

A Review of Human Microbiomes on the Regulation of Body's Hidden Ecosystem



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Abstract

Trillions of bacteria live in and on the human body that makes up the human microbiome, which is a key factor in determining both human health and disease. A diverse collection of bacteria, viruses, fungi, and other microbes that cohabit with their host is known as the human microbiome. Although it can be found throughout the body, it is primarily found in the colon. This intricate ecology is essential for functions including immunity, metabolism, and digestion. For example, bacteria in the colon contribute to the production of vital vitamins, the breakdown of complex carbohydrates, and the defense against infections. Studies have demonstrated the connection between dysbiosis, or an imbalance in the microbiome's composition, and several illnesses, such as inflammatory bowel disease, diabetes, obesity, and allergies. Technological developments, especially high-throughput DNA sequencing, have completely changed our capacity to research the microbiome. This review demonstrates how lifestyle, environmental, and genetic variables interact to shape each person's distinct microbiome. This knowledge has enormous potential for adjusting dietary and medicinal therapies according to a person's microbiome profile. In summary, the human

microbiome exerts a profound influence on health and is implicated in the pathogenesis of various diseases.

Keywords: Microbiome, Human Health, Dysbiosis, Metabolism

Introduction

Unlike the word "microbiota," which refers to the microbial population, "microbiome" refers to the total quantity of microorganisms and their genetic material present in the body's many ecosystems. There are 100 trillion microorganisms on the average person ten times more than the cells in the gut throughout the human body; hence, the fungus and commensal bacteria that live there are much surpass the number of human cells. The quantity and diversity of bacteria increases dramatically from the gastrointestinal tract's proximal to distal region, bulk of the gut flora being stored in the colon. Despite the widespread belief that these microorganisms only live on our skin, stomach and mucous membranes, it has developed into more and more obvious that our microbiome is essential to our health and well being (Korra, Y, et al.2022). Over millennia, the human microbiome has coevolved with humans, with the emergence of distinct microbial populations occupying distinct anatomical niches inside the body of a person (Afanas'ev, I. (2014). Microbial ecology of humans and macroscopic ecology share a lot of similarities that support the intellectual comprehension inside the microbiome. In line with expectations specific plant and animal species on various tropical beaches, comparable microbial ecologies in particular anatomical regions that will be shared by several Individuals because, despite

Significance | Understanding Disease Mechanisms and Potential Therapeutic Interventions

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Editor Md Asaduzzaman Shishir. And accepted by the Editorial Board Dec 02, 2023 (received for review Nov 09, 2023)

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Please cite this article:

Sayed UI Alam Shibly 1, Debananda S Ningthoujam. (2023). A Review of Human Microbiomes on the Regulation of Body's Hidden Ecosystem, *Microbial Bioactives*, 6(1), 1-10, 9374

their differences, microecosystems (such as the preponderance of firmicutes and Bacteroidetes in the colon and proteobacteria and Firmicutes in the oral cavity). (Sharma et al,2021).

All living things that make up the microbiome, which includes bacteria, fungus, algae, tiny protists, and archaea, are referred to as the microbiota. One of the most contentious additions to the description of a microbiome is the inclusion of viruses, phages, and mobile genetic components among its member (Corral et al,2020). Since then, though, the term "microbiome" has been expanded to include not just the community of microbes but also the entire range of chemicals that these organisms make, including their structural components, metabolites, and molecules that are produced by the coexisting host. Numerous host-related and environmental variables affect the makeup of the human microbiome. Genetics (Goodrich et al., 2014), age (O'Toole & Jeffery, 2015), immune system performance (Round & Mazmanian, 2009), and general health (Cho & Blaser, 2012) are host-related variables. Diet (David et al., 2014), antibiotic usage (Dethlefsen & Relman, 2011), hygiene habits (Biedermann et al., 2017), and exposure to outside microbes (Huttenhower et al., 2012) are examples of environmental influences. Microbes usually do best in conditions that are favorable to them. It follows that these microbes should possess methods for adjusting to human microbiome settings that mimic their ideal native habitat. Many environmental variables influence the variety and quantity of microbes at different places throughout the body, including temperature, pH, oxygen concentration, pressure, osmolarity, and nutrition supply. For example, the temperature of human bodies is ideal for harboring a wide variety of microorganisms. Other elements, such the availability of nutrition sources like sebum, alter the pH of the skin and serve as a source of carbon, which promotes the growth of specific microbial populations (Youn et al,2016).

