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Current Understating of Gut Microbiome Alterations and Therapeutic Approaches for Improving Human Health

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Abstract: Millions of microorganisms, including bacteria, fungi, and viruses compose the human gut microbiome. There is variation in the composition of species from the moment of birth throughout the whole human lifecycle. Gut microbiome play a central role in maintaining body equilibrium, influencing a range of physiological processes including metabolism, the maintenance of barriers, inflammation, and hematopoiesis, both within and outside the intestines. An imbalanced microbial environment within the gastrointestinal tract is at the core of numerous diseases, such as inflammatory bowel disorder, obesity, diabetes, and *Clostridioides difficile* infection, and plays a pivotal role in their development. In this review, we discuss the therapeutic approaches of gut microbiome-related therapies including fecal microbiota transplantation, anti-microbial therapies, prebiotics, probiotics and Dietary interventions to repair the altered gut microbiome composition. The pursuit of new therapies and their subsequent improvement is propelled by an ongoing requirement for evaluation, experimentation, laboratory procedures, and the ethical and technological limitations associated with clinical translation.

Introduction

The human gut microbiome is a complex and diverse community of all microorganisms, primarily bacteria, present in the gastrointestinal tract of humans. The wide range of microorganisms residing in the human gastrointestinal tract is known as the gut microbiota (Sekirov et al., 2010). All the microbes found on and within the human body, along with any associated metabolites or products, are collectively referred to as the human microbiome. More than 1,000 different bacterial species can be found in the human gut microbiome, although just a few major phyla namely, *Bacteroidetes*, *Firmicutes*, *Actinobacteria*, and *Proteobacteria* are prominent (Thursby and Juge, 2017). In a normal gut, *Bacteroidetes* and *Firmicutes* are the most prevalent bacteria. At the lowest taxonomy levels, a small number of taxa are often dominant; still, the overall composition of these microorganisms varies significantly, resulting in major inter-individual variability. *Akkermansia*, *Bifidobacterium*, and *Escherichia* are among the less common but still important genera of bacteria that can be found in the gut microbiome (Rinninella et al., 2019). Alterations in the human gut microbiome which result in an imbalance of the normal microbial community are termed dysbiosis. The function of gut microbiome in Homeostasis and in Dysbiosis is illustrated in Figure 1. This could potentially contribute to the onset of diseases. As our understanding of how the microbiota can impact

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the host deepens, it is also important to recognize that the diseased state can trigger alterations in the microbiota through several mechanisms. These may include shifts in dietary patterns, bowel function, and the introduction of medications, such as antibiotics (Shreiner et al., 2015). The presence of the host and the availability of dietary carbohydrates in the gastrointestinal tract are important factors influencing the composition and functionality of the gut microbiome.

In this review, we discuss the various types of therapeutic approaches related to gut microbiome alteration. The idea of modifying the gastrointestinal microbiome to enhance health outcomes has become firmly established in contemporary medicine. Microbiome-focused treatments can encompass various therapeutic approaches, including the role of prebiotics and probiotics, anti-microbial therapies, dietary interventions, and fecal microbiota transplantation (FMT).

