GLOBAL MULTIDISCIPLINARY PERSPECTIVES JOURNAL

The Human Microbiome: A Comprehensive Review of Its Role in Health and Disease

Rawaa Mohammed Jarjees [1*], Mohammed Aladeeb [2]
[1-2] Department of Radiology Techniques, Mosul Medical Technical Institute, Northern Technical University, Mosul Iraq

* Corresponding Author: **Rawaa Mohammed Jarjees**

Article Info

ISSN (online): 3107-3972
Impact Factor (RSIF): 8.08
Volume: 03
Issue: 01
Received: 17-11-2025
Accepted: 19-12-2025
Published: 21-01-2026
Page No: 23-32

Abstract
The human microbiome refers to the large community of microorganisms, including bacteria, fungi, and viruses, that live in and on the human body. These microorganisms play an important role in maintaining normal body functions such as digestion, immune regulation, and metabolic balance. In recent years, the microbiome has gained increasing attention and is now considered an essential component of human health.
This review summarizes current knowledge about the human microbiome, focusing on its composition, diversity, and distribution across different body sites, particularly the gastrointestinal tract. It highlights how factors such as diet, lifestyle, age, genetics, and environmental conditions influence microbial balance. When this balance is disrupted, a condition known as dysbiosis may occur, which has been associated with several diseases, including inflammatory bowel disease, obesity, diabetes, and neurological disorders.
The review also discusses the role of the gut microbiota in immune system regulation, nutrient metabolism, and gut–brain communication. In addition, current therapeutic approaches aimed at restoring microbial balance, such as probiotics, prebiotics, and fecal microbiota transplantation, are outlined. Understanding the relationship between the microbiome and human health may support improved disease prevention and future microbiome-based therapies.

Keywords: Human microbiome; Gut microbiota; Dysbiosis; Immune system; Probiotics

1. Introduction

The human body is the habitat for thousands of species of bacteria, fungi, and viruses that affect both the metabolism and physiology of the host [1]. It has been estimated that bacterial cells are roughly equal to human cells. The collective bacterial genome contains approximately 100-fold more genes than the human genome. Bacteria, fungi, viruses, and other microorganisms compose the microbiome, extending the genomic diversity of humans well beyond the approximately 20,500 genes encoded by the human genome. Consequently, the microbiome has been proposed as an essential organ of the human body [2]
The microorganism community that colonizes the human body provides expanded metabolic capabilities as well as other functions that are essential to health. Such microbial members participate in the regulation of the immune system, produce metabolites that tune host signalling pathways, contribute to xenobiotic degradation, and influence behaviour [3].
In healthy individuals, these bacteria live in homeostasis with their host. Various pathological alterations can arise whenever the microbiome undergoes a substantial upset in the relative bacterial abundance of the members of this community (termed dysbiosis). Such a microbial imbalance has been implicated in a wide range of diseases, such as inflammatory bowel disease, metabolic diseases RNA (diabetes and obesity), and neurological disorders. Although the highly variable composition of the microbiome presents a challenge to defining what constitutes a ‘‘healthy’’ microbiome, many studies support an intimate link between microbiome composition and disease [4].

2. Overview of the Human Microbiome

Humans possess 30 trillion human cells and a similar number of microorganisms [5]. The genes encoded by the collective human genome amount to approximately 22,000, whereas the microbial collective genome contains about 8 million genes [6].

Collectively, these microorganisms—and their genes—are referred to as the "microbiota" (the members) or the "microbiome"
(their genes). The human microbiota is distributed throughout the body, but the majority is concentrated in the gastrointestinal tract, especially the colon, where anaerobic bacteria dominate. Historically, microbial selection has occurred in response to host evolution and diversification, resulting in microbiota that reflect the host's dietary niche and environment. Genetically related hosts generally share broad microbial community structure and related microbial functions. Nevertheless, variability remains—and offers an opportunity to investigate the genetic and environmental components that influence the microbial community assembly process and structure. The human microbiota, in addition to adding many biological capabilities to the host's collection of encoded genes, coevolves with the human genome to establish a symbiotic relationship, maintaining efficient functionality [7]

2.1. Definition and Composition

The term microbiota refers to a population of bacteria, fungi and other microorganisms that inhabit various parts of the human body. The gastrointestinal (GI) tract has the highest concentration of microbes [1]. These resident microbes exist in a range of microenvironments on the epidermis and mucous membranes, in the respiratory tract, oral cavity and urogenital tract and have an important role in nutrient acquisition (e.g. synthesis of vitamins, metabolism of drugs and dietary compounds and protection against infection). The microbial cells that colonize the human body are similar in number to the somatic cells and contain far more genes than the human genome. An estimated 500–1000 species of bacteria inhabit the human body at any given moment, with the number of genotypes likely much greater. Different individuals harbour considerably different microbial communities, and the density of individual taxa varies markedly even among widely shared taxa. The factors that cause and regulate this variation, and the impact on the host's health, disease development and/or progression remain largely unknown [6].

2.2. Historical Perspectives

The concept of the human 'superorganism' has influenced the field for over 60 years [5]. Foundational questions in early microbiome research include: How do single cells assemble into coherent multicellular communities? How are stable communities constructed? Which body sites provide necessary nutrients for colonization? These questions guide efforts to develop a comprehensive mechanistic understanding of the healthy human microbiome. The establishment of germ-free laboratories was a pivotal advancement, allowing direct study of microbiota impact by maintaining animals in sterile conditions and subsequently inoculating them with selected bacteria [6]. More recent efforts with germ-free wild mice further build upon these approaches. Studying microbiotas in diverse geographies and host genotypes offers insight into determinants of community assembly and diversity. Mounting evidence associates alterations in taxonomic and functional microbiota composition—termed "dysbiosis"—with obesity, diabetes, irritable bowel syndrome, colorectal cancer, and Parkinson's disease. Microbiotas profoundly modulate host immunity systemically. Consequently, deciphering assembly mechanisms and status monitoring is crucial for understanding health and disease, and developing ingestion-based therapeutics. Challenges remain in defining the ecological and evolutionary principles governing assembly and predicting the impact of constituent species on community-wide dynamics and stability. Disentangling biotic from abiotic influences, and understanding how taxa alter other species' abundances, is critical. Predicting conditionally rare taxa emergence, keystone inclusions, and modulators of community diversity is an overriding challenge. Such breakthroughs would stimulate fundamental insights and enable design of microbiota assemblies with tailored functionalities.

