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Is Human Microbiome the Answer to Many Pathologies? Relation Between Microbiome and Dm

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Editorial Note

The human microbiome is confident of bacteria, archaea, viruses and eukaryotic microbes that consist in and on our bodies. These microbes have tremendous hidden to impact our physiology, both in health and in disease. They contribute metabolic functions, protect against pathogens, educate the immune system, and, through these basic functions, affect directly or indirectly most of our physiologic functions. The study of the human microbiome has been furthered by technological advancements for operating culture-independent analyses. In most studies, the bacterial component of a microbial population are defined by sequencing of the 16S rRNA-encoding gene (hereafter, 16S) followed by comparison to known bacterial arrangement databases.

The human body is a complex ecosystem,harboring trillions of microorganisms on its surface and in its interior.This diverse assemblage of organisms constitutes the human microbiome. As distinct microbial communities can be localized to certain parts of the body, investigations have been launched to survey the significance of the gut, respiratory, reproductive tract, oral, and skin microbiomes. An improved understanding of the human microbiome will allow for the prevention and control of chronic diseases, the remediation of suboptimal health, and a potential revolution in medical technologies.

Research into the interactions between the microbiome and health leads to the development of microbiome-based medicine, capable of not only treating diseases but preventing them as well. The interactions between the human microbiota and the host provide an overview of the microbial role in basic biological processes and in the development and progression of major human diseases such as infectious diseases, liver diseases, cancers, metabolic diseases, respiratory diseases, mental or psychological diseases, and autoimmune diseases.

The advances in techniques associated with microbial research, such as DNA sequencing, metabolomics, and proteomics combined with computation-based bioinformatics have become much more sophisticated and more comprehensive.The influence of diet on microbiota composition and function is well established.A number of other factors have been associated with variability in microbiota composition or function, including sex hormone, treatment with antibacterial or antifungal agents, pharmaceuticals such as proton pump inhibitors, xenobiotics, environmental toxicants or prescribed drugs .

Recent data has configured intestinal microbiota as modified in patients with type 2 diabetes, Firmicutes and Clostridium ratios being significantly reduced. They show the presence of Bacteroids at Firmicutes and have defined the proportions of the Bacteroides-Prevotella group in C. coccoides. E. Bacterial sequences specific to type 2 diabetes rather than obesity can be considered as signatures of the hyperglycemic sidrum. In insulin resistant individuals, serum BCAAs are shown to be elevated in insulin resistance, especially due to the intestinal microbial composition, P. copri and B. vulgatus being the major BCAA producers.

Interestingly, blood glucose lowering treatments, such as metformin, can alter the overall bacterial composition, for example by increasing the abundance of Lactobacillus and Escherichia species. It has also been shown that the diet causes short and long-term changes in the microbial intestinal wealth and composition. High fiber intake increases the abundance of Prevotella. Pasteurized probiotics offer another potential therapy for diabetes, allowing for the use of oxygen sensitive anaerobes in the treatment of diabetes. Pasteurized muciniphil has been shown to improve glucose metabolism in mice. Genetically modified bacteria can be designed to express therapeutic factors and are incorporated into the microbiota. L. Lactis (a "safe" bacterium) was genetically engineered to produce GLP-1 and, therefore, to improve glucose metabolism in mice.

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