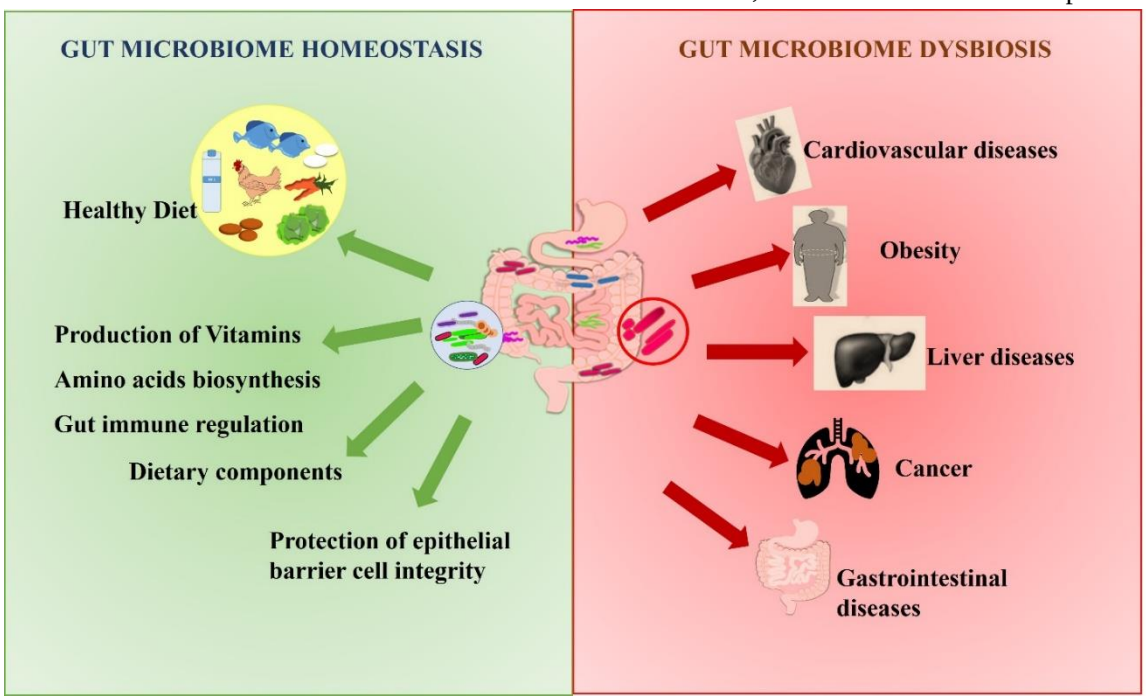

Figure 1. Gut Microbiome function in Homeostasis and Dysbiosis.

The human gut microbiota undergoes continuous evolution throughout life and appears to hold a central position in influencing both health and disease. In a state of good health, the gut microbiota serves various beneficial functions, such as extracting energy from the metabolism of indigestible components of foods, safeguarding the host against pathogenic threats, and modulating the immune system (Afzaal et al., 2022). The emergence of a disrupted microbial equilibrium state within the gut microbiota is now acknowledged as an environmental factor that interacts with the host's metabolism and contributes to various pathological conditions. These conditions can be systemic, including obesity, diabetes, and atopy, as well as gut-related issues like irritable bowel syndrome (IBS) and inflammatory bowel disease (IBD). However, the precise role of the gut microbiota in the development of these diseases remains unclear. The diverse causes of metabolic and gastrointestinal diseases have been linked to different microbial factors, although limited information is available regarding the causative direction of this association (Bull and Plummer, 2014).

Therapeutic approaches to gut microbiome alteration

Gut microbiome therapy is gaining prominence as alterations in the gut microbiome are linked to several diseases. Anti-microbial therapies work by altering metabolic, nutritional, and biological processes to repair dysbiosis and improve the host's ability to survive. These strategies include dietary modifications, probiotics, prebiotics, antibiotics, and fecal microbiota transplantation. Therapeutic approaches like fecal microbiota transplantation, and probiotics, involve introducing external microorganisms for the treatment of dysbiosis-associated conditions. Gut microbiome therapy has the potential to accomplish individualized therapy by addressing important aspects such as interpersonal variation and stability in a wide range of environments.

Antibiotic therapy

Antibiotics are therapeutic medications that save lives and have been used by people for decades (Yang et al., 2021). They are used to treat bacterial infections. Sepsis and the microbiome interact in a bidirectional connection that has not yet fully been explored (Looft et al., 2012). The bacteria are altered by sepsis, but treatment for all

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these critically ill individuals seems to have an indirect influence on the microbiome. The administration of medications results in a decrease in the variety of intestinal microbial diversity, including the extinction of numerous significant groups, resulting in an impact on metabolism, making the gut more hospitable to colonization, and encouraging the emergence of microbial-resistant strains.

Reduced diversity

The use of antibiotics is related to a decline in microbial diversity. According to reports, it takes around a month for microbial diversity in children to return after antibiotic therapy (Yassour et al., 2016). Meropenem, gentamicin, and vancomycin given to adults increased the prevalence of *Enterobacteriaceae* and other pathobionts while decreasing the prevalence of *Bifidobacterium* and other species that produce butyrate (Palleja et al., 2018). Antibiotic-resistant bacteria proliferate and replace the antibiotic-susceptible bacteria when the former is destroyed. After antibiotic treatment, species diversity decreases. However, the microbial load, which is a measure of the total number of microorganisms present within the system, increases mainly due to a significant increase in the number of Gram-negative bacteria (Panda et al., 2014).