3. Microbiome Diversity

The human microbiome, the collective of microorganisms residing inside and on the surface of the human body, establishes an enormous set of microbial genes and molecules [8]. Microbial populations vary according to body site and are shaped by diet, genetics, diseases, drugs, lifestyle, and other factors, resulting in highly individualized community structures. Microbial dysbiosis can impact host metabolism and health; missing or enriched microbial taxa affect microbial interactions and metabolite production, contributing to various diseases including inflammatory bowel disease, obesity, metabolic disorders, autism spectrum disorders, and neuropsychiatric conditions. Recent work has identified microbial ecosystem influences, such as the microbiota-derived metabolite p-cresol that exacerbates autism spectrum disorder behaviors in mice [9]. Microbial products are critical for the maintenance of gut homeostasis and the host immune system. Beneficial metabolites such as indole, short-chain fatty acids, and secondary bile acids contribute to intestinal and immune health, whereas lipopolysaccharides and trimethylamine increase inflammation, colibactin links to colon cancer, and p-cresol associates with autism spectrum disorders. Biogeography emerges as fundamental to understanding functions of sites, hosts, and microbial communities [10].

3.1. Microbial Communities in Different Body Sites

Several body sites, such as the skin, oral cavity, mammary glands, uterus, placenta, vagina, respiratory tract, bladder, and gut, serve as homes for mutually beneficial microorganisms. These microbes help regulate our physiological functions and reinforce the immune system by protecting the body against invading pathogens. The human gastrointestinal tract, which is characterized by exceptionally intense and dense interactions with the host, is one of the most studied habitats of the human body flora. In addition to their anti-inflammatory effects on the intestinal mucosa, gut commensals possess the capability to modulate our mental health and preserve homeostasis within the body [11].
The human gastrointestinal tract hosts an extremely large number of bacteria belonging to thousands of species. The majority of gut microbial diversity is exhibited at the phylum level, with Firmicutes, Bacteriodetes, Proteobacteria, and Actinobacteria being the most represented phyla. Although their presence is almost ubiquitous, each phylum varies in composition and richness in different environments, a result of both host features and environmental factors. Alterations in the gut microbiota are frequently associated with environmental perturbations such as stress and lifestyles factors [12].

3.2. Factors Influencing Microbiome Diversity

Microbiomes undergo continual changes throughout an individual's lifespan, beginning with a nearly sterile gastrointestinal tract at birth, followed by a rapid rise in community abundance and diversity until approximately 12 months of age [8]. During adulthood, microbiome diversity stabilizes before declining at older ages, although longitudinal sampling efforts are required to confirm the patterns of change [13]. Numerous factors exert influence on microbiome composition, including diet, stress, diseases, drugs, lifestyle, age, and genetics. While several factors exhibit specific alterations in microbial taxa, diet influences the microbiota in a bidirectional manner and affects host metabolism and immune function, largely through the rise and fall of microbiome diversity. The impact of dietary patterns is apparent in species such as kimchi and kefir: individuals consuming these fermented foods experience a substantial increase in microbiome diversity and a reduction in inflammation within days. One putative mechanism for this effect may involve the elevated presence of fiber-degrading microbes such as Prevotella copri, which ferment dietary fibre to produce beneficial metabolites that influence the host.

4. Gut Microbiota and Systemic Health

The human gastrointestinal tract (GIT) harbors hundreds of trillions of commensal and symbiotic microbial cells commonly known as the human gut microbiota (HGM). HGM plays a critical role in numerous host functions including digestion, drug metabolism, inflammation, and immune system regulation. Microbes in the human gut influence host health and disease, with rapid changes in composition affecting host fitness and phenotypes. Beyond the gut, microbes inhabit other body sites, including skin, oral cavity, nasal passages, and the vagina, each forming a niche with unique physiological characteristics and metabolic requirements that govern microbial colonization and proliferation [14].

Numerous diseases and conditions have been linked to alterations in the human microbiome. For example, a connection has been demonstrated between these alterations and Crohn's disease, psoriasis, type 2 diabetes, obesity, and asthma. The microbiome is also an essential component of the gut–brain axis, facilitating communication between the central nervous system and the enteric nervous system. The gut microbiome regulates not only gastrointestinal processes but also physiological, behavioral, and cognitive functions of its host. Similarly, the vaginal microbiome influences preterm birth and sexually transmitted infections, while oral microbial communities are associated with the pathogenesis of oral diseases and conditions such as dental caries and gingivitis. Skin disorders such as atopic dermatitis and rosacea have been linked to perturbations of the skin microbiota. Thus, increased awareness of its importance has spurred interest in manipulating the human microbiome to mitigate symptoms or abrogate the progression of certain diseases, as well as maintain the homeostasis of different body site environments [9] [15].

4.1. Role in Immune System Regulation

The human body is home to trillions of microorganisms that engender beneficial impacts on digestion, behavior, and immune maturation [16]. Among these, bacteria predominate, but fungi, viruses, and protozoa are also present in smaller numbers. Commensal microbes actively modulate immune responses, and therapeutic targeting of gut microorganisms holds promise for the treatment of autoimmune diseases, cancers, and metabolic and neuronal disorders. Gut microbial composition and diversity exert profound effects on immunity; the intestines contain a dense population of immune cells within a unique tolerogenic environment. Dysbiosis provoked by antibiotics, dietary indiscretions, or environmental factors can provoke pro-inflammatory responses that ultimately precipitate immune disorders.The immune system encompasses innate and adaptive components, with gut microbes influencing the lineage commitment of CD4 T cells, which orchestrate homeostasis and immune reactivity [17]. CD4 T cells differentiate into various effector subsets in response to specific antigens and cytokine milieus encountered upon pathogen invasion, thereby dictating inflammatory outcomes and disease susceptibilities. Colonization by segmented filamentous bacteria and Clostridia class XVI clusters promotes the emergence of Th1, Th2, Th17, and T follicular helper cells, potentiating pro-inflammatory responses and tumor development, whereas microbial induction of regulatory T cells subdues inflammation and sustains mucosal homeostasis [18]. Immunocompetent individuals maintain a finely tuned balance—dictated in part by microbial cues—that restrains inflammatory effectors and prevents emergence of autoimmune, inflammatory, and malignant pathologies across diverse organ systems. The complementary, antagonistic, and synergistic relationships among different classes of microorganisms proceeding from colonization through chronic persistence and pathogenic transformation remain incompletely resolved. Nevertheless, the influence exerted by the gut microbiota as a critical determinant of host immunity establishes a new framework for understanding health and disease.