Both internal and external variables influence the human microbiota's variety and quantity. As was previously said, intrinsic aspects include the characteristics of the bodily ecosystems since certain microorganisms may grow more easily in these habitats according to their physiology. Hereditary, ethnic, gender, and age characteristics are other fundamental factors that influence the composition of the microbiome. Once the microbe has acclimated to the environment, the human microbiome is often resistant and stable. Extrinsic variables including nutrition, lifestyle, medicine, geographic location, climate, and seasonality can alter the microbial population in addition to intrinsic factors that may induce a shift in the microbiome over time. Furthermore, it has been demonstrated that the technique of delivery during birth affects the microbiota. For instance, babies born vaginally have a distinct dominant gut microbiota group than babies born Caesarean. But by the time a child is three years old, their gut

microbiome has changed to resemble an adult's (Manary et al,2012). The gut's capacity to break down food and absorb nutrients varies in individuals over the age of 70, which has an impact on the gut microbiome's makeup. Because older persons have lower immune function, they are more vulnerable to infections, which affects the core microbiome and causes alterations in the entire microbiome. Bifidobacterium species activate the immune system and metabolic processes, a decline in Bifidobacteria in elderly persons may lead to malnourishment and a low level of systemic inflammation (Schiffrin et al,2008).

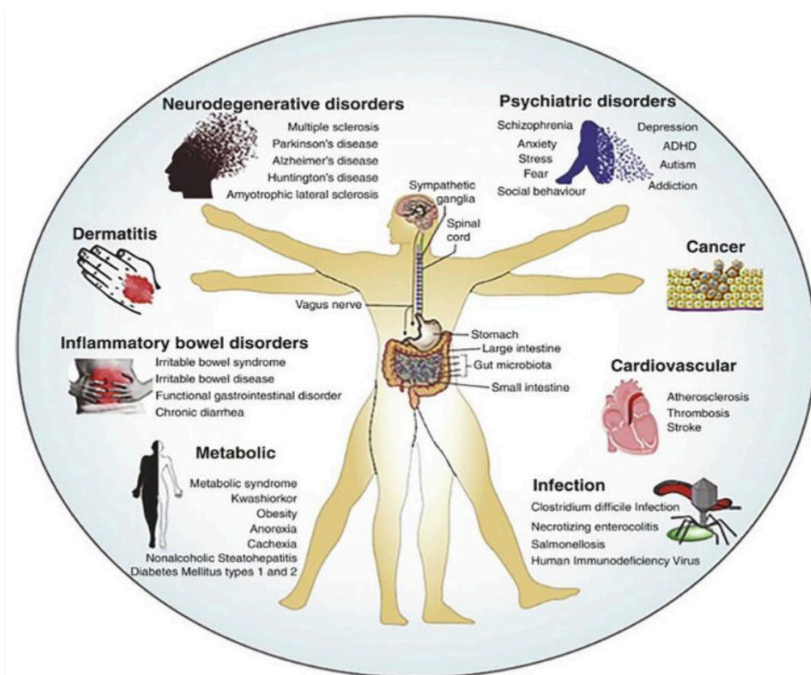
Microbiome and Health

The human gut microbiome is a complex and dynamic ecosystem of microorganisms inhabiting the gastrointestinal tract. This intricate community, comprising bacteria, viruses, fungi, and other microorganisms, plays a pivotal role in maintaining overall health and well-being. When in a balanced state, the gut microbiome performs a number of vital roles that are vital to human health. Its function in nutrition metabolism and digestion is among the most notable of them. Human enzymes would not be able to break down complex carbs without the help of the gut microbiota. Additionally, it aids in the fermentation of these carbohydrates, which results in the absorption and use of short-chain fatty acids (SCFAs) as an energy source. Furthermore, this microbial population produces vital vitamins, including biotin, vitamin K, and B vitamins (B2, B5, and B12), which are necessary for a number of physiological processes (Sonnenburg & Bäckhed, 2016). Immune system modulation is another essential role of a healthy gut microbiota. It serves as a crucial go-between for the immune system and the outside world, guiding and controlling immunological reactions. The ability to differentiate between potentially harmful microbes and commensal, benign microorganisms depends on this education. The immune system's development and regulation are greatly aided by the gut microbiome, which is also essential for immunological tolerance and response (Belkaid & Hand, 2014). In addition, the intriguing idea of the gut-brain axis—a bidirectional communication pathway between the gut and the brain has been revealed by current study. This axis emphasizes how mood and behavior are impacted by gut microbiota. It has been discovered that the makeup and activity of microbes in the stomach affect neurological and psychological well-being. Thus, it is possible that the gut microbiota has a significant impact on mental health, opening up new possibilities for diagnosing and treating mood disorders (Table 1) (Cryan & Dinan, 2012).