Altered metabolomes

The concept of "metabolome" defines the entire collection of tiny molecules (1500 Da) present in a biological system (Lamichhane et al., 2018). Less research has been done on how antibiotics affect the gut metabolome than they have on the variety of bacteria in the gut. Metabolomic redundancy is one aspect that complicates this connection's research (Cho et al., 2012; Choo et al., 2017). According to a different study, treatment with vancomycin-imipenem increased the concentration of sugar as well as arabinitol in feces. It has been suggested that higher amounts of these chemicals may make people more susceptible by functioning as a precursor molecule for *Clostridioides difficile* infection. The accumulation of microbes *Lachnospiraceae* but also *Ruminococcaceae*, which generally metabolize arabinitol to pentose sugars, were similarly decreased by vancomycin/imipenem. With the use of vancomycin/imipenem, arginine levels immediately decreased somewhat but significantly. This was linked to a decreased frequency of *Ruminococcaceae* and *Bacteroides* and an increasing incidence of *Escherichia* and *Shigella* species (Ramirez et al., 2020). Nine days after the vancomycin/imipenem treatment ended, the incidence of *Enterobacter* species increased while the prevalence dropped. Arginine is a precursor to several substances that have immunomodulatory properties (Choo et al., 2017). When someone is exposed to antibiotics, their gut metabolome changes, which may or not be correlated with alteration in their gut microbiota. Patients with metabolic syndrome received oral vancomycin, which resulted in a drop in fecal secondary bile salts and a rise in plasma primary bile salts after meals. Additionally, vancomycin reduced peripheral insulin sensitivity, which had an impact on host physiology (Vrieze et al., 2014).

Antibiotic resistance

The ability of a microorganism to tolerate antibiotic doses to prevent or eradicate entities of the same species is known as antimicrobial resistance (Sabtu et al., 2015). It was first used by bacteria that produce antibiotics as a defense mechanism against those products and as a means of interfering with other germs. Globally, overuse of antibiotics has evolved into a major concern for public health. The most widely treated medications consisted of amoxicillin and amoxicillin/clavulanic acid between 2000 and 2015 (Klein et al., 2018). The worldwide usage of antibiotics increased by sixty-five percent between 2000 and 2015 (Hernando-Amado et al., 2019). A few of the immune systems that bacteria have developed to combat antibiotic effects include antibiotic uptake via their living cells, the creation of cellular reactions that alter and impair this same treatment, the adjustment of the particles that antibacterial drugs approach, and the productive disposal of antibacterial agents from the cell through the use of special purpose efflux proteins. Antibiotics can be rendered inactive by microbial activities such as chloramphenicol acetyltransferases, aminoglycoside-modifying protease, and lactamases (Giedraitienė et al., 2011). The molecular targets of antibiotics can also be changed by bacteria, altering the antibiotic's targeted enzyme and its specific connection by way of minute structural changes. For instance, variations in deoxyribonucleic acid (DNA) enzymes topoisomerase II and IV result in susceptibility to quinolones and fluoroquinolones while changes in the protein ribosomal code provide tolerance against macrolides, lincosamides, and streptogramin B. The efficiency of beta-lactam antibiotics is also impacted by changes in penicillin-binding proteins. Bacteria can get rid of antimicrobial compounds by expelling them through efflux proteins located in bacterial cell membranes. While some of these proteins may be antibiotic-specific, the majority of them are multidrug transporters (Giedraitienė et al., 2011).