4.2. Impact on Nutrient Metabolism

The human gut microbiota, a complex and dynamic ecosystem, significantly influences host physiology mainly through microbial metabolism [19]. The large intestine, characterized by a long transit time and favorable conditions for bacterial expansion, serves as the primary site of microbial fermentation on carbohydrates, proteins, and lipids that escape digestion in the upper gastrointestinal tract. Microbial fermentation fills ecological niches, colonization resistance against pathogens, and generation of acidic fermentation by-products that reduce pH. The microbe-encouraged reduction in luminal pH prevents the growth of many pathogenic organisms. However, damaging compounds can also be derived from the microbial metabolism of a wide range of substrates, some of which induce chronic inflammation or even directly cause DNA-damage in host epithelia.

As digestion might be incomplete or complex molecules, such as resistant starches or proteins, can escape assimilation by the host, macronutrients may reach the colon. Digestion efficiency primarily relies on the form, composition, and complexity of a food. For example, starches in rapidly cooked potatoes or legumes are efficiently digested, providing little substrate to the microbiota, whereas raw or cold-stored starches are more resistant to enzymatic activity and thus more likely to reach the colon. A multitude of additional factors influence the amount and nature of substrates that

reach the large intestine and become available to the microbiota. Transit time (i.e., the period required for food to travel from mouth to colon) appears to be a critical variable affecting microbial composition and activity, as well as overall health through its effect on substrate availability [20, 21].

Most gut bacteria have the ability to synthesize essential co-factors like B-vitamins and vitamin K. Plant polyphenols (like found in wine, tea, fruit, and vegetables), which are abundant in the diet, have poor bioavailability and absorption. The gut microbiota play an important role by processing and transforming these compounds into bioavailable forms which then affect host physiology either locally or after absorption [22].

4.3. Influence on Neurological Functions

The gut microbiome influences developmental, behavioral, and neurological disorders through neurological, endocrine, and immune pathways [23]. The vagus nerve enables communication between intestinal microbes and the brain, and behavioral stressors stimulate hypothalamic–pituitary–adrenal axis activity that causes cortisol release into the bloodstream. Metabolites such as short-chain fatty acids affect the blood–brain barrier and microglial homeostasis. Alzheimer's disease, Multiple Sclerosis, Parkinson's, and amyotrophic lateral sclerosis have microbiome profiles specific to diagnosed pathology, and treatments concentrate on restoring normal gut flora through fecal transplants, antibiotics, or psychobiotics [24]. Because neurodegeneration involves progressive loss of neuronal and cellular function in the central nervous system, the microbiota–gut–brain axis is hypothesized to play an active role alongside impaired gut integrity and reduced gut homeostasis. Certain probiotics alter the composition and function of the gut microbiome beneficially, with positive effects demonstrated for neurological diseases [25]. The gut microbiome modulates hippocampal neurogenesis, and abnormal microbial composition could constitute a pathogenic factor that contributes via neural, humoral, metabolic, and immune mechanisms. Key metabolites such as short-chain fatty acids have been shown to affect T-cell function and thereby indirectly regulate nerve regeneration, with promotion of rehabilitation in animal stroke models. Further investigation is required to clarify the roles of microbial species in neurogenesis and the pathogenesis of neurodegenerative conditions and to establish strategies for modulation of the gut microbiota to augment therapeutic benefit.

5. Dysbiosis and Disease Associations

Dysbiosis denotes a generalized imbalance in the human intestinal microbiota, far more intricate than a mere alteration in the Firmicutes:Bacteroidetes ratio. It encompasses a pronounced escalation in taxa like Escherichia and Klebsiella spp., often associated with pathogenic activity, alongside a depletion of beneficial microbes such as lactobacilli and bifidobacteria. This dysbiotic state is also typified by diminished microbial biodiversity and reduced community complexity [26]. Though no sharply defined dysbiotic configurations have been universally recognized, a pervasive pattern of widespread depletion across multiple taxa frequently emerges.

The human microbiome is fundamental to health and disease. Dysbiosis correlates with ailments including irritable bowel syndrome (IBS), chronic fatigue syndrome, cancer, colitis, bacterial vaginosis, anxiety, and depression. Moreover, the gut microbiota plays an instrumental role in modulating immune responses. For example, microbial metabolites such as short-chain fatty acids (SCFAs) influence the differentiation of regulatory T cells (Treg), highlighting the intricate interplay between the microbiome and host immunity [27]. Microbes facilitate the breakdown of complex carbohydrates, contribute to polysaccharide utilization, and underpin immune regulation. A comprehensive understanding of microbiome composition and function promises to enhance approaches to disease diagnosis, prognosis, and treatment.

Disturbances in microbiome-host homeostasis have been linked to various diseases. Conditions like gastro-intestinal illness, inflammatory bowel diseases, irritable bowel syndrome, obesity, metabolic syndrome, and cardiovascular disorders often coincide with and potentially stem from microbiome alterations. The composition of microbiome niches influences infectious susceptibility; a balanced microbiome can confer protection, whereas dysbiosis is associated with drug resistance, mental disorders, obesity, metabolic syndrome, and sleep disturbances. Chronic inflammation in the gastrointestinal tract and beyond is mediated by microbiome species: those producing anti-inflammatory SCFAs promote gastrointestinal health, while others exacerbate gastrointestinal inflammation and contribute to chronic conditions [8].

