A Metagenomic Insight into the human microbiome:Its Implication in Health and Disese

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***Abstract*—The human microbiome comprises a diverse and dynamic community of microorganisms, including bacteria, archaea, viruses, and fungi, that inhabit various anatomical sites of the human body. These microbial populations play a crucial role in maintaining physiological homeostasis by contributing to metabolic processes, immune system development, and protection against pathogenic organisms. Among different body habitats, the gastrointestinal tract hosts the most complex and densely populated microbial ecosystem, significantly influencing host health (1). Recent advances in metagenomics and high-throughput sequencing technologies have expanded our understanding of microbiome composition and its functional implications. The dominant microbial phyla, including Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria, vary across body sites such as the gut, skin, oral cavity, respiratory tract, and urogenital system. Alterations in the composition and diversity of these microbial communities, referred to as dysbiosis, have been strongly associated with the pathogenesis of numerous diseases, including inflammatory bowel disease, metabolic disorders, autoimmune conditions, skin diseases, and infections. This review provides a comprehensive overview of the human microbiome, focusing on its composition across different body sites and its role in maintaining health and contributing to disease development. Furthermore, it highlights emerging therapeutic strategies targeting the microbiome, including probiotics, prebiotics, and microbiota modulation, which hold promise for future clinical applications. (2)**

***Index Terms*—Human microbiome; Gut microbiota; Dysbiosis; Metagenomics; Probiotics; Microbial diversity; Human health; Disease association**

I. INTRODUCTION

The human microbiome is a complex aggregate of the microbes residing at various sites in the human body and consisting of communities of a variety of microorganisms including Eukaryotes, Archaea, Bacteria, and the virus that reside in the different body habitat including the skin, the oral cavity, respiratory tract, gastrointestinal tract, urinary tract, reproductive tract etc. (1). Microbiome is a term that describes the genome of all the microorganisms, symbiotic and pathogenic, living in and on all vertebrates. The gut microbiome is comprised of the collective genome of microbes inhabiting the gut including bacteria, archaea, viruses, and fungi. Information about these microbes living in our guts is growing at a tremendous rate. Till recently, heterogeneity among human populations was attributed to various allelic forms of genes. The human intestine harbors trillions of bacteria which constitute more genome than all the human cells in the body. The distribution of microbes is spatial in the gut, with the colon containing the largest diversity and abundance of microorganisms. The colon also harbors more aerobes than the small intestine, owing to its proximity to the environment. Due to the anaerobic nature of the majority of commensals, especially in the upper gut, it has been difficult to culture them. Advances in omics-based approaches have helped further the understanding of intestinal ecosystem and the multitude of factors that impact its microbial composition. This technology has opened many areas of research focused on the role of intestinal microbiota in immune system homeostasis that impact health and disease.[1] The human microbiome project initiated by the National Institutes of Health (NIH) in 2007 has identified microbiota at various surfaces of human body. The dominant phyla in humans include Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria, with the intestine being dominated by Firmicutes and Bacteroidetes. The colonization of the intestine begins at birth and has been shown to be influenced by vaginal or C-section

birth.[2] However, the microbiota changes with exposure to various environmental factors during maturation. Much like a genetic imprint of an individual, each individual has a unique microbiota, though approximately one-third of the species are common across most humans. Many factors influence intestinal microbiota including hygiene, diet, geographical locations, and host genotype. In addition, studies in humans and animals have suggested a role of sex hormones and age in determining the intestinal microbial composition. Humans have coevolved with the commensals and maintain a symbiotic relationship. Intestinal microbes out-compete the pathogens and maintain the integrity of the epithelium which may be a key factor in preventing inflammation. Diverse microbial communities are essential for maintaining the intestinal ecosystem and play a vital role in harvesting energy from foods and producing micronutrients. In return the microbes receive food and a suitable environment for growth. (2)

Metagenomics has increased the number of microorganism genomes that are mappable up to 85%, which means they can be prioritized for analysis. Based on a recent large-scale metagenomic study of the microbiome across different body sites in individuals with both Westernized and non-Westernized lifestyles, the diversity of the human microbiome has been estimated at 25 phyla, an average 2,000 genera and 5,000 species, and 316 million genes.