Modulatory therapy

Intending to improve human health, modulatory

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therapy modifies the microbes in the gut or their relationship with the human host. This requires consideration for restoring the microbiome after it became depleted and modifying the current bacteria to create a more beneficial microbiome. The gut microbiome can be restored or modified through a variety of factors, including antibiotics, diet, exercise, and lifestyle choices (Bhalodi et al., 2019). Although the microbiome promotes a healthy diet, changing our dietary habits is a key strategy for altering the gut microbiome. The synthesis of short-chain fatty acids and a healthy microbiome are both correlated to physical activity. Athletes intake more proteins that affect the gut microbiome. Marathon participants have been identified with increased levels of *Veillonella*, enhancing exercise endurance (Scheiman et al., 2019). Following the ketogenic diet, children with severe epilepsy had lower levels of the gut bacteria *Eubacterium rectale, Bifidobacteria* and *Dialister*. Lindefeldt et al. (2019) used ketogenic diet as a drug-resistant epilepsy treatment. Long-chain fatty acid dietary supplementation relieved pathological circumstances and restored the *Lactobacillus* in ethanol-induced liver damage. Similar to this, the injection of glycerol tributyrate rectified the butyrate levels and improved health. Prebiotics, including fiber and galactooligosaccharides that enhance the abundance of *Bifidobacterium*, promote the positive bacteria and eliminate infections (Martinez et al., 2019). Drinking alcohol enhances the concentration of gram-negative bacteria, reduces the generation of short-chain fatty acids, and raises intestinal permeability. Alcohol decreases the quantity of *Lactobacilli* and *Proteobacteria* while increasing the number of Bacteroidetes. The abundance of *Proteobacteria* increases and *Faecalibacterium* decreases in the human stool because of higher alcohol intake (Kosnicki et al., 2018). Smoking also affects the gut microbiome composition, airway, and oral microbiomes. Quitting smoking alters the gut microbiome makeup by enhancing *Firmicutes* and *Actinobacteria* while simultaneously decreasing *Bacteroidetes* and *Proteobacteria*. Dysbiosis, smoking, and the beginning of a disease are all related. In *Clostridioides difficile* infection patients, *Bacteroidetes* are more prevalent, which includes the severity and progression of the disease. Additionally, antibiotics damage the gut microbiome by minimizing microbial diversity, altering metabolic processes, and stimulating the development of resistance to antibiotics, leading to *Clostridioides difficile* infection and diarrhea caused by antibiotics (Ramirez et al., 2020).

Role of probiotics and prebiotics in gut microbiome

An enhancement in the gut microbiome composition is one of the major advantages of probiotics. To improve the gut microbiome composition, next-generation probiotics like intestinal microorganisms are used (Depommier et al., 2019). Probiotics interact with other intestinal microbes for receptors and binding sites on the intestinal mucosa or may create antimicrobial agents or enzymatic substances that inhibit the development of parasitic microorganisms (Hemarajata and Versalovic, 2012). Probiotics contain some strains of bacteria including *Bifidobacterium, Propionibacterium, Lactobacillus, Streptococcus, Escherichia coli, Enterococcus,* and yeast such as *Saccharomyces* (Oniszczuk et al., 2021). The main benefit is that they have an impact on the microbiota that exists inside the organism, which helps to maintain the healthy balance between bacteria and pathogens that is essential for the organism to survive and function properly (Markowiak and Slizewska, 2017). An additional function of probiotics is preventing the activities of pathogenic bacteria in the gut that have been ingested from contaminated food as well as the environment (Iqbal et al., 2021). Hence, probiotics may prevent illnesses caused by food by easily inhibiting the growth of pathogenic microbes, including *Salmonella* Enteritidis, *Clostridium perfringens, Campylobacter jejuni, Escherichia coli,* multiple species of *Shigella, Staphylococcus,* and *Yersinia.* Probiotics have been proven to improve digestion and be effective in treating candidiasis (a fungal infection caused by *Candida* species), food allergies, and dental cavities (Markowiak and Śliżewska, 2017). It has been beneficial for treating many types of illnesses including Crohn's disease, ulcerative colitis, inflammatory bowel disorder, and cancer (Yadav and Chauhan, 2021). It possesses the potential to regulate microbial environments and alter the gut microbiota. To determine whether probiotics can have a similar effect on the human gut microbiota and whether these modifications are linked to therapeutic advantages for the host, more research on humans is necessary (Hemarajata and Versalovic, 2012).

Probiotics work by either establishing themselves in a specific part of the body or temporarily residing there, offering health benefits. These benefits involve enhancing immunity, hindering the spread of infections through resource competition, and directly eliminating harmful microbes using antimicrobials like bacteriocins (Gulliver et al., 2022). A new research study on individuals with diarrhea-dominant inflammatory bowel syndrome found that probiotic combinations containing *Lactobacillus acidophilus, Lactobacillus plantarum, Lactobacillus rhamnosus, Bifidobacterium breve, Lactobacillus longum,* and *Streptococcus thermophilus* improved patients feel better. Fascinatingly, denaturing gradient gel electrophoresis (DGGE) investigations of the fecal

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microbiota of these patients showed that probiotic-treated patients had a more similar microbial composition than the placebo group did. This observation revealed that the composition of the bacterial community was more consistent throughout the probiotic therapy period (Hemarajata and Versalovic, 2012). Probiotics can alter intestinal microbial communities, as demonstrated by a Preidis et al. (2012) study that employed 16S rRNA metagenomic sequencing to examine the effect of *L. reuteri* on microbial community composition in a neonatal mouse model. When comparing the distal intestine microbiome of animals treated with *L. reuteri* to that of animals treated with the vehicle, the results showed a transient improvement in both evenness and diversity (Preidis et al., 2012).