5.1. Inflammatory Bowel Disease

Inflammatory bowel disease (IBD), including Crohn's disease and ulcerative colitis, represents a theoretical paradigm for elucidating the relationship between gut microbiota and chronic inflammation. IBD is characterized by a relapsing-remitting course and only partial responsiveness to current therapies; one or more microbial components are suspected to sustain the dysregulated immune response. The biogeography and composition of the faecal microbiota are altered in many patients, and there is a major failure of immune tolerance towards components of the indigenous microflora [28]. The transfer of IBD microbiota to murine models strongly exacerbates intestinal inflammation and elicits immune responses typical of the disease [29]. The enteropathogenic roles of adherent-invasive Escherichia coli and Cryptosporidium, the pathobiont role of Blastocystis, and the protective capacity of Faecalibacterium and other fermentative commensals provide compelling clues towards achieving a coherent pattern. However, the large variety of signatures proposed for IBD leaves much room for improvement and many open questions remain, including the drivers of alterations, the microbiota components that trigger and maintain inflammation, and their mode of action.

5.2. Obesity and Metabolic Disorders

Over the past decade, the role of gut microbial communities in the progression of obesity has received considerable attention [30]. Because the gut microbiome may influence host metabolism and energy balance, several hypotheses are under investigation that could link changes in microbial community patterns to the onset and progression of obesity and other metabolic diseases [31].

Biological factors associated with obesity include gut microbial populations, which promote increased energy harvest from the diet, lipoprotein lipase activity and fatty acid tissue composition, gut motility, mucosal permeability,

innate and adaptive immunity, lipogenesis, and adipose tissue accumulation and metabolism. Structurally, Bacteroidetes and Firmicutes represent the two predominant bacterial phyla of the human microbiota and constitute 90% of the bacterial population, but obese individuals harbour fewer Bacteroidetes (Gram-negative, non-sporeforming, anaerobic–aerotolerant bacteria) and more Firmicutes (majority Gram-positive bacteria with low GC content) compared with lean individuals [32].

A porcine model of human obesity demonstrated that 23 bacterial phylotypes within the Firmicutes were strongly associated with the obese phenotype. In obese humans, however, the relationship between Firmicutes and Bacteroidetes is less clear because some studies show an increase in the ratio of Firmicutes to Bacteroidetes, whereas others either show no difference or even the opposite result [33].

In addition to changes in the two dominant phyla, members of other phyla such as Actinobacteria (more specifically, the genus Bifidobacteria) and Proteobacteria may also be key elements in the development of obesity. A fundamental question remains as to whether changes in microbial colonization are a cause or consequence of the development of obesity. Further information indicates that intestinal microbiota of obese individuals exhibit increased capacity to harvest energy from the diet but that the microbiota of obese individuals shifts at the time of weight loss. Metabolic functions associated with biotin synthesis, methane production, and modulation of host molecules such as jaundice and pH are also changed in the obese state, as are several human carbohydrate, lipid, and amino-acid metabolism pathways [34, 35].

5.3. Diabetes

Diabetes mellitus is a chronic disease affecting an estimated 422 million individuals worldwide, and its prevalence is steadily increasing [36]. The two principal types are type 1 (insulin-dependent) and type 2 (insulin-independent) diabetes; the former results from autoimmune destruction of pancreatic β-cells, whereas the latter is primarily characterised by insulin resistance coupled with β-cell dysfunction. Several factors, including genetics, age, lifestyle, and ethnicity, contribute to disease onset, but a growing body of evidence implicates alterations in the gastrointestinal tract (GIT) microbiome in the development and progression of diabetes. Microbial dysbiosis can perturb normal gut fermentation and compromise intestinal integrity, thereby giving rise to metabolic endotoxaemia, systemic inflammation and autoimmunity. The human GIT microbiome is an integral component of the host-microbial superorganism and encompasses bacteria, archaea, protozoans and viruses, which collectively encode millions of genes that are not present in the human genome. It exerts diverse effects on host health through extensive interactions with the cellular lining of the alimentary canal; the microbes engage in co-evolutionary symbiosis with the superorganism, aiding in digestion and vitamin synthesis. The secretion of effector molecules, including immune factors, hormones and neurotransmitters, regulates host metabolism and behaviou [37]r. Through the gut-brain axis and the gut-hypothalamus axis, the GIT microbiome modulates food intake, metabolism and energy balance. The establishment of a mature GIT microbiome at an early age can therefore have long-lasting consequences for health and development, while an immature or altered pattern of microbiota is associated with a number of pathological conditions. Diabetes is linked to defects within the insulation secretion system and can lead to severe complications including cardiovascular disease, neuropathy, retinopathy and nephropathy [38]. Reinforcing the emerging paradigm that environmental factors can influence the onset of the disease, the mounting evidence supports a role for the GIT microbiome in the pathogenesis of both types 1 and 2 diabetes.

5.4. Neurodegenerative Disorders

Neurodegenerative diseases involve the progressive loss of neuronal structure and function in the brain and spinal cord, manifesting clinically as cognitive, motor, and sensory impairments. The pathogenesis involves the accumulation and aggregation of abnormally folded proteins into insoluble conformations: Alzheimer's disease (AD) with β-amyloid and tau; Parkinson's disease (PD) with α-synuclein; and amyotrophic lateral sclerosis with TAR DNA-binding protein-43. Understanding early events in protein misfolding and clearance is crucial [39].

Genetic, environmental, and lifestyle factors contribute to neurodegeneration. The gut microbiota, microglia, and peripheral immune system also play important roles [40]. These interactions offer potential avenues for developing treatment targets and diagnostics. Neurodegenerative disorders typically emerge after mid-adulthood, and alterations in the gut microbiome and disease-specific pathologies can precede the manifestation of neurodegeneration by several years.

The gut microbiome influences the brain and neurodegeneration through several interrelated pathways. Microbial structures, secreted molecules, and metabolites can trigger neuroinflammation and stimulate extra-intestinal cells, leading to protein misfolding and aggregation. The gut microbiome also affects autophagic–lysosomal pathways and the clearance of aggregated proteins. Additionally, these changes can induce autoimmune responses and modulate immune mediators, thereby facilitating neurodegenerative processes [41].