An imbalance in the make-up and functionality of the gut microbiome is known as dysbiosis, and it can have serious effects on a person's health. Dysbiosis has far-reaching effects on many different facets of health. The development of gastrointestinal problems is one of the most obvious effects. Dysbiosis is closely

Table 1. Metabolites produced by gut microbiota and their functions

Metabolites	Functions
Bile acid metabolites; including deoxycholic acid (DCA) and lithocholic acid (LCA)	Regulate bile acid, cholesterol, lipid, glucose, and energy metabolism, show antimicrobial effects, and activate host nuclear receptors and cell signaling pathways.
Short-chain fatty acids (SCFAs) metabolites such as propionate and butyrate	Regulate food intake and insulin secretion, also aid in maintaining body weight
Branched-chain fatty acids (BCFA) including isobutyrate, isovalerate	Histone deacetylase (HDAC) inhibition, increased histone acetylation
Indole derivatives including indoxyl sulfate and indole-3-propionic acid (IPA)	IPA exhibits neuroprotective effects, acts as a powerful antioxidant, and regulates intestinal barrier function. Indoxyl sulfate is a uremic toxin that accumulates in the blood of individuals with impaired excretion system
Vitamins including thiamine (B1), riboflavin (B2), Niacin (B3), pyridoxine (B6), pantothenic acid (B5), biotin (B7), folate (B11-B9), cobalamin (B12), And menaquinone (K2)	Help in red blood cell formation, DNA replication, and repair, work as an enzymatic co-factor, and enhance immune functioning

**Figure 1.** Schematic diagram showing the microbiome implicated in a variety of disorder, including skin, metabolic, and cardiovascular disease, as well as cancer, infection, and neurodegenerative and psychiatric disorders

associated with diseases such as Inflammatory Bowel Disease (IBD) and Irritable Bowel Syndrome (IBS). Marchesi and Ravel (2015) state that alterations in the diversity and composition of microbes might worsen inflammation in the gut, which in turn can lead to the onset and advancement of these crippling conditions. Gut dysbiosis is closely linked to metabolic illnesses, specifically obesity and type 2 diabetes. Increased energy extraction from meals, which encourages excess energy storage and contributes to obesity, can result from an unbalanced gut microbiota. Moreover, dysbiosis might exacerbate metabolic dysfunction by causing inflammation and altering hormonal signaling (Cani & Van Hul, 2015). Interestingly, autoimmune disorders can develop as a result of dysbiosis. Immune tolerance can be lost as a result of modifications to the composition of the gut microbiome and its interactions with the immune system, which can result in diseases like lupus and rheumatoid arthritis (Figure 1) (Manfredo Vieira et al., 2018).

Microbiome and Disease

It is evident from the results of current epidemiological, physiological, and omics-based research—backed by cellular and animal experiments that intestinal microbiota plays an important part in both illness and health (Ding et al., 2019). Even while this field of study is still in its infancy, with less comprehension of the complex's functional properties intestinal microbiome, there have been some encouraging findings published and demonstrated a great deal of promise for changing the Pathophysiology of illnesses and available treatments (Ding et al, 2019). An altered gut microbiota has been linked to a number of serious human ailments, including obesity, diabetes, heart disease, cancer, hypertension, and IBD (Xu et al., 2019; Nie et al., 2019; Ding et al., 2019) have each been covered separately later in this assessment. An entity the variation in gut microbiota composition is referred to as "dysbiosis," which, as illustrates, is characterized in numerous disorders. It is a prevalent issue in the modern period because to bacterial antibiotics, dietary changes, and infections (Lindell et al., 2022). It's got been difficult to identify a suitable, healthy microbiota due to inter-individual variance in composition (Lloyd-Price et al, 2016). An equilibrium of gut microbiota is necessary for the coexistence of the microbiome and the host in a mutually advantageous partnership.

Obesity

Over the past forty years, the number of people worldwide who suffer from obesity has surpassed 650 million, which is six times the number that was recorded in the 1990s (Sørensen et al., 2022). The only way to justify that is to consume more calories with a decline in exercise (Pascale et al., 2019). Numerous other illnesses, like diabetes mellitus, heart disease and malignancies, according to Amin et al. (2019). Researchers are becoming increasingly interested in and focused on weight management and reduction.