Prebiotics are devoid of any bacteria in the gut microbiome composition rather, they are made up of substances that promote the growth of microorganisms. Prebiotics are the substances that are most frequently utilized to keep the gut microbiota in a normal condition and to prevent disruption to homeostasis (Davani-Davari et al., 2019).

Prebiotics are substances obtained in food that the microbiome utilizes to promote many kinds of healthy bacteria. They also offer beneficial health effects and are easily ingested (Gulliver et al., 2022). According to the research of Fidelis et al., 2021, castalagin, vescalagin, procyanidin A2, and ellagic acid act as bacterial metabolizing enzymes such as β-glucosidase, mucinase, β-glucoronidase, β-galactosidase, and nitroreductase which are suppressed. In turn, this prevents iron ions from detoxifying in the gut and inhibits bacterial growth, which adversely affects the proliferation of aerobic microbes, in particular gastropathogenic microorganisms (Fidelis et al., 2021). Prebiotics are considered non-digestible food substances that enhance host health by selectively promoting the proliferation and activity of particular bacteria in the gut (Gibson et al., 1995). Prebiotics changed the predominance of four commensal microbiota in these individuals (Bacteroides, *Bifidobacterium, Escherichia coli*, and *Enterococcus*). These contentious data imply that additional study is required to fully understand their therapeutic impact in lowering the burden of colorectal cancer at population-based levels (Xie et al., 2019). Studies have shown that inulin-rich nourishment may improve *Bacteroidetes* populations of prominent propionate makers, predominantly as an outcome of significant increases in the *Porphyromonadaceae, Bacteroidaceae,* and specifically species of *Prevotellacea* (Fernandez et al., 2019).

Prebiotics are linked to the possible improvement of human health by regulating the balance of the intestinal microbiome. These materials are fermented by gut microbes, producing acetate, propionate, and butyrate. Positive effects of producing these short-chain fatty acids include improved absorption of minerals and integrity of the intestinal membrane, decreased body weight and glycemic levels, improved immunity, altered metabolic processes, heart disease, and biomarkers of inflammation (Farias et al., 2019).

Fecal microbiota transplantation

By giving a dysbiotic recipient the healthy recipient's gut microbiota, a technique known as fecal microbiota transplantation (FMT) can be used to restore eubiosis (Khanna, 2018). It is based on the hypothesis that treating illnesses characterized by changed microbial composition may benefit by changing the microbiome. There have been studies where dietary fibers, probiotics, and prebiotics have been shown to enhance gut microbiome diversity (Banerjee et al., 2023). However, the results of treatment with probiotics have been mostly mixed. This might have something to do with the probiotics' diversity of species vs. the bacteria in a healthy human gut. Fecal microbiota transplantation, therefore represents the gut microbiome in its totality when it occurs naturally, making it possibly an advanced substitute for probiotic bacteria. This swiftly established itself as a practical substitution for managing recurrent *Clostridioides difficile* infection (Gupta et al., 2020). In 1983, *Clostridioides difficile* infection with fecal microbiota transplantation was successfully treated for the first time with retention enemas (Schwan, 1983). This administration method was used until the 1990s, when newer ones such as nasogastric infusion, anterior endoscopic and colonoscopy methods, and a self-conducted laxative, started to gain favor (Kassam et al., 2013). Stimulant laxatives were used to enhance the variety of the gut microbiome and approximately 85% of diseases are cured (Brandt, 2013). To ascertain its potential use in illness conditions including *Clostridioides difficile* infection, extensive investigation is being conducted in ongoing clinical studies. The use of fecal microbiota transplantation as a novel therapeutic strategy for several conditions with altered gut microbial compositions is slowly gaining acceptance. These diseases range from *Clostridioides difficile* infection to inflammatory bowel disease to inflammatory bowel syndrome to non-alcoholic fatty liver disease, adiposity, psychiatric illnesses, and antibiotic-resistant organisms,

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among others (Zhou et al., 2019). Figure 2 represents the process of fecal microbiota transplant.

