

Significance of Gut Microbiome Role in Human Diseases

Sana Farooq*

Department of Microbiology, The University of Delhi, New Delhi, India

DESCRIPTION

The human gut microbiome is a huge microbial community that shows an irreplaceable role in human life. With the further expansion, the influence of intestinal flora on human diseases has been progressively excavated. Gut Microbiota (GM) dysbiosis has contrasting health effects on the human body that will major to a variety of chronic diseases [1]. The fundamental mechanisms of GM on human diseases are incredibly difficult. Recent studies focusses on regulation and mechanism of cardiovascular diseases, GM on neurodegenerative diseases, metabolic diseases and gastrointestinal diseases, thus providing a potential target for the prevention and treatment of disease. The human gut Microbiota (GM) is a dynamic, complex, and spatially heterogeneous ecosystem inhabited by a myriad of microorganisms interrelating with each other and with the human host, including bacteria, archae, fungi, and viruses. The collection of all intestinal microorganisms genes represent a genetic repertoire, which is one order of magnitude advanced than that of human genome. As the leading micro-ecosystem in the human body, GM is interdependent with the host and preserves normal physiological procedures in a dynamic equilibrium state [2]. The composition of GM mainly includes four categories, including Bacteroides, Firmicutes, actinomycetes, and Proteus. Firmicutes and Bacteroidetes ratio is an important parameter to reproduce GM disorder. Once the GM disorder happens, the structure and function of the intestinal flora will modify and even cause some diseases [3]. The fundamental regulatory mechanisms are complex. In recent years, with the rapid development of molecular biology, bioinformatics analysis technology, genomics, and high-throughput sequencing technology, the GM has made rapid progress. A great deal has produced evidence that GM disorder and its metabolites play a key role in maintaining host intestinal homeostasis and influencing the expansion of many diseases, including neurodegenerative diseases, metabolic diseases, cardiovascular diseases, and gastrointestinal diseases. The imbalance of GM will affect the health of the host through many ways, such as energy absorption, Short Chain Fatty Acids (SCFAs), choline, gut-brain axis, Bile Acids (BAs), and so on. However, the mechanism of GM on human diseases has not yet

been completely clarified. As findings related to the regulation and mechanism of GM on human diseases, and then summarized the characteristics of intestinal microflora changes associated with various diseases, and the possible mechanisms of microbial metabolism and derivatives complicated in driving the occurrence and development of diseases [4]. The association between GM and neurodegenerative disease has lately increased a lot of attention in the medical community. An increasing number of studies suggested that GM can modulate nervous, endocrine, and immune communication finished the gut-brain axis which takes part in the occurrence and development of central nervous system diseases, especially in Alzheimer Disease (AD) and Parkinson Disease (PD). GM is closely connected to human health and diseases, which bring great occasions for the diagnosis, treatment, and prevention of diseases [5]. This paper designates the research progress of the pathogenesis and mechanism of GM in multi-system diseases. For the past few years, metagenomic research has become a prevalent research method to study the correlation between gut microbes and diseases. Procurement high-quality reference genome sets can significantly improve the resolution and accuracy of metagenomic research, and provide a data basis for the correlation analysis between the human gut microbiome and phenotype. The mechanism of GM complicated in the occurrence and expansion of diseases is not yet clear. Additionally, intestinal microbes are beneficial to disease treatment and promote overall immune health, finally the interactions between host immune systems, gut microbes, and diseases are not only complex but also highly dynamic, dissimilar gut microbiota treatments are wanted to be adopted through the course of disease treatment. At present, there are few effective methods for the treatment of clinical diseases by regulating intestinal flora. Therefore, it is very essential to combine advanced techniques such as transcriptomics, metagenomics, proteomics, and metabolomics to conduct potential studies with large samples. In the context of precision medicine, it is conceivable to use personalized, genetically modified microbiota for the anticipation and treatment of certain diseases in the future. Aiming the composition and metabolic function of intestinal flora may be a new option for the prevention and treatment of diseases.

Correspondence to: Sana Farooq, Department of Microbiology, The University of Delhi, New Delhi, India, E-mail: sanafarooq0000@gmail.com

Received: 12-Jan-2022, Manuscript No. JPH-22-16223; **Editor assigned:** 15-Jan-2022, PreQC No. JPH-22-16223 (PQ); **Reviewed:** 31-Jan-2022, QC No. JPH-22-16223; **Revised:** 04-Feb-2022, Manuscript No. JPH-22-16223 (R); **Published:** 10-Feb-2022, DOI:10.35248/2329-8901.22.10.255.

Citation: Farooq S (2022) Significance of Gut Microbiome Role in Human Diseases. J Prob Health.10:255.

Copyright: © 2022 Farooq S. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

CONCLUSION

There are great opportunities for studies at all levels, from basic and translational research to clinical and epidemiological analysis, which can advance the understanding of this complex intestinal ecosystem. This necessitates reasonable experimental design and long-term dynamic following of vicissitudes in intestinal microbes and disease expansion, collective with multi-omics analysis and more comprehensive high-throughput sequencing. Go deeper into the single strain level of research, so as to find disease-related conditional pathogenic bacteria. It may make obtainable new ideas for disease treatment and give full production to the potential of precision medicine.

REFERENCES

1. Almeida A, Nayfach S, Boland M, Strozzi F, Beracochea M, Shi ZJ, et al. A unified catalog of 204,938 reference genomes from the human gut microbiome. *Nat Biotechnol.* 2021;39(1):105-114.
2. Aoki R, Kamikado K, Suda W, Takii H, Mikami Y, Suganuma N, et al. A proliferative probiotic *Bifidobacterium* strain in the gut ameliorates progression of metabolic disorders via microbiota modulation and acetate elevation. *Sci Rep.* 2017;7(1):1-0.
3. Bakay M, Pandey R, Grant SF, Hakonarson H. The genetic contribution to type-1 diabetes. *Curr Diab Rep.* 2019;19(11):1-4.
4. Bedarf JR, Hildebrand F, Coelho LP, Sunagawa S, Bahram M, Goeser F, et al. Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. *Genome Med.* 2017;9(1):1-3.
5. Beyer K, Domingo-Sabat M, Ariza A. Molecular pathology of Lewy body diseases. *Int J Mol Sci.* 2009;10(3):724-745.