Research on the relationship between gut bacteria and obesity is expanding and maybe helpful in treating obesity. Interestingly, the diet's impact on the composition of the gut microbiota has become a particular area of study. Regarding this, recent data from a number of human and mouse studies has shown suggesting variations in the makeup of the gut microbiota may be essential contribution to the onset of obesity (Davis, 2016). Obesity can be caused by a number of gut microbiota species known as the obesogenic gut microbiota, including Firmicutes, Clostridium (Cao), Lactococcus, Rhizobium, and Bacteroidetes as well as (Cao et al, 2019). Specifically, obesity-promoting gut microbiome may promote obesity by the production of SCFAs such butyrate, giving the host more energy and causing low-quality inflammation brought on by metabolites of the gut microbiota (Cao et al, 2019). Both genetic and epigenetic factors are involved in an important part in the relationship between the composition and the role of the gut microbiota in obesity and the creation of metabolic products. Various mechanisms have been proposed to explain the role of gut microbiota in the development of obesity. Gute Mikroben können die Oxidation von Fettsäuren reduzieren, indem sie die Aktivität von adenosin hemmen monophosphatekinase (AMPk) Diese Enzyme ist enthalten in Muskelfasern und Leber und fungiert als Zellkern energiemarker. Die Reduzierung von AMPk führt zu einer verringerten Oxidation of fatty acids and, as a consequence, a greater amount of fat accumulation. Durch die Auslöschung systematischer Entzündungen in den Darmbakterien can also cause obesity-related metabolic problems (Pindjakova et al., 2017).

Inflammatory bowel diseases

The incidence of inflammatory bowel disease has increased significantly in newly industrialized Asian countries, yet it is still a substantial disease with the largest frequency in western countries South America, Africa, and the Middle East (Kaplan and Ng, 2017). Additionally, it is crucial to investigate the precise etiology and the etiology of IBD. Significant progress has been made in determining how IBD has evolved over the past few years. The most important and advantageous therapeutic feature of this breakthrough was the discovery of gut microbiota as a important multipurpose inflammatory agent. Lately, The gut microbiota in the etiology of inflammatory bowel disease has been highlighted. Numerous lines of evidence point to the crucial component of the intestinal inflammation caused by the gut flora. Most research have shown a decline in the variety of gut microbiota in patients with IBD (Willing et al., 2010). The most significant indications of changed gut microbiota composition in IBD patients are significant reductions in Firmicutes and Proteobacteria. The decline in variety of patients with IBD had gut flora that was predominantly because there are less Firmicutes. A reduction in Clostridium leptum groups have been noted, especially F.

Prusnitzii between Firmicutes (Wang et al., 2014). When a biologically vulnerable changes in the gut microbiota have been linked to hosts involves abnormal immune reactions to the mucosa that lead to a range of extraintestinal and intestinal conditions, including IBS. Therefore, in order to restore immunological homeostasis. Currently, altering the gut microbiome is thought to have a possible treatment plan for individuals with IBD (Facciotti, 2022). Proteobacteria, which have been found to comprise the bulk of human pathogenic bacteria, are becoming more and more significant in IBD (Mukhopadhyaya et al., 2012). Evaluation microbiological diversity indicates an increase in the quantity of bacteria species from this phylum, suggesting a proactive involvement in causing persistent inflammation in IBD patients (Hold et al 2014).

Cardiovascular disease

Heart disease remains a major cause of death worldwide, despite the advancements in atherothrombosis prevention and therapy. It will continue to climb as a result of increased prevalence in nations with low and moderate incomes (Odutayo et al,2016) Within the etiology and development of the gut has also been affected by CVDs, mainly because reduced intestinal circulation resulting in intestinal barrier breakdown. Regulating the intestinal endothelial barrier is many mechanisms of a healthy, balanced gut microbiome (Sabatino and associates, 2015). The gut microbiota has been investigated recently as a potential risk factor for heart disease and stroke due to mounting data (Tang et al., 2017; Leustean et al., 2017).. New evidence has demonstrated believed there was a correlation between the creation of many metabolites from the gut microbiome and additionally promoted interference with the gut endothelium barrier's ability to function. Additionally, a crucial relationship between the quantity of the microbiota in the feces and the degree of intestinal patients with CVDs were shown to have permeability (Pasini et al, 2016) Conversely, individuals with bacterial DNA in the peripheral blood's plasma levels of were noticeably elevated in indicators of inflammation, especially extremely sensitive C-reactive amounts of protein and interleukin-6, in contrast to those who did not contain DNA from bacteria. Furthermore, coronary artery disease is associated with an increased abundance of Enterobacteriaceae and Streptococcus (Jie et al., 2017). People suffering from coronary artery disease have changed the most common bacterial species' populations so that comprise the gut microbiota, with Bacteroidetes declining in number as well as a rise in Firmicutes. N-oxide trimethylamine is a metabolite that contributes significantly to atherosclerosis and helps forecast the risk of cardiovascular disease (Ramírez-Macías et al.,2022).