There are microbial community members that may be potentially crucial taxa, but which are not easily detectable with cutting-edge metagenomic approaches. For instance, host cells and their DNA in the samples analyzed can hinder the discovery of relevant microbial taxa. Often, eukaryotic microbes and viruses are under sampled by metagenomic protocols. This is the case, for example, with bacteriophages, as reproducible protocols for analyzing them using metagenomics have only recently emerged and are considered relevant colonizers of the human gastrointestinal tract. (4)

In this project we mainly focus on a role and their function on a human body and in this project, we collect or compile the all data about microbiome present all over body or part.

II. MATERIALS AND METHODS

Study Design

This study is a narrative review aimed at summarizing current knowledge on the human microbiome and its association with health and disease. The review focuses on microbial composition across different body sites and their functional roles in physiological and pathological conditions.

Literature Search Strategy

A comprehensive literature search was conducted using electronic databases including PubMed, Google Scholar, Scopus, and ScienceDirect. Relevant articles published between 2000 and 2026 were considered to ensure inclusion of both foundational and recent advances in microbiome research. The search was performed using combinations of keywords such as “human microbiome,” “gut microbiota,” “microbial diversity,” “dysbiosis,” “metagenomics,” “skin microbiome,” “oral microbiome,” and “microbiome in disease.”

Inclusion and Exclusion Criteria

Studies were selected based on their relevance to the topic. Inclusion criteria comprised:

- Peer-reviewed research articles and review papers
- Studies focusing on human microbiome composition and function
- Articles addressing the role of microbiome in health and disease

Exclusion criteria included:

- Non-English publications
- Conference abstracts without full text
- Studies with insufficient or unclear data Data

Extraction and Analysis

Relevant data from selected studies were systematically reviewed and categorized based on microbiome composition, body site distribution, functional roles, and disease associations. Key findings were compiled and synthesized to provide a structured understanding of the topic.

Methodological Approach

The review emphasizes findings obtained through advanced microbiological and molecular techniques, including

- 16S rRNA gene sequencing
- Whole-genome metagenomic sequencing
- Bioinformatics analysis for microbial diversity and functional profiling

These approaches have significantly improved the identification and characterization of microbial communities that are otherwise difficult to culture.

Gut Microbiomes [9][1]

The gut of the human is a natural habitat that harbors a large and dynamic population ofmicroorganism.The term 'gut microbiota' is used to describe the large collection of vari-ous microorganisms consisting the human gastrointestinal tract (GI tract) that includes the bacteria, archaea, virus, and eukarya. The gut microbiome com-prises this diverse community of diferent microorganisms which difer from each other depending upon their location along the length of GI tract (esophagus, stomach, the small and the large intestine with colon at the end) (Aragón et al. 2018). The microbial cell are more than 10 times the eukary-otic cells present in a human body with more than 100 trillion microbes pre-sent in the human gut alone. These organisms colonize different region of the human gut and influences many aspects of health. The stomach, along with the small intestine has presence of very few species of bacteria in comparison to large intestine that contains a more complex and highly dynamic ecosystem of microbes. The structure of the microbiota depends not only on location but also on a variety of factor such as age, diet, medication, sex, GI infection etc. Actinobacteria, Firmicutes, Bacteroidetes and Proteobacteria are four predominant major bacterial phyla found to be present in the human gut. The subdominant bacterial phyla that are found in the human gut are Fusobacteria and Verrucomicrobia. The microbial genera belonging to Bacteroides, Bifidobacterium, Eubacterium, Pepto streptococcus, Clostridium, Peptococcus and Ruminococcin are the principal microbes in the human gut, whereas aerobes and the facultative anaerobes namely Enterobacter, Klebsiella, Enterococcus, Lactobacillus, Escherichia, Proteus, etc. are some of the subdominant genera present in the gut of human.In the stomach and the small intestine, the most prevalent bacterial genera are Helicobacter, Streptococcus, Staphylococcus, Prevotella, Veilonella, Lactobacillus, Actinomyces, Rothia etc.. In addition to these bacterial genera, the human gut contains some other pathogenic bacteria like Campylobacter jejuni, Vibrio cholera, Salmonella enteric. There is also presence of various rare microbial taxa which are largely overlooked but can have a great impact on the human physiological functions. Oxalobacter formigenes is an example of a rare microbial species present in the gut microbiota and plays a role in oxalate homeostasis. Mechanophore stadtmanae and Methanobrevibacter smithii are the dominant archeal species in the gut microbiota along with presence of low-abundance taxa i.e. Methanomassiliicoccus luminyensis and members belonging to the genus Nitrososphaera. The human gut is also inhabited by various eukaryotes although the knowledge regarding this component of the gut is less. They may have a potential role in human health e.g.Saccharomyces boulardii plays a role as a probiotic, whereas giardiasis disease is associated with a rare eukaryote Giardia duodenalis present in the gut.

