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ORIGINAL ARTICLE

Dysfunction of the Gut Microbiome and its Onset Progression of Chronic and Mental Health Disorders

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ABSTRACT

The gut microbiome is a complex community of microbes that inhabits the gastrointestinal tract and plays a crucial role in maintaining human health. Recent research has demonstrated that gut dysbiosis, or an imbalance in the microbiome, is associated with the development of various chronic and psychiatric diseases, such as obesity, cardiovascular disease, and depression. The mechanisms by which gut dysbiosis contributes to disease development involve alterations in the gut-brain axis, gut-liver axis, and gut-immune system interactions. Studies have shown that gut microbiome dysbiosis can cause up-regulation of certain pathways involved in disease development, including systemic inflammation, oxidative stress, and intestinal permeability. Additionally, gut dysbiosis has been linked to alterations in neurotransmitter synthesis and gut hormone secretion, which can influence the brain and contribute to mood and cognitive disorders. Further research is necessary to fully comprehend the mechanisms underlying this relationship and to develop effective strategies for the prevention and treatment of chronic and psychiatric diseases. In conclusion, gut microbiome dysbiosis plays a critical role in the up-regulation and development of chronic and psychiatric diseases and is an area of growing interest in the scientific community. Further investigation is needed to fully understand the mechanisms underlying this relationship and to develop effective treatments and interventions.

Keywords: Gut microbiome , chronic, mental health, dysfunction

INTRODUCTION

A gut microbiome is defined as the community of microbes including viruses, bacteria, archaea, and some unicellular organisms sharing a specific gut environment. The microbiome is also the genomic element of the entire microbiota, and the genomics is the field of study to these microbiomes extensively. Human body is considered as an entity of all metabolic reactions, also including immune system development, detoxification, and digestion. There are two genomes in the human body, one is inherited from the parents and the other is acquired from the environment and diet called the microbiome, the most critical difference in both is the one that is inherited stays the same during the lifetime but acquired one is highly dynamic and changes with many factors including age, diet, exercise, hormonal cycles, and therapies. Humans are born sterile but develop their gut colonization later in combination with many factors. Age plays a big role in alteration of the gut microbiome, there is a huge difference in the gut microbiome of infants, adults and the elderly. The human gut microbiome contains more than 1000 genes and a few phyla which include *firmicutes, Bacteroides, actinobacteria,* and *proteobacteria* [1]. In human, bacterial level rise in lumen of intestine and bacterial numbers can be as high upto 10 million bacteria /ml in fecal sample. Food induced effects and addition of probiotics, prebiotics can increase the beneficial microbial diversity in gut while antibiotics can decrease it and can shift whole gut microbiota. Antibiotics remained very popular for long time to save human lives but its access use have caused resistance and disturb the gut bacteria resulting increase in diseases. The short term effects of antibiotics are diarrhea and *clostridium deficile* infection or long term effects include asthma, allergic reactions and obesity leading to alteration of gut microbiome. In intestinal cells, antibiotic abuse can lead negative effects on the levels proliferation and apoptosis to enterocytes and endocrine cells by releasing lots of intracellular proteins. They may be useful markers for the detection of gut dysbiosis [2].

Keeping in mind the importance of the gut microbiome, it is mandatory to maintain it through diet and a healthy lifestyle. Changes in microbiome composition can lead to many diseases; it will become possible in the future to target disease by gut microbiome therapeutic through the keen study of microbial dysbiosis and the development of specific diseases. Microbial studies are based on the conventional methods of cultivation and identification of microbes and these facilities are currently used for the diagnostics of disease. Next generation sequencing and 16s rna sequencing methods have replaced the use of these conventional culturing techniques in research due to unfavorable growth of many anaerobic bacteria. The study of all the anereobic and aerobic bacteria is important and useful to get the knowledge of dysbiosis in normal and diseases individuals. The gut microbiome study is highly variation and individuals use as subjects for the study are highly different in composition and diversity of the gut microbiome. It is difficult to find out all the microbes by using conventional methods with variations of microbiomes with specific diseases [3].