Diabetes mellitus

Globally, diabetes mellitus has a substantial negative impact on people's health conditions. Risk factors for diabetes include things

like being overweight, having a bad diet, and having a family history of the disease. Considering the ongoing urbanization trend, dietary changes, and the rise in the number of unhealthy lifestyles, the increasing Diabetes incidence is a major global health issue. As stated by a approximately 463 million people worldwide reported having diabetes in 2019 and subsequent projections indicate that by 2045, the number more than 700 million people worldwide will have diabetes (Saeedi et al.,2019). Recent research has shown a strong correlation between changes in the gut microbiota's composition and the advancement of diabetes (Sender et al., 2016).. One of the primary determinants of the gut microbiota's makeup and an important contributing element to the onset of diabetes (Meijnikman et al.,2018). Considering that the growth and structure of the gut the availability of nutrients is essential for the microbiota crucial to show how metabolite synthesis is dependent on about food intake. It has been discovered that the composition of the microbiome altered when a low-fat, high-sugar diet was replaced with one high in fat and low in plant polysaccharides quite quickly (Turnbaugh et al., 2009). Human consumption habits have changed during the previous few decades, favoring fats over fibers, Due to current dietary practices, intestinal microbiome has also altered. Consequently, it was proposed that diabetes may be connected to the systemic changes in the gut microbiome (Sircana et al, 2018). The gut microbiota composition of participants with newly diagnosed type 1 diabetes differed from controls in the diabetes prevention and prediction (DIPP) research (Brown and others, 2011). It was discovered that mucin synthesis was brought on by bacteria that produced butyrate and lactate in the control group to maintain intestinal health. Conversely, mucin Non-butyrate generating lactate-utilizing bacteria that contribute to β -cell autoimmunity decreased production diabetes type 1 (Brown et al., 2011).Also, an increase in the occurrence of Akkermansia muciniphila has been observed to be inversely related to the probability of developing type 1 Diabetes (Hansen et al., 2012).

The Immune System and Microbiome Crosstalk

Research into the relationship between the human immune system and the microbiome a complex community of trillions of microorganisms living inside the body has become essential. This thorough assessment of the research dives deeply into the various functions that the microbiome plays in immune system control and explores how it might be used to avoid autoimmune illnesses. We will study the immune system's education by the microbiome, the impact of metabolites originating from the microbiota, and the involvement of the microbiome in gut-associated lymphoid tissues. We will also look at probiotics, prebiotics, fecal microbiota transplantation (FMT), and lifestyle changes as means of preventing autoimmune illnesses.

Role of the Microbiome in Immune System Regulation: Immune education is a key component of the microbiome's function in immune system regulation. The immune system receives essential training from early exposure to a wide variety of microbes, which helps it differentiate between benign and hazardous substances. An individual's later life sensitivity to allergies and autoimmune illnesses is greatly impacted by this training process. The gut microbiota is fundamentally responsible for generating intestinal immune responses and teaching the immune system in both health and illness, as demonstrated by groundbreaking research by Round and Mazmanian (2009). The immune system's maturity is aided by the microbiome, which makes this immunological education process an amazing example of symbiosis in action. Early exposure to a variety of microbial patterns aids in the immune system's ability to distinguish between self and non-self. The prevention of autoimmune responses—in which the body's own cells and tissues are mistakenly attacked by the immune system—is made possible by this education. Crucially, the development of immunological tolerance depends on the microbiome's capacity to affect immune cell growth and function, particularly in the gut. Such studies emphasize the importance of the microbiome as an early-life immune system instructor (Round & Mazmanian, 2009).