Clostridium difficile infection (CDI)

Nosocomial diarrhea is mostly caused by *Clostridioides difficile* infection, and during the past few decades, its prevalence has increased in the population as well. Hospitalization, stomach acid-suppressing drugs, exposure to antibiotics, and chronic conditions such as immunocompromised states are also often linked risk factors (Tariq et al., 2017a). Since alteration in the gut microbiome plays a significant role in the pathophysiology of *Clostridioides difficile* infection, fecal microbiota transplantation may be able to stop further infection by repairing the microbiota's ordinary variety and functions (Gupta and Khanna, 2017).

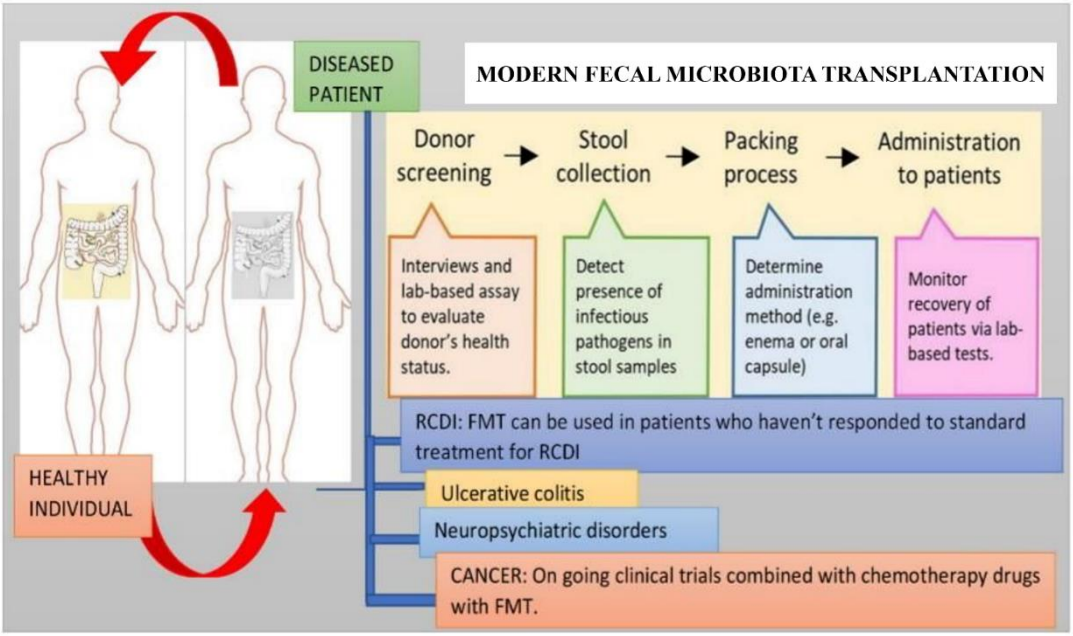

Figure 2. The process of fecal microbiota transplant.

Microbiome against inflammatory bowel disease

Inflammatory bowel disease, a chronic inflammatory gastrointestinal disorder, is significantly influenced by changes in the microbiome of the gut. Bacterial dysbiosis in inflammatory bowel disease is caused by a decline within communities of *Bifidobacteria* but also *Clostridia* or a rise in *Acinetobacter*, and *Enterobacteriaceae* (Colombel, 2014). Results of bacterial hormone replacement in inflammatory bowel disease that are less impressive can be explained by the hypothesis that additional factors, such as diminished mucosal barrier function, inflammation, and ecological and biological factors, contributed to disease formation (Vindigni et al., 2016). Further randomized, double-blinded, placebo-controlled, large-scale study is necessary to evaluate the current function of fecal microbiota transplantation in the treatment of inflammatory bowel disease because this role is currently unknown (Qazi et al., 2017). The possibility of an inflammatory bowel disease flare is another one more issue with fecal microbiota transplantation. Twenty publications on the use of fecal microbiota transplantation in inflammatory bowel disease have been published, with the earliest case report published in 1989. These papers include a collection of cohort studies, case reports, and randomized, controlled trials.

Therapy against inflammatory bowel syndrome

By giving a dysbiotic recipient the healthy recipient's gut microbiome, a technique known as fecal microbiota transplantation can be used to restore eubiosis. According to studies, patients with inflammatory bowel syndrome have less microbial diversity in their guts than people without the condition (Kassinen et al., 2007). In a recent analysis, research with 55 patients indicated that 36% of inflammatory bowel syndrome patients who underwent fecal microbiota transplantation experienced complete symptom clearance, while a smaller, uncontrolled trial with 13 patients showed that 70% of patients experienced symptom reduction (Pinn et al., 2014). Before such a therapy can be implemented in clinical practice, however, large randomized controlled trials (RCTs) are needed because the data on fecal microbiota transplantation's effectiveness in inflammatory bowel syndrome is currently inconclusive.