Immune cell interaction with gut microbiome: The gut microbiome refers to the collection of microorganisms, including bacteria, fungi, viruses, and parasites, that live within the human digestive tract. Immune cells play a critical role in maintaining a healthy gut microbiome by recognizing and responding to harmful microorganisms and regulating the growth of beneficial microorganisms. There are several types of immune cells that interact with the gut microbiome, including T cells, B cells, dendritic cells, and natural killer cells. T cells, for example, can differentiate between harmful and harmless bacteria and respond by producing cytokines and other signaling molecules that recruit other immune cells to the site of infection. B cells produce antibodies that can directly neutralize harmful microorganisms, while dendritic cells serve as sentinels that capture and present antigens to T cells to initiate an immune response. The gut microbiome also influences the development and function of immune cells. For example, certain species of bacteria can stimulate the production of regulatory T cells, which play a key role in controlling inflammation and promoting tolerance to harmless antigens. In addition, the gut microbiome can modulate the function of innate immune cells such as natural killer cells, which play a critical role in defending against viral infections. The interaction between immune cells and the gut microbiome is bidirectional and complex. On one hand, the gut microbiome helps to shape and regulate the immune system, while on the other hand, the immune system helps to regulate the composition and function of the gut microbiome. Disruptions to this delicate balance, such as those caused by antibiotics or diet, can lead to alterations in the gut microbiome that contribute to the

development of various diseases, including inflammatory bowel disease, obesity, and allergies [4].

In conclusion, the gut microbiome and immune cells have a complex and reciprocal relationship, with each influencing the other. Understanding the interplay between these two systems is essential for developing new strategies to maintain gut health and prevent disease.

Metabolites production and gut microbiomes: Over the last few years it was identified by the scientist that obesity and metabolic syndromes is the result of shift in gut microbiome at phylum level. Scientists are still not satisfied by these findings and confused about to go deeper at strain and specie level because of much variation and extensive studies required on metabolic activity of microorganisms. The production and shift of metabolites can be the cause of strain shifting or the gut is considering new environment to work on. Numerous metabolites produced in gut and can influence metabolism. To obtain the complete details about gut microbiome on health, studies should be conducted on it with co-relation to environmental factors such as diet, amount of consumption of different variety of drugs, and also in relation to variation in physiological conditions and chronic diseases.

When a correlation is found in beneficial and deleterious bacteria or disease, it's complicated to find its implication on candidate onset of disease [5]. Researchers usually start from the correlation of isolated bacteria and identified metabolites; the role of new microbes is not identifiable due to conventional cultural techniques. The advances in metagenomics and 16s ribotyping has given scientist a new direction to find the community of anaerobic bacteria and their produced metabolites. It is also important to culture the quantities of putative anaerobic bacteria that are compatible to chronic testing in vivo.

A tremendous amount of microbes are present in human gut, advancements in research on gut microbiome have opened up many direction of assessments of composition and metabolites production by various bacteria, novel bacteria were also identified for in this research. Various studies have informed us the differences in gut microbiome with under different conditions. Complete analysis is required to get the clear concepts of correlations e.g multiomics and time series measurements. Differences in gut microbiota composition are directly related with specific disease [6].

Diet, Obesity and role of Gut Microbiome: Scientists are more interested to explore the gut microbiome's impact on the health of obese and lean individuals. Many studies reported that the gut microbial composition and diversity is mostly different in healthy (lean) and unhealthy (obese) individuals. The diversity of microbiota varies from person to person and it is also dependent on various factors. Besides bacteria, the gut microbiome also includes archaea, viruses, fungi, and protozoa. Obesity is defined as the abnormal or excessive amount of fat accumulation in body that can be a risk to health. Body BMI of more than 25 is considered over weight and more than 30 is considered obese. This obese condition is directly related to the gut microbiome distinctive features with low microbial gene richness and functional alterations. It also associated with inflammation and type -2 diabetes. The studies on mouse model have clearly found out that gut microbiome low gene richness is associated with dysbiosis and cause obesity. Many bacterial species and their genes are not functional enough to cope up the pressure of environmental factors and result in low metabolism and high obesity. Bariartic surgeries are recommended to individuals with more than 40 BMI but this procedure is not a long term solution for the obese patients [7].

A healthy gut microbiome is a key regulator of health, it must contain *bifidobacteria* to digest healthy sugars in milk and other dairy products, also contain gram negative and positive bacterial strains that can enhance the production of short chain fatty acids, can metabolize long chain fatty acids and limited the production of peptides produce by gram positive bacteria. Healthy gut microbiota has also balance the immune cell production, activation and maintenance in individual's body. Gut microbiota re-shaping is influenced by diet pattern, living arrangements, smoking, depression and also the environment in which an individual live. Gut microbiota-dysbiosis promote different chronic disease conditions in individuals suffered in obesity which includes high blood sugar level, low synthesis of short chain fatty acids leads to obesity ,production of non- commensal peptides and changes in the gut barrier and activation of immune cells by receptors [8]. Microbial communities in high fat diet [9].