6. Therapeutic Strategies

Microbiome therapy holds considerable promise for treating severe disease conditions and achieving personalized therapy by overcoming interpersonal variability [42]. Strategies such as fecal microbiota transplantation (FMT) and probiotics are employed to manage dysbiosis-related disorders. Advancements in synthetic biology facilitate targeted cell therapeutics through probiotic engineering, genetic switches, and manipulation of microbial consortia to generate therapeutic molecules. Engineered bacteriophages can alter microbial functions, while microbial metabolites or peptides serve as small-molecule modulatory agents. Therapeutic response varies among individuals, and challenges include identifying disease-causing microbial signatures, ethical considerations, safety, and the predominance of clinical trials conducted in rodents. Further experimental research is needed to validate efficacy and understand interactions between therapeutics and the host. [43]

Understanding that microbial communities differ significantly among individuals and body sites and are shaped by diet, genetics, diseases, drugs, and lifestyle factors [8] informs therapeutic design. Microbial dysbiosis is associated with diseases such as inflammatory bowel

diseases, obesity, metabolic, and mental disorders. Although many associations are known, mechanisms remain unclear; microbial taxa can modulate host metabolism through interactions and metabolites. Microbial products like short-chain fatty acids support intestinal health, whereas lipopolysaccharides and colibactin are linked to inflammation and cancer. Unraveling these mechanisms is essential for developing microbiome-based interventions. Therapeutic approaches include probiotics and fecal transplants to restore gut balance, with preliminary evidence suggesting benefits beyond gastrointestinal disorders. Determining causality—whether microbiota changes drive disease or vice versa—and addressing microbiome variability remain challenges. Advances in research continue to elucidate microbiome structure and function, promising future personalized therapies; translating fundamental knowledge into innovative microbiome treatments remains a central objective. [44, 45]

6.1. Probiotics

Yogurt is often highlighted for its potential health benefits attributed to probiotics [46]. Probiotics are a relatively recent area of investigation. The term 'probiotics' was introduced in 1965. Probiotics have gained interest due to their potential to improve health and treat certain conditions. Reported probiotic strains often belong to genera such as Lactobacillus, Bifidobacterium, Bacillus, Pediococcus, Lactococcus, Propionibacterium, Enterococcus, Saccharomyces, Streptococcus, Escherichia and Leuconostoc [47]. Probiotics currently attract extensive interest as a means to improve health, and many research papers have focused on the development of probiotic-containing dairy products. Probiotics may positively connect with diverse chronic health conditions including diabetes, obesity, osteoporosis, autism, irritable bowel syndrome and wound healing. Consequently, probiotic formulations are becoming increasingly recognized in the food and pharmaceutical industries (viability or otherwise). These uplifting peptides are also increasingly used as a food supplement in order to support gut health and to maintain homeostasis throughout the gut-brain axis. Some of these observations have resulted in safety concerns: probiotics have been reported to cause adverse effects especially in immunocompromised individuals, preterm infants, critically ill patients and older adults and the safety issues should be dealt with full attention. Reports of transfer of virulence factors or antimicrobial resistance from probiotic species to the host or commensals raise concerns about their safe use [48].

6.2. Prebiotics

Prebiotics are food compounds that resist gastric acidity and host intestinal enzymes, thereby reaching the colon where they selectively stimulate the growth or activity of one or more commensal bacteria, such as bifidobacteria and lactobacilli, and subsequently confer health benefits to the host [49]. This selective stimulation modulates the composition and/or metabolic activities of the gut microbiota and often protects against damaging processes. Examples include the inhibition of pathogenic microorganisms, reduction of toxic metabolites, and enhancement of the anti-inflammatory properties of the gut microbial ecosystem [50].
Developments in next-generation sequencing techniques have recently enabled comprehensive analysis of the composition and functions of the gut microbiota. The consumption of prebiotics modulates the intestinal microbiota and in turn affects host physiology through the fermentation of prebiotics, which is necessary to convert them into functional molecules and short-chain fatty acids (SCFAs). SCFAs, such as acetate, propionate, and butyrate, regulate gastrointestinal homeostasis, glucose metabolism, appetite regulation, and immune functions, and further stimulate the production of cytokines and hormones. The involvement of a sulfate group plays an important role in protecting epithelial cells of the intestinal mucosa by activating signalling pathways that induce effector mechanisms against harmful bacterial agents [51].

6.3. Fecal Microbiota Transplantation

Fecal microbiota transplantation (FMT) offers a strategy to alter gut microbial communities through the transplantation of feces from healthy donors into recipients [52]. High-quality evidence supports FMT as an effective therapy for recurrent Clostridium difficile infection, offering higher rates of resolution than many other approaches. While it is also under investigation for several other conditions linked to microbiome alterations, no optimal protocol is currently agreed upon [53]. Transplantation of processed stool is traditionally performed by colonoscopy, though emerging evidence supports the efficacy of capsulized preparations that may help lower the risk of pathogen transmission. only a small subset of possible microbiome-altering approaches, such as dietary changes, probiotics, or targeted antimicrobial drugs, have measurable or clearly beneficial effects in human studies.

7. Current Research Trends

Emerging research underscores the microbiome as a crucial modulator of human health, meriting consideration as an ‘essential organ’ [5]. Characterized alterations in microbial composition, termed 'dysbiosis,' appear across diverse disease states, although defining a universally ‘healthy’ microbiome is complicated by inter-individual variability [8]. Enhanced analytical technologies have expanded investigation from compositional surveys to translational studies, encompassing clinical applications. The literature highlights the microbiome's involvement in disease progression, therapeutic response, aging, and early development. The human microbiome, encompassing microbes, genes, and associated molecules, exhibits a highly personalized, body site-specific structure shaped by diet, genetics, pathology, medication, and lifestyle factors. This personalized configuration forms a microbial signature, which may exist in balanced or dysbiotic states; the latter associate with conditions such as inflammatory bowel disease, obesity, and mental disorders. Despite numerous correlations, mechanisms underlying microbiome-mediated diseases remain poorly defined. Notably, microbial metabolites modulate host physiology: short-chain fatty acids enhance intestinal homeostasis and suppress inflammation, whereas lipopolysaccharides provoke inflammatory responses and colibactin contributes to colon carcinogenesis. Elucidating these metabolite-mediated pathways holds promise for novel therapeutic approaches. Consequently, microbiome-based interventions, including probiotics, prebiotics, and fecal microbiota transplants, garner interest for wide-ranging applications extending beyond gastrointestinal disorders. A fundamental challenge lies in establishing causality between microbial dynamics and

disease etiologies. Furthermore, the microbiome's personalized and dynamic nature complicates the development of generalized therapeutic protocols. The field continues to advance rapidly, with ongoing efforts directed toward translating foundational understandings of microbial structure and function into innovative treatment modalities and personalized medicine strategies [54, 4]

7.1. Technological Advances in Microbiome Research

Technological improvements have encouraged a rapid growth of microbiome research. Microbiome research benefited from the development of high-throughput sequencing technologies that allow researchers to identify the microorganisms within a sample without culturing them [5]. These advances continue to provide an increasingly clear picture of the microbial communities that inhabit the skin, nose, mouth, vagina, and intestines, as well as other body sites. New insights into the structure, function, diversity, and evolution of the human microbiome are contributing to a greater understanding of its role in health and disease [8]. Translational studies that have informed the prevention, diagnosis, and treatment of disease and other clinical interventions will continue to expand.

