and promote the growth of potentially harmful bacteria, such as *Enterococcus* and *Streptococcus* species[140]. Antipsychotic medications have been linked to changes in gut microbiota that may contribute to metabolic side effects, including weight gain and insulin resistance[141]. The interactions between medications and gut microbiota are complex and influenced by multiple factors, including the type of medication, dosage, duration of treatment, and individual patient characteristics[142]. Understanding these interactions is crucial for developing strategies to mitigate negative effects on the gut microbiome and enhance overall health outcomes.

The impact of antibiotics and medications on gut microbiota and disease is increasingly clear, with antibiotic use significantly altering microbiota composition. This disruption can lead to conditions such as antibiotic-associated diarrhea, *Clostridioides difficile* infection, and the development of antibiotic-resistant infections[143-145]. Recent research has highlighted the critical role of gut microbiota in influencing drug metabolism, efficacy, and safety[146]. Gut bacteria can chemically modify drugs, affecting

their bioavailability and activity, with some species activating or deactivating drugs through enzymatic actions. Specific bacterial strains such as *Gammaproteobacteria* have been found to metabolize chemotherapy drugs like gemcitabine into inactive forms, reducing its effectiveness in cancer treatment[146]. Conversely, commensal bacteria such as *Enterococcus hirae* and *Barnesiella intestinihominis* have been shown to enhance the efficacy of other drugs like cyclophosphamide by stimulating immune responses in cancer therapies. These microbiota-related interactions offer promising potential for using specific bacterial markers as indicators of therapeutic outcomes, guiding the development of personalized treatments based on an individual's microbiome composition[147].

Long-term antibiotic use has been linked to chronic conditions like IBD, Crohn's disease, and metabolic syndrome by disrupting microbial balance[148,149]. Dysbiosis, or an imbalance in the gut microbiota, is implicated in obesity, asthma, allergies, cardiovascular disease, and depression, where altered microbiota affect metabolism, immune function, and neurotransmitter production[150-152]. Non-antibiotic medications, such as NSAIDs and PPIs, also contribute to intestinal inflammation, dysbiosis, and conditions like ulcerative colitis, small intestinal bacterial overgrowth, and lactose intolerance[153-155]. In diseases like celiac disease, CKD, and colorectal cancer, gut microbiota alterations influence inflammation, uremic toxin production, and cancer progression[156,157]. Additionally, early-life antibiotic exposure is associated with increased risks of asthma, allergies, autism spectrum disorder, eczema, and psoriasis, highlighting the critical role of gut microbiota in immune regulation and disease susceptibility across various conditions[158].

GAPS IN THE CURRENT UNDERSTANDING

Current research on the gut microbiota's involvement in disease and cancer faces several key gaps. One major challenge is the substantial variability in microbiota composition among individuals, influenced by factors like diet, genetics, and lifestyle. This variability complicates efforts to establish clear causal relationships between

specific microbial profiles and disease states. Mechanistic understanding also remains limited; while correlations exist between microbiota composition and diseases like colorectal cancer, the precise biological mechanisms underlying these associations are often unclear (Table 6)[159-170]. Many studies are cross-sectional, providing snapshots rather than longitudinal insights into how microbiota changes over time correlate with disease progression. Addressing these gaps requires large-scale, longitudinal studies that integrate multi-omics data to elucidate microbiota-host interactions comprehensively.

FUTURE RESEARCH DIRECTIONS

Future research directions should focus on integrating multi-omics data to better understand the intricate interactions between gut microbiota and disease. This approach will help identify microbial biomarkers and therapeutic targets, facilitating personalized medicine strategies tailored to individual microbiota profiles. Exploring the impact of diet and lifestyle interventions on microbiota composition and disease outcomes is crucial. Investigating microbiota engineering techniques, such as precision microbiome editing and synthetic ecology, holds promise for developing novel therapies. Ethical considerations surrounding microbiota-based therapies also demand attention, including issues of informed consent, privacy protections for microbiota data, and equitable access to emerging treatments.

To advance our understanding of the role of gut microbiota in health and disease, it's crucial to integrate multi-omics data, including genomics, transcriptomics, proteomics, metabolomics, and microbiomics. This comprehensive approach allows for the study of interactions between gut microbiota and disease, helping to identify microbial biomarkers, therapeutic targets, and molecular pathways that underlie disease mechanisms[171,172]. Investigating the impact of dietary patterns, prebiotics, probiotics, dietary fibers, and lifestyle factors such as exercise and stress management on gut microbiota composition and function is essential[144]. Understanding these impacts can lead to personalized dietary and lifestyle recommendations tailored to

individual microbiota profiles, ultimately aiding in disease prevention and management[173,174].

The exploration of advanced microbiota engineering techniques, including precision microbiome editing, synthetic biology, and microbial ecosystem engineering, offers promising avenues for manipulating microbiota composition and function to promote health or treat diseases[175]. These innovative approaches have the potential to provide novel therapeutic interventions based on microbial modulation. Alongside these scientific advancements, it is important to address ethical considerations in microbiota-based therapies[176]. This includes ensuring informed consent for research and therapy participation, protecting privacy related to microbiota data, and ensuring equitable access to emerging treatments. Ensuring transparency, safety, and fairness in the implementation of microbiota-related interventions is crucial for maintaining ethical standards and public trust in these healthcare innovations[177].

CONCLUSION

Human gut microbiota plays a critical role in maintaining overall health, influencing various physiological processes, and modulating disease susceptibility, including cancer. The complex ecosystem of beneficial and harmful bacteria within the gut impacts digestion, immune function, and systemic health through intricate mechanisms involving microbial metabolites and interactions with the host immune system. Dysbiosis, or the disruption of this microbial balance, is implicated in a wide range of diseases, from metabolic and autoimmune disorders to various cancers. Current research has highlighted the profound impact of specific gut bacteria on disease progression and cancer development, underscoring the importance of maintaining healthy microbiota for disease prevention and management. Therapeutic strategies such as probiotics, prebiotics, FMT, dietary modifications, and emerging approaches like phage therapy and microbial ecosystem therapeutics offer promising avenues for restoring microbial balance and improving health outcomes. Despite significant advancements, gaps in understanding remain, particularly concerning the variability in

microbiota composition, the precise mechanisms by which microbiota influence disease, and the long-term effects of therapeutic interventions. Future research directions should focus on integrating multi-omics data to unravel the complex interactions between microbiota and host, exploring the impact of diet and lifestyle interventions, and advancing microbiota engineering techniques. Ethical considerations must also be addressed to ensure informed consent, privacy protection, and equitable access to microbiota-based therapies. By continuing to investigate the role of gut microbiota in health and disease, we can develop personalized, effective treatments and preventive measures, ultimately contributing to better health outcomes and advancing the field of microbiome research.

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PRIMARY SOURCES

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