

Opinion Article

Human microbiomes and their applications in daily life

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DESCRIPTION

Human microbiome refers to the entire collection of microbes (the micro biota) that inhabit humans and, more specifically, the group of microbial genomes that contribute to a person's metagenome, or more comprehensive genetic profile. A remarkable variety of microorganisms, including bacteria, archaea (primitive single-celled creatures), fungi, and even certain protozoans and non-living viruses, are represented by the genomes that make up the human microbiome. The majority of the human microbiome is made up of bacteria, which are believed to number between 75 trillion and 200 trillion distinct organisms, compared to the 50 trillion to 100 trillion somatic (body) cells that make up the total human body. The vast amount of microorganisms in the human body raises the possibility that it is a "supraorganism," a combination of human and microbial genes, cells, and features.

Numerous metabolic processes in humans are impacted by the relationship between the human microbiome and immune system, which also has an effect on our wellbeing. To correctly diagnose and treat these conditions, a deeper comprehension of the host-microbe interaction is required. Because of the importance of the microbiome to host health, new treatment modalities have emerged that centre on manipulating the host microbiome as directed, either by eradicating toxic taxa or reintroducing missing good taxa and the functional functions they play. Large numbers of microbial taxa are difficult to cultivate in the lab, if not impossible. This makes it very challenging to fully catalogue the different components of a given microbiome and to comprehend how microbial communities work and affect host-pathogen interactions. Also included are developments in high-throughput sequencing tools for studying host-microbe interactions.

The genetic makeup of all the bacteria, fungi, protozoa,

and viruses that inhabit and survive inside the human body is known as the microbiome. The total number of genes in the bacteria that make up an individual's microbiome is 200 times more than those in the human genome. The microbiome might be up to five pounds heavy.

Human growth, immunity, and nutrition depend on the microbiome. The bacteria that reside in and on us are helpful colonisers rather than foreign invaders. Dysfunction in the microbiome is linked to autoimmune disorders such as diabetes, rheumatoid arthritis, muscular dystrophy, multiple sclerosis, and fibromyalgia. As disease-causing microorganisms build up over time, they alter metabolic and gene activity, which causes an aberrant immune response against cells, tissues, and substances that are typically found in the body. The family's microbiome appears to carry autoimmune illnesses down across generations rather than through DNA inheritance.

The HMP aims to describe the human microbiome and analyse its function in human health and disease by studying the human as a supraorganism made up of non-human and human cells. The HMP's main objective is to characterise the metagenome the collective genomes of all the microbes of the 300 healthy individuals' microbiomes across time. Skin, mouth, nose, colon, and vagina are the five bodily regions that are tested.

Microbes are necessary for all life on this planet. They both create and are created by the environment. However, knowledge of host-pathogen systems is still in its infancy. The ability to investigate microbial communities dwelling within various hosts has been made possible by considerable advancements in sequencing technology and bioinformatics tools during the past two decades. It is widely acknowledged that the diversity of microorganisms found in arid settings has largely gone unexplored.

Through fermentation, microorganisms have been used

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for thousands of years to extend the shelf life of foods and beverages. Carbohydrates are oxidised during fermentation to create mostly organic acids, alcohol, and carbon dioxide. Some of these foods that have been preserved also have extra health advantages, like increased nutritional content or probiotic qualities.

Although yeasts and other moulds have also been linked to these processes, bacteria are the most frequent microbe used in them. The Lactobacillaceae family of bacteria, which converts carbohydrates into lactic acid, is the most frequently used group in these activities. *Acetobacter* and *Bacillus* are two more typical bacteria that are used in the fermentation process.