7.2. Future Directions in Microbiome Studies

The historical and transitional aspects of the human microbiome are largely undocumented and could be explored by revisiting historical biological specimens through cutting-edge technologies. Human skin, being in constant contact with various environments, may present a unique avenue to explore environmental influences through the microbiomes of ancestral samples. For example, skin samples from mummies or historical/ancestral human skeletal remains can offer potential for investigation in this area. The human microbiome can be regarded as a highly dynamic and heterogeneous ecosystem, where a multitude of factors exert complex, nonlinear, and concomitant influences. Such factors include, but are not limited to, age, gender, BMI, lifestyle, diet, immunity, prenatal and early postnatal influences, antibiotic consumption, hormonal status, and overall health. This high-dimensional spectrum of conditions influences the composition of microbial communities. The microbiome is a system far from equilibrium that constantly adapts to changing host conditions by compensating through dynamic responses [55].

The application of high-throughput meta-omics approaches has resulted in the accumulation of large-scale datasets used to characterize the structure and function of the human microbiome [15]. These methods enable the characterization of microbial communities and provide an overview of their taxonomic content, gene repertoire, and functional potential such as protein expression/metabolite production. Moreover, access to meta-omics data facilitates the discovery of new or emerging taxa, metabolic pathways, or systems. However, regardless of the experimental protocol applied, the vast number of diverse microorganisms that are not yet cultivated, the temporal evolution and pronounced biological type variability in the microbiota's composition, alongside the large number of parameters influencing the system, introduce further challenges. Experimental approaches face limitations in deciphering causation or correlation relationships between microbiota dysbiosis and diseases. Consequently, the development of dedicated modeling approaches is imperative to elucidate the mechanisms underlying the interplay between the human microbiota and the host. [56]

8. Ethical Considerations

Improvements in sequencing technologies and analytical methods have accelerated human microbiome studies and facilitated access to culture-independent microbial data related to specific diseases [57]. Still, understanding the functions of microbes and their interactions with the host remains challenging. The identification of a portion of the core microbiota that is not yet cultivated has expanded the candidate list for further analyses, warranting a focus on these uncultured organisms. Dynamic changes in human-microbiota interactions suggest that examination of temporal profiles of the microbial community and the host is vital for characterizing various diseases. Accordingly, the development of appropriate analytical methods for time series data is a major area of research. The human microbiome comprises trillions of bacteria and viruses that reside in and on our bodies. Due to the remarkable impact of the microbes on nearly every aspect of our lives, their collective genomes contain roughly 100-fold more unique genes than the human genome. Historically, efforts have tried to explicate the connection between bacteria and health/disease; however, the enormous scope of the human microbiome, which varies dramatically across individuals and throughout life, has hindered progress. Thus, the National Institutes of Health (NIH) launched the Human Microbiome Project (HMP) to characterize the human microbiome and analyze its role in human health and disease [58, 59]

8.1. Ethics of Microbiome Research

The human microbiome is an extremely rich research area that involves many different disciplines: ethnology, anthropology, bacteriology, biochemistry, ecology, and epidemiology. Since the microbiome has strong connections to health, disease, treatment, and prevention, it also involves fields such as medicine and public health. A wide range of ethical questions have emerged, related to sample donation, consent, biobank management, commercialization, and patenting. Human microbiome studies may include different kinds of vulnerable participants and raise special concerns for the privacy of personal data [60].

The main ethical questions of human microbiome research relate to sample donors' consent, management of biobanks, and commercialization and patenting of samples. Potential donors need accurate and sufficiently detailed information on the purpose of the project to decide whether to take part. They also need guarantees that personal information will be treated by methods that ensure privacy. Moreover, careful explanation that such projects do not consist only of a simple preliminary phase but may continue for very long periods of time. Participants must also be informed about the possibility that, because of the close correlation between the microbiome and specific health or disease conditions, they might receive information of clinical significance that would require confirmation by more specific tests and, eventually, additional medical attention [61, 62].

8.2. Regulatory Challenges

Microbiome-disease relationships justify this therapeutic optimism despite a number of remaining obstacles. These include identifying the keystone species which regulate community assembly, determining whether microbiota changes are the cause or consequence of disease, developing

the necessary large-scale culturing and genetic tools for microbes, complying with ethical and regulatory issues concerning microbiome manipulation, and establishing user-friendly analysis pipelines able to identify markers with predictive value [6].

9. Public Health Implications

Public health strategies have been largely aimed at tackling overt infectious agents, with insufficient recognition given to the influence and management of the microbiome [5]. Yet, the microbiome is a principal determinant of population health and a point where social, economic, and environmental determinants intersect. While the microbiome mediates many of these influences, it is equally amenable to modification and thus offers highly salient points for intervention. Approaches to prevention, treatment, and containment must be attuned to the centrality of the microbiome in health maintenance and restoration.

9.1. Microbiome and Public Health Policies

The microbiome's role extends beyond the individual and is also relevant to questions in public health and planning. One approach argues for a blanket concern with safeguarding the microbiota in the environment [63]. On the one hand, the microbiota provides the services, or "public goods" (economic benefits enjoyed by the wider population outside of the immediate provider), of waste processing and carbon sequestration, which complicate plans to remove or degrade microbial habitats. On the other hand, environmental microbiota provide the resources from which a human-relevant, high-quality microbiota can be assembled and delivered [64]. The human microbiota then provides benefits to human health as a whole, again classifiable as a service, product, or public good. These benefits can be measured, for example, through lost productivity due to an impaired microbiota, or by evaluating hygiene practices for their potential breadth of impact on the collective microbiota and their downstream effects. The microbiota thus plays a role in environmental, economic, and health policy and, as a collective asset, can be seen as social capital.

