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# The Importance of Normal Microflora in the Occurrence and Course of Diseases

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**Annotation:** Since its discovery, many studies have been conducted on the role of microbiota in health and disease. Microbiota are divided into intestinal, oral, respiratory and skin microbiota depending on where they are located. Microbial communities interact with the host to maintain homeostasis and regulate the immune system. However, microbiota dysbiosis can disrupt the regulation of body functions and diseases such as cancer, respiratory diseases, cardiovascular diseases, etc. In this review, we discuss current knowledge about how the microbiota is related to host health or its pathogenesis. First, we summarize microbiota studies in healthy settings, including immune modulation, the gut-brain axis, and resistance to colonization. Then we consider the causes of microbiota dysbiosis in the development and spread of diseases. First of all, we consider the problems associated with a change in the composition of the community, a change in the host's immune response and the occurrence of prolonged inflammation. Finally, we propose clinical treatments for diseases using microbiota, such as microbiota modulation and fecal microbial transplantation.

**Keywords:** Microbiota, dysbiosis, microbial communities, human intestinal microbiota, multisystem diseases.

**Introduction.** The term "microbiota" appeared in the early 20th century. Numerous microorganisms, including bacteria, yeast and viruses, live in the lungs, mouth, skin and intestines.

In addition, the human microbiota, or "hidden organ", contains more than 150 times more genetic information than the entire human gene. The terms "microbiota" and "microbiome" are often used to refer to the same thing, but there are certain differences between them. Microbiota, for example, in the oral cavity and intestines, are living microorganisms that live in certain environments. The set of genomes of all microorganisms in the environment is called the microbiome. Microbiomes include a community of microorganisms, structural elements, metabolites, and conditions [1,2]. In this regard, the microbiome is not as widespread as the microbiota. The microbiota consists of different species depending on the location, but the gut microbiota is considered the most important for maintaining our health. Gut bacteria perform many tasks, including digesting food, protecting against pathogens, boosting immunity, and producing vitamins. As a rule, the gut microbiota consists of six types of bacteria: *Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, Fusobacteria* and *Verrucomicrobia. Firmicutes and Bacteroidetes* are the most common types. Currently, *Candida, Saccharomyces, Malassezia* and *Cladosporium* are the most studied fungi known as intestinal mycoses. The human gut microbiota also includes bacteria, fungi, phages and archaea, mainly *M. Smithii* [3,4,5].

The human gut microbiota consists of thousands of microorganisms that fight pathogens in infectious diseases and suppress or cause inflammation in various immunological contexts. The gut microbiome is a dynamic and complex ecosystem that promotes the reproduction, growth and differentiation of epithelial and immune cells to maintain intestinal homeostasis. Disorders that cause changes in this microbiota lead to an imbalance in the immune regulation of the body. There is increasing evidence that the gut microbial community is associated with the development and progression of various infectious and inflammatory diseases. Thus, understanding the interaction between the gut microbiota and the host immune system is fundamental for understanding the mechanisms involved in the development of various pathologies, as well as for finding new treatments. In this article, we consider the main intestinal bacteria capable of influencing the immune response in various pathologies, and discuss the mechanisms by which the interaction between the immune system and the microbiota can influence the course of diseases [7,8,9,10].

**The main purpose** of the presented manuscript is a brief analysis of scientific and practical research conducted on the importance of the microbiota located in its cavities for the health and diseases of the human body

**Intestinal metabolome: the relationship between microorganisms and the host.** Recent discoveries that allow us to collect more data on DNA sequences and metabolites have expanded our understanding of how the gut microbiota and metabolites relate to each other at a system-wide level. We can now better study the effects of certain microbes on certain metabolites. We consider how the microbiota determines certain levels of metabolites, how the profile of metabolites is formed in infants, and how the physiological state of a person can be assessed based on microbes and/or metabolites. Despite improvements in data collection technologies, the computational challenges associated with integrating data from multiple layers remain complex. Developments in this area will significantly improve our ability to interpret current and future datasets.in the intestine: the interaction of the microbiota and the host [11,12,13].

For a long time, people believed that healthy human lungs were sterile. However, some studies have shown that microbiota is also present in lung tissues. *Actinobacteria, bacteroidetes, Firmicutes* and *Proteobacteria* are the main types of lung microbiota, and its composition is based on three factors: the immigration of microorganisms, the elimination of microorganisms and the rate of reproduction of microorganisms. The skin glands and hair follicles are distributed and differ depending on the geographical location. The composition of the microbiota varies depending on the physical and chemical characteristics of the skin areas. As a rule, *Actinobacteria, Bacteroides, Cyanobacteria, Firmicutes* and *Proteobacteria* make up the composition of the skin microbiota. A huge amount of research in recent decades has revealed a link between the microbiota and diseases such as cancer, diabetes and neurological disorders. In addition, the management of microbiota in the human body can be vital for the treatment of diseases. Here we summarize and discuss current information on how the human microbiota affects the development of disease-mediating diseases and possible clinical applications of microbiota in the treatment of diseases [14,15,16,17].