The predominant phyla of human being [6][1]

Bacterial phylum	class	Example	Body location	Characteristics
Actinobacteria	cidimicrobiia, Actinobacteria, Coriobacteriia, Rubrobacteria, Thermoleophilia, Nitriliruptoria	Corynebacterium, Mycobacterium, Nocardia, Bifdobacterium, Streptomyces	intestine, oral cavity, skin	Gram-positive, flamentous, physiologically aerobic, they can be heterotrophic or chemoautotrophic, but most are chemoheterotrophic and able to use a wide variety of nutritional sources
Bacteroidetes	Bacteroidia, Flavobacteria, Sphingobacteria	Bacteroides, Prevotella	intestine, oral cavity	Aerobic and anaerobic, non-spore- forming, Gram-negative rods

Firmicutes	Bacilli, Clostridia, Erysipaelotrichia, Thermolithobacteria, Negativicutes	Clostridium, Staphylococcus, Enterococcus, Lactobacillus spp	intestine, skin, stomach	Gram-positive, rod, coccoid, spiral in shape, anaerobic, aerobic, include commensal and beneficial bacteria
Proteobacteria	Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria Deltaproteobacteria, Epsilonproteobacteria	Escherichia, Salmonella, Vibrio, Helicobacter, Yersinia, Legionellales	Large intestine, skin	Gram-negative bacteria

III. ROLE OF GUT MICROBIOME IN HUMAN HEALTH AND DISEASE

The gut microbiome affects the host physiology of human notably. Humans and their microbiota of the gut maintain a close relationship beginning right after birth and advances in a concerted and coordinated manner throughout the lifespan of man. The microbiota of the gut plays a paramount role in both health and disease in a human which depends on the overall state of composition and distribution of different microbial community. Some of them have highly important role in many vital processes including biosynthesis of vitamin and amino acids. They also help in immune development, providing some other essential nutrients, regulating epithelial development, protection against pathogens that help in maintaining the gut health. In addition, the gut microbiome might be an important factor in certain pathological disorder including colon cancer, inflammatory bowel disease (IBD), multisystem organ failure, cardiovascular disease, obesity and diabetes etc. Moreover, it has been seen that the trans-domain diversity of microbial gut plays a role in human health and disease with findings showing a direct relationship between kidney stone disease related to alteration on not only the species composition of the bacteria but also fungus, archea and eukayotes in the gut.

Trophic function: The principle trophic functions carried out by human gut microflora includes control of proliferation and differentiation of the epithelial along with the development and maintenance of gut homeostasis. SCFs produced by some gut microbiome can play an essential role in the trophic function of the human gut. The three main SCFs (butyrate, acetate, and propionate) stimulate the proliferation and differentiation of the epithelial cells. However, butyrate serves as a major source of energy for the intestinal epithelial cells that inhibits cell proliferation and stimulates epithelial cell differentiation). In addition, the human gut microbiome is responsible for development and regulation of gut immune system and this microbiota-driven immune.

IV. BENEFICIAL FUNCTION OF GUT MICROBIOTA

Metabolic function, trophic function, and protective function are the main benefits of the human gut microbiota (Sheerin 2011). Metabolic function: The gut microbiome in the humans, helps in the degradation of undigested carbohydrate that includes large polysaccharides such as cellulose, hemicelluloses, pectin; unabsorbed sugar and alcohol which are degraded into various short-chain fatty acids (SCFs) including butyrate, acetate, propionate. Acetate (with two carbons), propionate (with three carbons) and butyrate (with four carbons) are SCFs used by the epithelial cells of the colon and acts as a major player in the continuation of gut homeostasis. SCFs induce the secretion of small peptides like the glucagon-like peptide (GLP-1) and peptide YY (PYY), which increase nutrient absorption from the intestinal lumen. Firmicutes such as Clostridium spp. and Bifidobacterium spp. are the ones responsible for producing SCFs (Elson and Alexander 2015). The gut microbiome also helps in synthesis of vitamins (e.g. Escherichia coli produces Vitamin-K) and help in absorption of ions such as magnesium, iron and calcium.