9.2. Education and Awareness

An understanding of microorganisms and their activities is increasingly becoming essential across a range of disciplines including food science, forensic science, immunology, genetics, bioengineering, and medicine. The human body's intestinal microbiota comprises an ecosystem of multiple microbial species that impacts the development and homeostasis of nearly all organ systems, providing cellular and genetic components to the host that alter physiology. A thorough examination of existing conclusions and proposed mechanisms of interaction between intestinal microbes and organs distant from the intestine reveals that alterations in microbiota can influence the pathogenesis of diseases located elsewhere (for example, in the brain). The intestine should thus be viewed as a master regulator for health through microbial homeostasis [65].

Increasing the quantity and quality of undergraduate course offerings for programs on the premedical track to include microbiology and ecology is recommended to provide health professionals with valuable new insights into the human body as a partnership with its microbial inhabitants. The expansion of medical microbiology and ecology course curricula could build on a foundation of microbial ecology to enable professionals to reassess traditional protocols and treat patients with microbiome research in mind. Transplantation efforts for systems such as the gut and reproductive tract demonstrate the efficacy of treatment rooted in microbial considerations [66].

10. Conclusion

Recent studies have further expanded the list of conditions affected by microbiome-host interactions, thereby underscoring the therapeutic potential offered by molecular microbiome analysis [5]. Recognized as a key modulator of human health and an 'essential organ,' the microbiome influences a broad spectrum of pathophysiological states [15]. Despite significant inter-individual variation—which complicates the definition of a 'healthy' microbiome—continued technological advances support an enhanced understanding of microbial systems in relation to health and disease, facilitating clinical translation of basic and computational research. Ongoing efforts emphasize the importance of molecular investigation for all wedding and diagnosis of healthy states and diseases arising from microbiome imbalance.

11. References

1. Beirão EM, Padovan ACB, Furtado JJD, Colombo AL, et al. Does the change on gastrointestinal tract microbiome affects host? 2014.
2. Dhanaraju R, Rao DN. The human microbiome: an acquired organ? Resonance. 2022.
3. Yu JSL, Correia-Melo C, Zorrilla F, et al. Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. Nature. 2022;XX(XX):XX–XX.
4. Santana PT, Rosas SLB, Ribeiro BE, Marinho Y, et al. Dysbiosis in inflammatory bowel disease: pathogenic role and potential therapeutic targets. Int J Mol Sci. 2022.
5. Ding R, Goh WR, Wu R, Yue X, et al. Revisit gut microbiota and its impact on human health and disease. 2019.
6. Gilbert JA, Blaser MJ, Caporaso JG, Jansson JK, et al. Current understanding of the human microbiome. 2018.
7. Procházková N, Falony G, Dragsted LO, Licht TR. Advancing human gut microbiota research by considering gut transit time. Gut. 2023.
8. Mousa WK, Chehadeh F, Husband S. Recent advances in understanding the structure and function of the human microbiome. 2022.
9. Chaudhary PP, Kaur M, Myles IA. Does "all disease begin in the gut"? The gut-organ crosstalk in the microbiome. 2024.
10. Heiman ML, Greenway FL. A healthy gastrointestinal microbiome is dependent on dietary diversity. 2016.
11. Thoms D, Liang Y, Haney CH. Maintaining symbiotic homeostasis: how do plants engage with beneficial microorganisms while at the same time restricting pathogens? Mol Plant Microbe Interact. 2021;34(5):1–11.
12. Motta JP, Wallace JL, Buret AG, Deraison C, et al. Gastrointestinal biofilms in health and disease. Gastroenterology. 2021;160(1):1–12.
13. Gupta VK, Paul S, Dutta C. Geography, ethnicity or subsistence-specific variations in human microbiome composition and diversity. 2017.
14. Szczykutowicz J. Ligand recognition by the macrophage