Microbiota-Derived Metabolites: Metabolites generated from the microbiota, specifically short-chain fatty acids (SCFAs), have become important players in the regulation of the immune system. When dietary fiber ferments, gut bacteria produce short chain fatty acids (SCFAs). Notably, three of the most well-known SCFAs with immunomodulatory qualities are butyrate, acetate, and propionate. These metabolites—particularly butyrate—are essential for stimulating regulatory T cells' (Tregs') differentiation, which is necessary to preserve immunological homeostasis. According to Arpaia et al. (2013), commensal bacterial metabolites such as SCFAs are essential for stimulating the production of peripheral regulatory T cells. Immune cells known as "Tregs" have a strong immunosuppressive ability. They aid in limiting overreactions of the immune system to both self and non-self antigens. Tregs are essential for sustaining immunity to self-antigens, averting autoimmunity, and reducing the body's reaction to benign environmental antigens, such as allergens. In this situation, the microbiota's SCFAs function as signals, aiding in Treg formation and activation and promoting immunological homeostasis in general.

Gut-Associated Lymphoid Tissues (GALT): The immune system's gut-associated lymphoid tissues (GALT) are an essential part. The microbiota has a significant impact on GALT formation and function. An imbalance in the composition of the gut microbiota known as dysbiosis can kick off aberrant immune responses, which may eventually result in the development of autoimmune

and inflammatory illnesses. The importance of the microbiota in maintaining adaptive immunological homeostasis and its possible participation in autoimmune disorders was highlighted by Honda and Littman (2016). The gastrointestinal tract's complex system of immunological tissues, known as the GALT, consists of isolated lymphoid follicles, mesenteric lymph nodes, and Peyer's patches. It is essential for coordinating immune responses and keeping an eye on the gut environment. Dysbiosis has the potential to upset the balance of the GALT, leading to inflammatory reactions, inflammation, and a distorted immune system. Numerous studies have connected the onset of autoimmune diseases such as inflammatory bowel disease (IBD), rheumatoid arthritis, and type 1 diabetes to changes in the composition of the gut microbiota.

Prevention of Autoimmune Disorders through Microbiome Interaction

Fecal Microbiota Transplantation (FMT): Fecal Microbiota Transplantation (FMT) has become well-known as a potentially effective method for microbial balance restoration and autoimmune condition symptom relief. During this process, the recipient's gut is given healthy donor microbiota, which successfully resets the gut microbiome and restores immunological equilibrium. FMT has demonstrated outstanding efficacy, especially in the management of recurrent *Clostridium difficile* infection (CDI), a bacterial infection resistant to antibiotics. According to Paramsothy et al. (2017), FMT dramatically decreased the inflammatory status in CDI patients, and favorable alterations in the metabolome and fecal microbiota were linked to increased immunity and a lower risk of recurrence. The ability of FMT to reestablish a diversified and well-balanced microbiota is what accounts for its efficacy; this microbiome can aid in immune modulation and prevent autoimmune reactions.

Probiotics and Prebiotics: There are encouraging options for the prevention of autoimmune illnesses with probiotics, which are live beneficial microorganisms, and prebiotics, which are indigestible substances that promote the growth of healthy gut flora. Certain probiotic strains have shown promise in regulating immune responses and slowing the development of several autoimmune diseases. The potential of probiotics in immunological control was highlighted by Vaghef-Mehrabany et al. (2014), who discovered that probiotic administration improved the inflammatory status in patients with rheumatoid arthritis. Beneficial bacterial strains like *Lactobacillus* and *Bifidobacterium*, which have a favorable effect on the composition of the gut microbiota, are frequently found in probiotic supplements. By improving immunological tolerance and balancing the microbiota, these probiotics may be able to stop autoimmune reactions.

Diet and Lifestyle Modifications: Lifestyle and dietary decisions have a big influence on the gut microbiome's makeup. A healthy microbiota is encouraged by a diet high in fruits, vegetables, and

dietary fiber, which also supports the growth of beneficial bacteria. Furthermore, because of their impact on the microbiota, regular exercise and stress reduction help maintain a well-regulated immune system. There is rising interest in the role that diet and lifestyle alterations have in regulating the immune system through interactions with the microbiome. The shifting ecosystem of the gut microbiota across age groups, settings, diets, and illnesses was covered by Rinninella et al. (2019). They highlighted the potential for dietary changes to affect the risk of autoimmune illnesses and stressed the significance of a balanced diet in maintaining a healthy gut microbiome. A healthy and diversified microbiota is promoted by consuming a diet high in fruits, vegetables, and fiber, which gives beneficial bacteria the nutrition they need. Additionally, stress reduction and physical activity enhance general health and may have a secondary influence on immunological control by influencing the microbiota. To sum up, the link between the immune system and the microbiome is complex and dynamic, with significant ramifications