Recent advancements in sequencing technology, characterization and probing of obese gut microbiome, the potential to provide valuable clues for the diagnosis and prognosis of obesity and associated diseases [10]. One possibility is that restoration of the gut microbiome to "normal" may help to trigger the normal gut-metabolism in obese and in turn reduce the severity of obesity with other chronic ailments [11].

Neurological disorder and role of gut microbiome: The gut microbiome has been linked not only to gastrointestinal and chronic diseases but also to psychiatric disorders. There is a strong correlation between the diversity of gut microbes and these psychiatric conditions. Factors like stress, the role of pre and probiotics, and bidirectional communication through the microbiome-gut axis play an important role in this connection. The alterations in the gut microbiota can lead to the development of various psychiatric disorders, including Major Depressive Disorder, Schizophrenia, Bipolar Disorder, and Autism Spectrum Disorder. [12].

Depression: Depression is a widespread mental disorder, characterized by intense feelings of sadness and emotional disturbance that can take up to two weeks to recover from. Patients with depression often feel isolated and helpless and avoid social gatherings. This condition can result in serious mental distress and even suicide. Studies have revealed alterations in the microbiome diversity in individuals with depression. One study found a higher abundance of the Alistipes genus, associated with inflammation, and a high presence of oscillibacter producing valeric acid in depression patients. Another study, using a mouse model, showed that changes in the gut microbiome, referred to as dysbiosis, led to increased gut permeability and systemic inflammation. This dysbiosis resulted in a decrease in the relative abundance of *Bacteroidetes,* an alteration in the Firmicutes/Bacteroidetes ratio, and growth of Lactobacillus [13]. The study also found that these changes in the microbiome were associated with a reduction in endogenous melatonin, leading to increased gut permeability and systemic inflammation. [14].

Bipolar disorder: Bipolar Disorder is a neurological disorder that resembles schizophrenia and causes episodes of depression and inflammation. Studies have found a connection between the diversity of the intestinal microbiome and the development of this disorder. An increased abundance of *Coriobacteriaceae* in the gut has been linked with elevated cholesterol levels, while a high amount of *Lactobacilli* has been associated with the development of obesity in individuals with Bipolar Disorder [15]. On the other hand, a low abundance of *Faecalibacterium*, a naturally occurring gut bacterium, has also been linked to this disorder. In patients diagnosed with Bipolar Disorder, the number of *Clostridiaceae*, which are involved in the fermentation of carbohydrates and production of Short Chain Fatty Acids, was four times lower compared to the control group, leading to obesity. [16].

Schizophrenia: Schizophrenia is a complex mental disorder that affects around 1% of the world's population. While the exact causes of schizophrenia remain unknown, a growing body of evidence suggests that the gut microbiome, the community of microorganisms living in the gastrointestinal tract, may play a role in the development and progression of the disorder. Studies have found that individuals with schizophrenia have a different gut microbiome compared to healthy individuals, characterized by changes in the abundance and diversity of gut bacteria [17]. This phenomenon is referred to as gut microbiome dysbiosis. The exact mechanisms behind this dysbiosis are not yet clear, but it has been suggested that changes in the gut microbiome could affect brain

function and behavior through various pathways, including the gut-brain axis, the immune system, and the metabolism.

One of the key ways in which gut microbiome dysbiosis might contribute to schizophrenia is through alterations in the gut-brain axis [18]. The gut-brain axis is a complex network of communication between the gut and the brain that involves the release of hormones, neurotransmitters, and other signaling molecules. Studies have found that changes in the gut microbiome can disrupt the gut-brain axis and alter the balance of signaling molecules, leading to changes in behavior and cognition. Another potential mechanism linking gut microbiome dysbiosis to schizophrenia is through the immune system. The gut microbiome plays an important role in regulating the immune system, and alterations in the gut microbiome can lead to changes in immune function. In individuals with schizophrenia, research has found elevated levels of inflammation and oxidative stress, which have been implicated in the pathogenesis of the disorder.