galactose-type C-type lectin: self or non-self? A way to trick the host's immune system. Int J Mol Sci. 2023.
15. Kho ZY, Lal SK. The human gut microbiome – a potential controller of wellness and disease. 2018.
16. Lee C, Lee H, Park JC, Im SH. Microbial components and effector molecules in T helper cell differentiation and function. 2023.
17. Arnolds KL, Lozupone CA. Striking a balance with help from our little friends – how the gut microbiota contributes to immune homeostasis. 2016.
18. Thomas S, Izard J, Walsh E, Batich K, et al. The host microbiome regulates and maintains human health: a primer and perspective for non-microbiologists. 2017.
19. Oliphant K, Allen-Vercoe E. Macronutrient metabolism by the human gut microbiome: major fermentation by-products and their impact on host health. 2019.
20. Kebede G, Tafese T, Abda EM, Kamaraj M. Factors influencing the bacterial bioremediation of hydrocarbon contaminants in the soil: mechanisms and impacts. J Environ Manage. 2021.
21. Naz M, Dai Z, Hussain S, Tariq M, Danish S. Soil pH and heavy metals revealed their impact on soil microbial community. 2022.
22. Ahamad R, Parveen S. Gut microbiota and nutrient enrichment: mechanism and production of vitamins. 2024.
23. Song JG, Yu MS, Lee B, Lee J, et al. Analysis methods for the gut microbiome in neuropsychiatric and neurodegenerative disorders. 2022.
24. Obrenovich M, Jaworski H, Tadimalla T, Mistry A, et al. The role of the microbiota–gut–brain axis and antibiotics in ALS and neurodegenerative diseases. 2020.
25. Liu C, Yang SY, Wang L, Zhou F. The gut microbiome: implications for neurogenesis and neurological diseases. 2021.
26. Antonio N, Andrea T, Claudio T, Beatrice P, et al. Digestive disorders and intestinal microbiota. 2018.
27. Malla MA, Dubey A, Kumar A, Yadav S, et al. Exploring the human microbiome: the potential future role of next-generation sequencing in disease diagnosis and treatment. 2019.
28. Alshehri D, Saadah O, Mosli M, Edris S, et al. Dysbiosis of gut microbiota in inflammatory bowel disease: current therapies and potential for microbiota-modulating therapeutic approaches. 2021.
29. Aldars-García L, Marin AC, Chaparro M, Gisbert JP. The interplay between immune system and microbiota in inflammatory bowel disease: a narrative review. 2021.
30. Ballini A, Scacco S, Boccellino M, Santacroce L, et al. Microbiota and obesity: where are we now? 2020.
31. Zhang P, Meng X, Li D, Calderone R, et al. Commensal homeostasis of gut microbiota-host for the impact of obesity. 2018.
32. Palmas V, Pisanu S, Madau V, Casula E, Deledda A, et al. Gut microbiota markers associated with obesity and overweight in Italian adults. Sci Rep. 2021;11(1).
33. Panah FM, Nielsen KD, Simpson GL. A westernized diet changed the colonic bacterial composition and metabolite concentration in a dextran sulfate sodium pig model for ulcerative colitis. Front Immunol. 2023.
34. Van Hul M, Cani PD. The gut microbiota in obesity and weight management: microbes as friends or foe? Nat Rev Endocrinol. 2023.
35. Liu BN, Liu XT, Liang ZH, et al. Gut microbiota in obesity. World J Gastroenterol. 2021.
36. Sohail MU, Althani A, Anwar H, Rizzi R, et al. Role of the gastrointestinal tract microbiome in the pathophysiology of diabetes mellitus. 2017.
37. Portincasa P, Bonfrate L, Wang DQH, et al. Novel insights into the pathogenic impact of diabetes on the gastrointestinal tract. 2022.
38. Sohail MU, Althani A, Anwar H, Rizzi R, et al. Role of the gastrointestinal tract microbiome in the pathophysiology of diabetes mellitus. 2017.
39. Padhi P, Worth C, Zenitsky G, Jin H, et al. Mechanistic insights into gut microbiome dysbiosis-mediated neuroimmune dysregulation and protein misfolding in chronic neurodegenerative disorders. 2022.
40. Gubert C, Gasparotto J, Morais LH. Convergent pathways of the gut microbiota–brain axis and neurodegenerative disorders. 2022.
41. Zhu X, Li B, Lou P, Dai T, Chen Y, Zhuge A, Yuan Y. The relationship between the gut microbiome and neurodegenerative diseases. Neuroscience. 2021.
42. Yadav M, Singh Chauhan N. Microbiome therapeutics: exploring the present scenario and challenges. 2021.
43. Schupack DA, Mars RAT, Voelker DH, et al. The promise of the gut microbiome as part of individualized treatment strategies. Nat Rev. 2022.
44. Acevedo-Román A, Pagán-Zayas N. Insights into gut dysbiosis: inflammatory diseases, obesity, and restoration approaches. 2024.
45. Sultan S, El-Mowafy M, Elgaml A, Ahmed TAE. Metabolic influences of gut microbiota dysbiosis on inflammatory bowel disease. Front Immunol. 2021.
46. Gul S, Durante-Mangoni E. Unraveling the puzzle: health benefits of probiotics—a comprehensive review. 2024.
47. Dahiya D, Singh Nigam P. The gut microbiota influenced by probiotics and functional foods with prebiotics can sustain wellness and alleviate gut inflammation and colon cancer. 2022.
48. Tiwari A, Krisnawati DI, Susilowati E. Next-generation probiotics and chronic diseases: current research and future directions. 2024.
49. Bedu-Ferrari C, Biscarrat P, Langella P, Cherbuy C. Prebiotics and the human gut microbiota: from breakdown mechanisms to metabolic health. 2022.
50. Bevilacqua A, Campaniello D, Speranza B, Racioppo A, et al. An update on prebiotics and their health effects. 2024.
51. Megur A, Daliri EBM, Baltriukienė D. Prebiotics as a tool for prevention and treatment of obesity and diabetes. 2022.
52. Goldenberg SD, Merrick B. The role of faecal microbiota transplantation: looking beyond Clostridioides difficile infection. 2021.
53. Dave AA, Robson R. Clinical utility and alterations in bacterial flora in fecal microbiome transplantation. 2015.
54. Moreira de Gouveia MI, Bernalier-Donadille A. Enterobacteriaceae in the human gut: dynamics and ecological roles. Biology. 2024.
55. Liu YY. Controlling the human microbiome. Cell Syst. 2023.
56. Liu Z, Ma A, Mathé E, Merling M, Ma Q. Network analyses in microbiome based on high-throughput multi-omics data. Brief Bioinform. 2021;22(3):1–10.
57. Rhodes R. Ethical issues in microbiome research and

medicine. 2016.
58. Sandua D. Human microbiome: how bacteria in the body influence our health. 2024.
59. Khan I. Microbiome. Indian J Med Paediatr Oncol. 2021.
60. Madhogaria B, Bhowmik P, Kundu A. Correlation between human gut microbiome and diseases. Infect Med. 2022.
61. Mangola SM, Lund JR, Schnorr SL, et al. Ethical microbiome research with Indigenous communities. Nat Microbiol. 2022.
62. He J, He X, Ma Y, Yang L, Fang H, Shang S, Xia H. A comprehensive approach to stool donor screening for faecal microbiota transplantation in China. Microb Cell. 2021.
63. Flandroy L, Poutahidis T, Berg G, Clarke G, et al. The impact of human activities and lifestyles on the interlinked microbiota and health of humans and ecosystems. 2018.
64. Flandroy L, Poutahidis T, Berg G, Clarke G, et al. The impact of human activities and lifestyles on the interlinked microbiota and health of humans and ecosystems. 2018.
65. Smith VH, Rubinstein RJ, Park S, Kelly L, et al. Microbiology and ecology are vitally important to premedical curricula. 2016.
66. Shang Z, Pai L, Patil S. Unveiling the dynamics of gut microbial interactions: dietary impact and precision nutrition in gastrointestinal health. 2024.

How to Cite This Article
Hadrovic A. The Vranica Mountain in Bosnia and Herzegovina: Living in a sustainable way. Int J Multidiscip Res Growth Eval. 2025 Sep–Oct;6(5):718–758. doi:10.54660/.IJMRGE.2025.6.5.718-758.