**Human intestinal microbiota and neurodegenerative diseases.** The relationship between the human gut microbiota and neurodegenerative diseases has recently attracted a lot of attention from the medical community. More and more studies show that the human intestinal microbiota can modulate the nervous, endocrine and immune systems through the "gut-brain" axis, which is involved in the occurrence and development of diseases of the central nervous system, especially Parkinson's disease and Alzheimer's disease [18,19,20].

**Human intestinal microbiota and cardiovascular diseases.** Cardiovascular diseases such as hypertension, atherosclerosis and heart failure are the leading cause of death worldwide. More and more studies show that the human intestinal microbiota and the products of its metabolism interact with the host body in various ways, affecting the development and occurrence of cardiovascular diseases. The role of trimethylamine oxide, bile acids and short-chain fatty acids in the development of cardiovascular diseases has been confirmed by a large number of studies that are products of the metabolism of the intestinal microbiome [21, 22, 23].

**Human intestinal microbiota and metabolic diseases.** Although the incidence of metabolic diseases is related to genetic factors and environmental conditions, the incidence of metabolic diseases in people with the same genetic background and energy consumption correlates with the presence of intestinal flora. In recent years, more and more studies have shown that intestinal dysbiosis is closely associated with many metabolic disorders, including obesity, diabetes and non-alcoholic fatty liver disease [24,25,26,27].

**Human intestinal microbiota and gastrointestinal diseases.** During a long evolutionary process, the intestinal flora constantly adapts to individual adaptation and natural selection, as well as interacts with the host and restricts it to regulate intestinal homeostasis. Intestinal microorganisms absorb nutrients from the host, decompose food residues that cannot be digested by the host, and participate in the metabolism of nutrients in the intestine. Accumulating evidence suggests that GM dysbiosis can cause diseases of the digestive system, including inflammatory bowel diseases and colorectal cancer [28, 29, 30.31].

**Discussion.** The gut microbiome is closely related to human health and diseases, which opens up wide opportunities for the diagnosis, treatment and prevention of diseases. This article describes progress in the study of the pathogenesis and mechanism of action of the intestinal microbiome in multisystem diseases. Over the past few years, metagenomic studies have become a popular method of studying the relationship between gut microbes and diseases. Obtaining high-quality reference sets of genomes can significantly increase the resolution and accuracy of metagenomic studies and provide a basis for analyzing the relationship between the gut microbiome and the human phenotype. In the course of the latest study, a set of genes was compiled from 200,000 genomes and 171 million protein sequences representing the human gut microbiome [1,4,5,7,11].

Among 4,644 species, 71% of the strains are not amenable to cultivation, and the high variability of strains between continents indicates that most microorganisms still need experimental studies. At the same time, there are still many unsolved mysteries in research on the relationship between intestinal microbes and diseases. Firstly, there is no consensus on what a “good” gut microbiome is. How to clinically identify intestinal microbial disorders and develop reliable microbiota screening methods for accurate diagnosis in order to recognize people with intestinal microbial disorders. [12,13,17,18,20]. Secondly, it is still unclear whether the intestinal microbial disorder is the cause or consequence of the disease, whether it is a specific strain of bacteria or the intestinal microbe as a whole as the cause of the disease. The mechanism of GM involved in the occurrence and development of diseases is not yet clear. In addition, whether intestinal microbes useful for the treatment of diseases can prevent diseases and contribute to the overall strengthening of immunity [21,24]. Finally, the interactions between intestinal microbes, the host immune system and diseases are not only complex, but also very dynamic, which may mean that various methods of treating the intestinal microbiota must be used throughout the course of treatment of the disease. Currently, there are several effective methods of treating clinical diseases by regulating the intestinal flora. Therefore, it is imperative to combine advanced techniques such as metagenomics, transcriptomics, proteomics and metabolomics to conduct prospective studies on large samples. In the context of precision medicine, it is possible to use personalized genetically modified microbiota for the prevention and treatment of certain diseases in the future. Targeting the composition and metabolic function of the intestinal flora may become a new option for the prevention and treatment of diseases [28,29,30,31,32].

**Conclusion.** In conclusion, it should be noted that there are great opportunities for research at all levels, from basic and translational research to clinical and epidemiological analysis, which can advance understanding of this complex intestinal ecosystem.

This requires a reasonable experimental plan and long-term dynamic tracking of changes in intestinal microbes and disease development, combined with multidimensional analysis and more comprehensive high-performance sequencing.

Delve into research at the level of individual strains to find opportunistic bacteria associated with the disease. This can provide new ideas for the treatment of diseases and fully unlock the potential of precision medicine.

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