The Role of Microbiome in Precision Medicine

A new age in healthcare has been brought about by precision medicine, which focuses on customized treatment plans that take into account a person's genetic and environmental makeup. The human microbiome, a dynamic population of microorganisms living within the human body, is becoming a key role in precision medicine. The goal of this thorough review is to examine how the microbiome has shaped the field of precision medicine, highlighting its enormous importance in comprehending health and investigating therapies that are customized to a person's microbial makeup.

Personalized Medicine and Microbiome Composition: The microbiome has become a crucial predictor of a person's health in recent years. Overall health is strongly correlated with having a diversified and balanced microbiome, while imbalances have been connected to a number of illnesses, such as mental health issues (Cryan & Dinan, 2012), inflammatory bowel disease (Sartor, 2008), and obesity (Turnbaugh et al., 2009). Thus, the composition of the microbiome functions as a crucial health indicator. Comprehending the complex relationship between microbiome makeup and genetic data is essential to the personalized therapy idea. Studies have demonstrated the significant impact of genetic variables on the organization and makeup of the microbiome (Goodrich et al., 2014). On the other hand, host gene expression can be influenced by the microbiome (Goodrich et al., 2016). Precision healthcare's incorporation of the microbiome is made possible by this reciprocal relationship. Technological developments in microbiome profiling—most notably, metagenomic sequencing have made it possible to forecast a person's propensity to develop particular diseases. Researchers can find microbial indicators and risk factors by examining the

microbiome; this presents a special chance for early intervention and the creation of customized preventive measures (Franzosa et al., 2015). Precision medicine is being reshaped in large part because of this predictive power.

Potential Interventions Based on an Individual's Microbiome:

Customizing food regimens is a particularly useful use of microbiome knowledge in precision medicine (Wu et al., 2011). Because the human microbiome reacts to food ingredients in a very personalized way, medical professionals can create dietary plans that promote the growth of good bacteria while suppressing harmful ones. This strategy is especially helpful for people who suffer from diseases like obesity and irritable bowel syndrome, where food is quite important. Precision medicine has seen a rise in the use of novel treatments, such as fecal microbiota transplantation (FMT) (Cammarota et al., 2019). Based on a patient's distinct microbial makeup, FMT, which entails transferring healthy donor germs to them, can be customized for each individual. FMT has demonstrated exceptional efficacy in treating ailments such as *Clostridium difficile* infection and shows promise in treating a wider range of illnesses. Pharmaceutical companies are increasingly focusing on the development of drugs targeting the microbiome (Shanahan, 2012). These medications can be tailored to an individual's microbial profile. The potential benefits are substantial, including enhanced drug efficacy and minimized side effects. This development is fundamental in achieving the goals of personalized healthcare.

A revolutionary era in healthcare is almost here thanks to the microbiome's significance in precision medicine. Beyond genetic influences, the future of personalized medicine will be greatly influenced by our ability to comprehend the complex interactions between the human genome and microbiome, as well as the composition of each individual's microbiome. Predictions regarding illness risk are made possible by the microbiome, which acts as a vital health indicator. Additionally, the ability to create customized interventions from dietary advice to medications and therapies aimed at the microbiome highlights the potential of the microbiome to improve health outcomes and lessen the burden of disease. The microbiome is expected to play a key role in the development of precision medicine as research in this area progresses, opening up new avenues for individualized treatment.

Future recommendation and challenges

The study of microbiomes has become essential to comprehending the function of the human microbiome in both health and illness. Numerous research projects and technological developments have paved the way for both encouraging suggestions and future difficulties. The creation of tailored microbiome treatments is one suggestion for the future, as noted in the research by Lloyd-Price et al. (2019) in "Strains, Functions and Dynamics in the Expanded Human Microbiome Project." The study highlights how highly

individualized the human microbiome is and how personalized medicines, such as fecal microbiota transplantation (FMT) or precision probiotics made to match each person's specific microbial makeup, have the potential to transform therapeutic approaches.