Finally, gut microbiome dysbiosis can also impact brain function and behavior through alterations in metabolism. The gut microbiome is involved in the breakdown and utilization of nutrients, and changes in the gut microbiome can alter metabolic pathways, leading to changes in brain function and behavior. For example, studies have found that alterations in gut microbiome composition can lead to changes in the production of neurotransmitters, such as dopamine, which are involved in the regulation of mood, cognition, and behavior [19].

Overall, the relationship between schizophrenia and gut microbiome dysbiosis is a complex and dynamic one, with multiple potential mechanisms of interaction. While more research is needed to fully understand this relationship, the growing body of evidence suggests that the gut microbiome may play a critical role in the development and progression of schizophrenia, and may represent a promising target for novel treatment and prevention strategies.

However, it is important to note that gut microbiome dysbiosis is not the sole cause of schizophrenia and is likely to interact with other genetic, environmental, and lifestyle factors. Further research is needed to fully understand the role of the gut microbiome in the development of schizophrenia and to determine the most effective strategies for addressing gut microbiome dysbiosis in individuals with the disorder [20].

Gut microbial Dysbiosis: Gut microbiome dysbiosis refers to an imbalanced state of the gut microbiome, the collection of microorganisms living in the digestive tract. This imbalance can result in numerous negative effects on health and is associated with a growing number of diseases and conditions, including obesity, type 2 diabetes, inflammatory bowel disease, and psychiatric disorders. The gut microbiome is a complex and diverse ecosystem that is composed of trillions of microorganisms, including bacteria, viruses, fungi, and parasites. These microorganisms play a crucial role in maintaining overall health and wellness by helping to digest food, regulate the immune system, and produce various essential molecules such as vitamins and neurotransmitters[21].

Dysbiosis can occur due to a variety of factors, including diet, use of antibiotics, and exposure to toxins and pollutants. An unhealthy diet, for example, can lead to a decline in beneficial bacteria, an increase in harmful bacteria, and a shift in the overall composition of the microbiome. Antibiotic use can also disrupt the gut microbiome by killing both harmful and beneficial bacteria, leading to an imbalanced state. Additionally, exposure to toxins and pollutants can also harm the gut microbiome, causing dysbiosis and reducing its ability to maintain health. The effects of gut microbiome dysbiosis can be significant and far-reaching. For example, an imbalanced gut microbiome can result in increased inflammation, which is associated with a number of chronic diseases and conditions. Additionally, imbalanced gut microbiome can also lead to alterations in gut-brain communication, which can result in a number of neurological and psychiatric disorders, including depression and anxiety. Furthermore, gut microbiome dysbiosis can also lead to an increase in body weight and the development of obesity. This occurs because imbalanced gut microbiome can lead to changes in metabolism and the absorption of nutrients, resulting in increased fat storage and weight gain. Additionally, gut microbiome dysbiosis can also lead to insulin resistance, which is a major factor in the development of type 2 diabetes. To address gut microbiome dysbiosis, it is essential to adopt a healthy lifestyle that promotes a balanced gut microbiome [22]. This includes eating a diet rich in fiber and fermented foods, avoiding processed foods and antibiotics when possible, and reducing exposure to toxins and pollutants. Additionally, probiotics and prebiotics can be helpful in restoring balance to the gut microbiome. Probiotics are live microorganisms that can help to restore balance to the gut microbiome by increasing the number of beneficial bacteria. They are found in fermented foods, such as yogurt and kefir, and can also be taken in supplement form. Prebiotics, on the other hand, are non-digestible fibers that serve as food for beneficial bacteria, helping to promote their growth and maintain balance in the gut microbiome.

In conclusion, gut microbiome dysbiosis is a growing concern in modern society and is associated with a number of negative health outcomes. To address this issue, it is essential to adopt a healthy lifestyle that promotes a balanced gut microbiome, including a diet rich in fiber and fermented foods, reducing exposure to toxins and pollutants, and taking probiotics and prebiotics. With the right lifestyle changes, it is possible to promote gut health and prevent the negative effects of gut microbiome dysbiosis [23].