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Fecal microbiota transplantation may be used to treat several additional illnesses that are currently being researched. In one research, nearly three-quarters of patients with recurrent *Clostridioides difficile* infection who tested positive for the germs had vancomycin-resistant enterococci removed successfully by fecal microbial transplantation (Dubberke et al., 2016). In *Clostridioides difficile* infection patients, fecal microbiota transplantation has been demonstrated to reduce the frequency of persistent bladder infections as well as the characteristics of bacteria's antibiotic resistance that result in recurrent infections of the bladder (Tariq et al., 2017b). Multiple sclerosis, Parkinson's illness, fibromyalgia, myoclonus dystonia, autism, fibromyalgia, and idiopathic thrombocytopenic purpura are among more potential, less well-researched indications for fecal microbiota transplantation usage. However, in clinical practice, microbial replacement therapies are presently only used to treat *Clostridioides difficile* infection because the evidence for treating other disorders is still poor, and further research is warranted (Colman and Rubin, 2014). Figure 3 depicts the factors affecting gut microbiome composition and the working of probiotics and fecal microbiota transplantation.

improper diet may increase the risk (Bear et al., 2020). IBS Patients have been found to gain advantages from diet modifications, with some patients being recommended to eat fewer fermentable oligo-, di-, and monosaccharides and polyols (FODMAPs) (Gibson and Shepherd, 2005). Various diets have been investigated for use in treating Crohn's disease (CD) or ulcerative colitis (UC), both of which dietary interventions have been extensively researched with IBD treatments (Gulliver et al., 2022). Dietary modification of the gut microbiome is a promising therapeutic and prophylactic approach for numerous diseases (De Filippis et al., 2018). To maintain the beneficial effects of EEN, CDED was created to allow patients to consume entire meals while limiting their consumption of inflammatory food components such processed foods, gluten, milk products and chemical additives to food. Bacteria belonging to the Firmicutes phylum are more abundant than those belonging to the Proteobacteria and Actinobacteria species, according to both EEN and CDED (Lee et al., 2015). In an observational trial, the researchers observed that melanoma patients who stated they consumed enough fiber responded better to ICIs than patients who reported eating inadequate fiber in their diets. In melanoma mouse