Another crucial suggestion is to monitor the microbiome continuously, as covered in a review by Gagnière et al. (2016) in "Gut Microbiota and Laparoscopic Surgery for Colorectal Cancer." It emphasizes how crucial it is to track the microbiome in real time in order to identify microbial alterations early on. Innovative, non-invasive monitoring techniques are essential for the future of healthcare related to the microbiome. As demonstrated by David et al. (2014)'s work, "Diet Rapidly and Reproducibly Alters the Human Gut Microbiome," dietary interventions have been the subject of substantial investigation and offer a promising recommendation. Nutritional recommendations that support a diverse and well-nourished microbial community can be developed as a result of an understanding of how nutrition affects the microbiome.

Future research will concentrate on how medications affect the microbiome, as demonstrated by the paper "Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome" by Shoaie et al. (2015). To reduce side effects and improve medication efficacy, this field of research advises having a thorough understanding of how the microbiota and drugs interact. As stated by Qin et al. (2012) in "A Human Gut Microbial Gene Catalogue Established by Metagenomic Sequencing," data integration is also crucial. In order to have a more thorough picture of human health, this advice highlights the necessity of having extensive databases and analytical tools that can integrate microbiome data with information on genetics, lifestyle, and environmental factors. There are many obstacles in the way of studying the human microbiome. According to Yatsunenکو et al. (2012)'s study, "Human Gut Microbiome Viewed across Age and Geography," microbiome heterogeneity is a major problem. There are significant individual variations in the makeup of microbes, making it challenging to develop general guidelines or solutions. Knights et al. (2011) discuss ethical and privacy concerns with microbiome data in their publication "Rethinking 'Enterotypes.'" The ethical use of microbiome data and the preservation of human privacy have become urgent concerns as data accessibility has increased. The study of Li et al. (2017) in "An Integrated Catalog of Reference Genes in the Human Gut Microbiome" highlights the intricacy of microbiome data processing. Advanced computational and bioinformatics techniques are needed to analyze data from the various microorganisms that make up the microbiome. It is difficult to validate clinical findings, as Khoruts and Sadowsky (2016) noted in "Understanding the Mechanisms of Faecal Microbiota

Transplantation." The safety and effectiveness of microbiome-based therapies must be confirmed by rigorous clinical trials, which can be a time- and resource-consuming procedure.

The International Scientific Association for Probiotics and Prebiotics (ISAPP) has addressed regulatory barriers as a major obstacle. Standardization is necessary as the regulatory frameworks for microbiome-based treatments and diagnostics continue to develop. Baquero and Nombela (2012) discuss patient acceptance and trust in microbiome-based methods in "The Microbiome as a Human Organ." It is difficult to persuade patients and healthcare professionals of the advantages of microbiome therapies because of the current skepticism and the relatively new nature of this subject. Baquero and Nombela (2012) discuss patient acceptance and trust in microbiome-based methods in "The Microbiome as a Human Organ." It is difficult to persuade patients and healthcare professionals of the advantages of microbiome therapies because of the current skepticism and the relatively new nature of this subject. Wu et al.'s (2021) work, "Longitudinal Analysis of Taxonomic and Functional Changes of Gut Microbiota in Patients with Cirrhosis," focuses on the long-term benefits of microbiome therapies. Long-term monitoring and research are required to comprehend the effects.

The intricate and crucial field of "Gut Microbiota, Metabolites and Host Immunity," reviewed by Rooks and Garrett (2016), is the interaction between the microbiome and the environment. More research is needed to determine how environmental influences affect the microbiome and, in turn, human health. In conclusion, there is a lot to be excited about in the field of microbiome research, which has much to offer. Numerous studies and papers that highlight the potential and complexity of the human microbiome have served as inspiration for the problems and recommendations listed below. Future studies and applications in the field of microbiome-related healthcare will be guided by these insights.

In summary, the human microbiome is critical to both the development of numerous diseases and our general state of health. This complex web of bacteria affects our immune system, digestion, and even mental health. Advances in our comprehension of the microbiome present opportunities for customized medicine and therapeutic approaches. Understanding the need of preserving a balanced microbiome is crucial for advancing human health and averting a variety of diseases. The intricate relationship between our microbiota and health will continue to be clarified by more research in this area, opening us new avenues for enhancing our wellbeing going forward.

Author Contributions

S.U.A.S. drafted the manuscript and made substantial contributions to the design of the study. D.S.N. reviewed and drafted the paper.

Acknowledgment

The authors are thankful to their university to support this study.

Competing financial interests

The author has no conflict of interest.

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