Autoimmune diseases and pathogenesis of gut microbiome: Human microbiota is composed of ~100 trillion microorganisms which include over 500 genera of most prevalent bacteria from two main phyla, namely Bacteroidetes and Firmicutes. The impact of gut microbiota dysbiosis and its linkage with pathogenesis of Autoimmune diseases is evident from increasing studies on human and murine models [24]. These studies support the effect of altered microbiota composition on several autoimmune diseases including multiple scelerosis, systemic seclerosis and inflammatory bowel disease etc. Despite many studies done of gut microbial dysbiosis and their linkage with autoimmune diseases, many scientists are not able to completely understand the association and mechanism of effect of these autoimmune diseases on gut microbiome. The manipulation and characterization of gut microbiome could represent an important therapeutic strategy for the improvement and restoration of microbial diversity to maintain normal immune system in different autoimmune diseases [25].

Autoimmune disorders have been triggered by disruption in gut microbiome. This disruption in the diversity of microbiota can also increase pathogenesis of disease. Several environmental effects e.g smoking, pesticides and heavy metals play a basic role in autoimmune disease pathogenesis. The gut microbiome is recently being identified that plays role in anti-inflammatory and immune deregulatory (dysbiosis) of gut microbiome. A change in immune hemeostatsis leads to the pre-dominace of effector Th1, Th17 lymphocytes and plasma cells which is an important component for the development of autoimmune disease states, dendritic cells and macrophage. This is critical for the connection between gut microbiota and the immune system where these antigen presenting cells can transport or exchange microbiota derived antigens in lumin. They also present to effectors T and B lymphocytes by activating it. Changes in gut microbiota profiles of individuals with a genetic predisposition can also lead to pathogenic autoimmune pro-inflammatory responses [26]. The induction and activation of Th17 by certain gut microbiota species (*Enterococcus gallinarum*, *Bifidobacterium adolescentis*, and *Prevotella copri*) is an example of pathologic sequelae. The effects of specific gut microbiota species on the immune system are context dependent [27].

The mono-colonization of *Akkermansia muciniphila* in humanized mice C57BL/6 mouse models hinders I the activation of follicular T helper cells and no activation of other immune cells.

Inoculation of same species in pathogenic free mice increases the activation of all phenotypes of CD4+ Th cells. Evidence from the previous studies linked up AIDS with gut microbiota. Many scientist suggests that alteration in gut microbial diversity rapid the chances of development of AIDs [28]. The translocation of *Enterococcus gallinarum* from gut to liver tissues produce autoimmune anti bodies and pro-inflammatory consequences in mono-colonized gnobiotic mice. This effect was prevented by the use of antibiotics and vaccines against mono-colonization of *E. gallinarum* [29].

The pathogenesis of one of the most critical autoimmune disease SLE is still not completely understood. Many environmental factors such as infections, chemicals, drugs, UV radiation , hormonal and genetics elements may trigger its development but also gut microbiome alteration is playing a potential role in disease induction. More casual experimental studies are required to know the mechanistic and casual effects of gut microbial diversity alteration and development of SLE on mouse and human subjects [30].

SLE patients have lower amount of important microbes from phyla firmicutes and bacteriodes, Increase in the abundance of lachnospiraceae and decrease in the colonies of lactobacillaceae. The patients of SLE show increases in *Ruminococcus gnavus* of Lachnospiraceae family and serum sCD14 with high level of fecal secretory IgA and calprotectic. Due to leaky gut, patients also have high levels of endotoxin lipopolysacharides, this study also suggests that chronic microbial translocation that also contribute to the development of SLE [31]. The experimental study on lupus-prone murine has shown the results of depletion of lactobacilli and increases in lachnospiraceae when compared with healthy controls. Addition of retinoic acid in to the diet of mice results in increase of lactobacillus colonization and also improved lupus disease symptoms. A comparison of gut microbiota between mice strains (NZB/W F1, MRL/lpr, and SNF1) and a cohort of SLE patients showed gut microbiota in different mouse models were more diverse as disease progressed, while the diversity was lower in SLE patients with active disease However, the exact role of either symbiotic or pathogenic microbes in this disease has yet to be elucidated [32] [33].

Asthma: The increase in asthma patients due to industrialization over the past several decades cannot be explained by genetic risk factors alone and also related to altered environmental exposures. Observational studies and molecular characterization of bacterial species in asthma patients in humans have identified *Proteobacteria* colonization to be the most prevalent phylum in patients with asthma compared with non-asthmatic controls across several studies. The *Proteobacteria* phylum is represented by potentially pathogenic bacteria, including those that belong to the genera *Haemophilus*, *Moraxella*, and *Neisseria* [34].