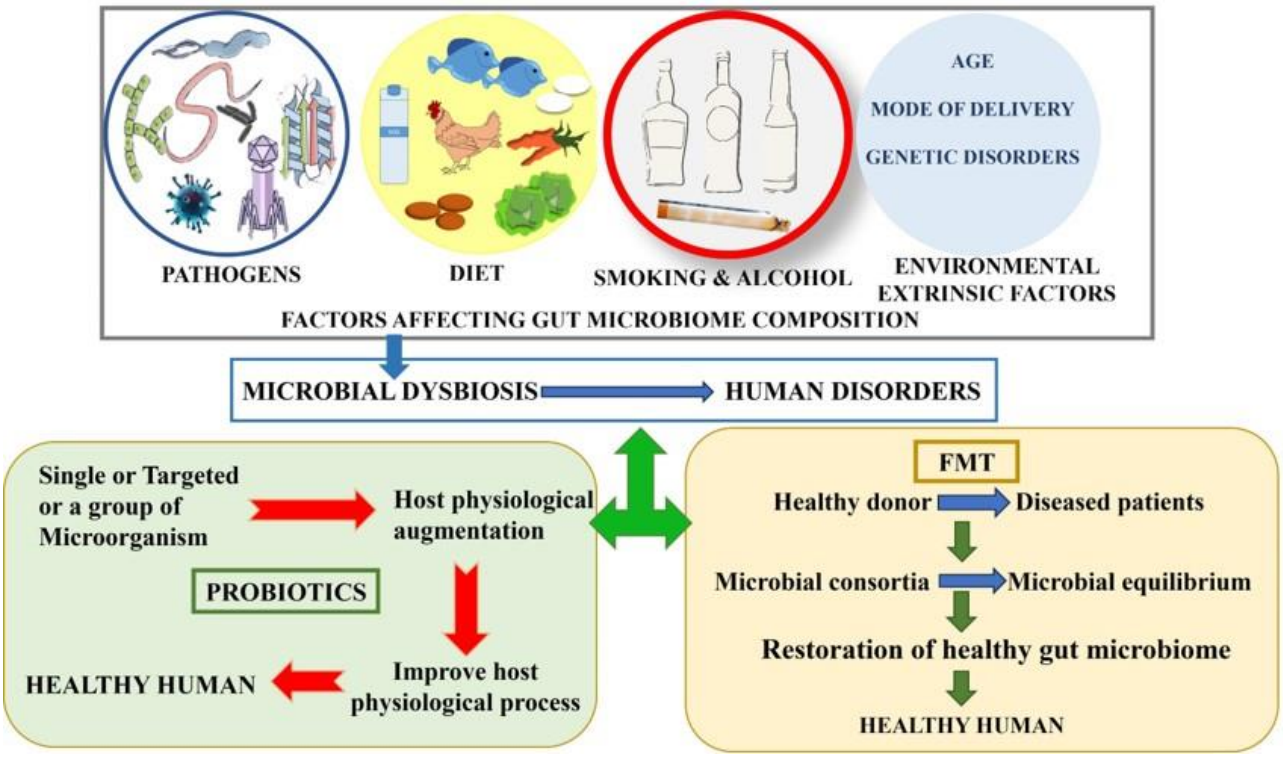

Figure 3. The factors affecting gut microbiome composition and the working of probiotics and fecal microbiota transplantation.

Dietary interventions

Diet plays an essential role in health and disease (Gulliver et al., 2022). There exists increasing evidence that consuming a healthy diet might reduce the possibility of developing anxiety or depression, whereas having an

models that were given adequate fibers, delayed tumor spreading was also noted; however, this effect wasn't observed in germ-free animals, showing that the gut microbiota of the mice was essential for the effect of dietary fiber (Spencer et al., 2021).

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Future perspective

Over the past decade, microbiome-based medicines have made significant strides, progressing from interventions like dietary changes, prebiotics, and probiotics to the utilization of fecal microbiota transplantation Advances in culturing gastrointestinal bacteria and the application of metagenomic sequencing have successfully addressed previous technical challenges in this field. Even though studies have demonstrated the effectiveness of microbiome therapies, more work is still needed to fully comprehend the microbiome and how it interacts with the host to forward the idea of microbiome therapeutics into clinical trials and develop treatment guidelines. To increase the effectiveness of the treatments, the pharmaceutical and microbiome therapeutic sectors must collaborate.

Conclusion

The gut microbiome composition has been altered causing severe health illness. Strategies used to reduce the impact on human health with the gut microbiome include Dietary intervention, probiotics, prebiotics, antibiotics, and fecal microbiota transplantation, which act as gut bio-modulators, and microbe-based therapies. Dietary intervention can indeed have a positive impact on the composition and function of the gut microbiome. Fecal microbiota transplantation repairs the altered microbiome into a changed microbiome composition. It is used for *Clostridioides difficile* infection, inflammatory bowel disease, and inflammatory bowel syndrome. Although studies have demonstrated the efficacy of treatments based on the microbiome, additional research is necessary to fully understand the microbiome and its intricate interactions with the host. To move the idea of microbiome therapies into clinical trials and eventually create a road map for more effective treatment regimens, further study is necessary. When combined with cooperative efforts, the era of gut microbiome therapeutics has the potential to completely transform the healing process of disease and its applications in medicine.

Figure legends

Figure 1. Gut Microbiome Function in Homeostasis and Dysbiosis

Figure 2. The process of fecal microbiota transplant.

Figure 3. The factors affecting gut microbiome composition and the working of probiotics and fecal microbiota transplantation.

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Conflict of interest

None. All authors declare that there are no conflicts of / or competing interests.

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Authors' contributions

AKR and AB designed the study and conceptualized the work. AB, RAT, AM prepared the original draft and wide-ranging aspects of the manuscript preparation and pictorial representations. AKR, AB and DI have critically reviewed the draft manuscript and provided feedback on data analyses. All authors read and approved the final manuscript.

Ethics Approval and Consent to Participate

Non-applicable. This research does not involve human/animal participants, human/ animal material, or human data.

Consent for publication

All authors have approved the final version of the manuscript and given consent for publication.

Availability of data and materials

Not applicable

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