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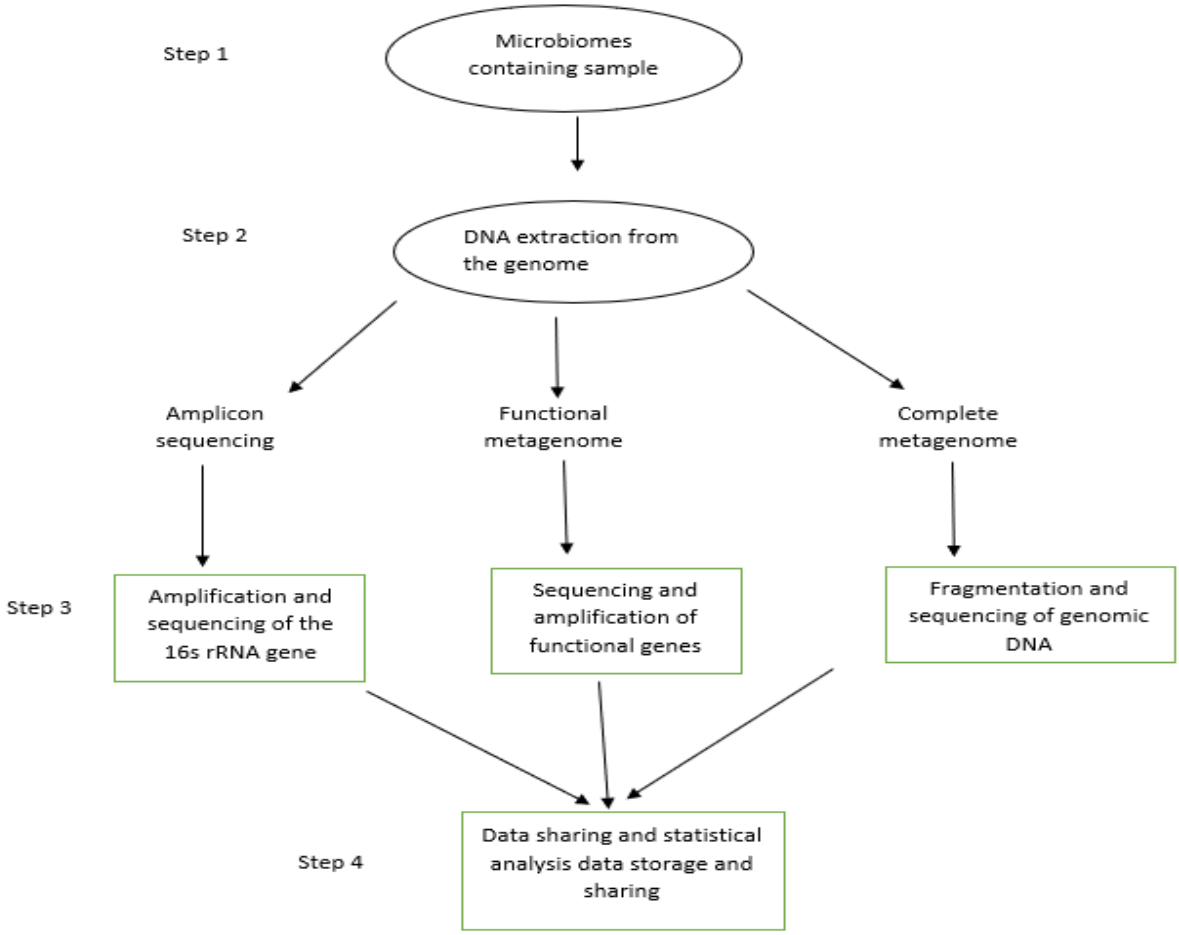

Human health and oral microbiota [13][1]

The oral bacterial population has a highly diverse structure, and some of the bacteria contribute significantly to human health by aiding in digestion, conferring immunity, preventing colonisation, synthesising vitamins, etc.

The microbiota of the oral cavity is extremely diverse containing as many as 700 or more species, of which the vast majority belong to the phyla Firmicutes, Actinobacteria, Bacteroidetes, Proteobacteria, Fusobacteria, and Spirochaetes. Bacterial colonization in the oral cavity and oropharynx occurs mainly on the lips, teeth, cheeks, subgingival and supragingival surfaces, hard and soft palate, and tonsils. The Human Microbiome Project sampled many of these locations and found that, in most, the dominant genera were Streptococcus, followed by Haemophiles, Actinomyces, and Prevotella in the buccal mucosa (cheek), supragingival, and subgingival plaque, respectively

V. FUNCTION IN DIGESTION

Certain oral microbes aid in the digestion of nutrients, especially complex carbohydrates that cannot be broken down by human digestive enzymes. [15] The non-digestible polysaccharide can be hydrolyzed by these bacteria into small chain fatty acids, which can then be metabolised by a person. It has also been discovered that some locally present microbes that break down gluten are present in the oral cavity. The endo-protease produced by some oral bacteria breaks

down gluten, a food protein that is difficult for the human proteolytic enzyme to digest, aiding in its digestion.