Type 1 diabetes (T1D): In humans, gut microbiota dysbiosis, including loss of bacterial diversity alteration, preceded the onset of metabolic symptoms associated with T1D. The recent findings from many studies include increased numbers of Bacteroides species, and deficiency of bacteria that produce SCFAs and produce the high amount of long chain fatty acids in cases of T1D. Specifically, the butyrate producer *Faecalibacterium prausnitzii* has been found to be decreased in abundance in children and adults with diabetes-related autoantibodies [35].

Gut microbial diversity dysbiosis with antibiotics: Gut microbiota diversity and host immunity are influenced by dietary factors and the gut environment. In mammals, the gut microbiome has established an interdependent relationship with metabolism and nutrition. This relationship has been recognized as crucial in the fight against infectious diseases. However, recent studies on the impact of antibiotics on the gut microbiome have raised questions about its potential dysbiosis. The severity of microbial community disruption in the gut varies with different antibiotics. This has spotlighted the need for gut microbiome restoration, particularly due to the adverse effects of antibiotics, which require proper care and time to recover. The gut is the largest reservoir of microbes, but the identification of bacterial species using conventional culture techniques is limited, with anaerobic bacteria being particularly difficult to culture. Recent advancements in culturing techniques, metagenomics, and proteomics have opened up new avenues for the study of bacterial community composition, function, and restoration in the context of antibiotics [36]. The gut microbiome also comprises fungi, phages, viruses, and protozoa, which contribute to gut homeostasis. The five major bacterial phyla in the gut are Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, and Verrucomicrobia, accounting for over 90% of the total gut bacterial population. These microbial species inhabit different segments of the gut and perform diverse tasks, such as regulating the immune system, aiding in digestion and food utilization, and synthesizing essential amino acids. Antibiotics are widely used to combat pathogenic diseases and are synthesized from various natural substances. However, excessive use of antibiotics has resulted in gut microbiome dysbiosis, causing neurological and chronic diseases like depression, autism, diabetes, inflammatory bowel disease, arthritis, and superinfections in critically ill patients. Antibiotics can directly or indirectly impact gut microbiota, with direct effects being the depletion of pathogenic bacteria and indirect effects being the disruption of commensal bacteria [37]. The impact of antibiotic combinations on the gut microbiome varies, with vancomycin decreasing fecal microbial diversity and the number of gram-positive bacteria from the *Firmicutes* phylum. A combination of ampicillin, gentamycin, and neomycin reduces the number of beneficial bacteria in the gut and shifts the gut microbiome composition. To understand the effect of antibiotics on the gut microbiome and host health, the relationship between antibiotics and specific gut bacteria needs to be studied. The increased use of antibiotics has led to the rapid dissemination of antibiotic-resistant genes, as sensitive strains are eliminated, giving antibiotic-resistant strains a growth advantage. Horizontally transferred antibiotic resistance genes account for approximately 6% of all resistance genes, which is 4.8% higher than the transmission of antimicrobial peptide resistance genes. Antibiotics also alter host cell metabolism and signal transduction, with epithelial and immune cells being particularly affected [38]. Depletion of commensal bacteria from the gut results in reduced fiber fermentation, leading to less production of short-chain fatty acids in the large intestine and increased risk of inflammatory diseases [39]. Antibiotic-induced changes in amino acid production and increased proline levels in the gut can also negatively impact Clostridium difficile [40]. Gut microbes communicate with the host through host pattern recognition receptors, and depletion of gram-negative bacteria from the gut reduces host-microbe interaction by inactivating these receptors. Vancomycin is known to cause this depletion of commensal bacteria from the gut microbiome [41]. Antibiotic disruption also affects group 3 innate lymphoid cell recruitment and development, reducing IL-22 production and making the host more susceptible to invading pathogens [42] [43]. Strategies to reduce gut microbial diversity disruption by antibiotics include microbiological examination and meta-analysis studies, which have involved 12 countries and 6,708 patients [44].

CONCLUSION

In conclusion, gut microbiome dysbiosis has been shown to play a significant role in the development and up-regulation of chronic and psychiatric diseases. Research has established a strong correlation between gut microbiome imbalances and various health conditions, including obesity, diabetes, depression, and anxiety. However, more research is needed to fully understand the mechanisms behind these correlations and to develop effective treatments that target the gut microbiome. Nevertheless, the findings to date suggest that gut microbiome health should be considered an important aspect of overall health and wellness, and that further research in this area is of significant importance.

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