Grant immunity

The oral microbiome contributes significantly to immunity in humans, some of which control immune cell formation, pro-inflammatory response down-regulation, immunological priming, and immune system function. Another crucial feature of the oral microbiota is nitrate metabolism, which converts nitrate to nitrite. Nitrite controls stomach integrity, blood pressure, and blood flow. Nitrite is then converted to nitric oxide which has antimicrobial property and is essential for vascular health.

Synthesis of vitamins

One of the crucial processes carried out by some oral bacteria is vitamin synthesis. The oral cavity also contains specific lactic acid bacteria strains that provide vitamin B12. (16) (15) The most common oral probiotic bacteria that generate vitamin are Lactobacillus and Bifidobacterium.

Resistance to colonization

Some oral microbes support the host's deffences by preventing the establishment of numerous other microbes. They prevent the infection from colonising by creating an unfavourable environment. One well-known example of such an organism is the Streptococcus salivarius

VI. APPLICATIONS OF THE HUMAN MICROBIOME

The human microbiome has emerged as a critical area of research due to its vast potential in diagnostics, therapeutics, and disease prevention. With advancements in metagenomics and bioinformatics, the microbiome is now considered a promising tool in modern medicine and pharmaceutical sciences.

Probiotics and Prebiotics

Probiotics are live microorganisms that confer health benefits when administered in adequate amounts, while prebiotics are non-digestible compounds that promote the growth of beneficial microbes. Common probiotic genera include Lactobacillus and Bifidobacterium, which help restore gut microbial balance, enhance immune function, and prevent gastrointestinal infections. These are widely used in the management of conditions such as diarrhea, irritable bowel syndrome (IBS), and inflammatory bowel disease (IBD).

Fecal Microbiota Transplantation (FMT)

Fecal microbiota transplantation involves the transfer of stool from a healthy donor to a diseased recipient to restore microbial balance. It has shown remarkable success in treating recurrent Clostridium difficile infections and is being explored for other conditions such as ulcerative colitis, metabolic syndrome, and neurological disorders.

Disease Diagnosis and Biomarkers

The microbiome can serve as a diagnostic tool by identifying disease-specific microbial signatures. Alterations in microbial composition have been associated with diseases such as cancer, diabetes, and cardiovascular disorders. Microbiome-based biomarkers provide a non-invasive and early detection method for various diseases.

Drug Metabolism and Pharmacomicrobiomics

The microbiome plays a significant role in drug metabolism, influencing drug efficacy and toxicity. This field, known as pharmacomicrobiomics, studies how microbial enzymes modify drugs, affecting their bioavailability and therapeutic outcomes. Understanding these interactions can lead to personalized medicine approaches.

Therapeutic Modulation of Microbiome

Targeting the microbiome through diet, antibiotics, probiotics, postbiotics, and synbiotics has become an important therapeutic strategy. Modulation of gut microbiota has shown potential in treating obesity, diabetes, liver diseases, and mental health disorders through the gut–brain axis.

Cancer Therapy and Immunomodulation

The microbiome influences the host immune system and plays a role in cancer progression and treatment response. Certain gut bacteria enhance the efficacy of immunotherapy and chemotherapy. Microbiome modulation is being explored to improve cancer treatment outcomes.

Nutritional and Metabolic Applications

The microbiome contributes to digestion, nutrient absorption, and synthesis of essential vitamins such as vitamin K and B-complex vitamins. It also regulates metabolic pathways and energy homeostasis, making it a key factor in managing obesity and metabolic disorders.

Personalized Medicine

Microbiome profiling allows for individualized treatment strategies based on a person's unique microbial composition. This approach can optimize therapeutic interventions, improve drug response, and reduce adverse effects.

VII. CONCLUSION

The human microbiome plays a fundamental role in maintaining health and influencing disease outcomes. Advances in sequencing technologies have revealed its immense diversity and functional significance. Understanding microbiome interactions provides new opportunities for therapeutic interventions and disease prevention. Future research should focus on personalized microbiome-based treatments and clinical applications.

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