Phylogenetic and Marker Gene Analysis of Human Microbiome

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Perspective

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ABOUT THE STUDY

Human microbiome refers to the aggregation of all microorganisms that inhabit the skin, seminal fluid, saliva, oral mucosa, conjunctiva, mammary glands, lung, biliary tract and gastrointestinal tract as well as the corresponding anatomical sites in which they do so. Archaea, fungus and viruses are some examples of human microbiota species, even though they can exist on the human body. Numerous bacteria that contain roughly the same number of non-human cells as human cells live inside of humans. Some microbes that live on humans are commensal, which means they live together without causing harm to people. Others interact with their human hosts in a mutualistic way. Identifying the individuals who make up a microbial community, which includes bacteria, eukaryotes and viruses are the main challenge in understanding the human microbiome.

Deoxyribonucleic acid based studies are usually used for this, while ribonucleic acid, protein and metabolite based research are also carried out. Targeted amplicon studies and more recently shotgun metagenomic investigations are the two main types of DNA based microbiome studies. One of the key questions surrounding the human microbiome aside from merely describing its makeup is whether there is a core or if there is a portion of the community that is characteristic of most humans. Metagenome assemblers typically have lower quality and many recovered genes are incomplete or fragmented, the computational constraints for this type of study are larger than for single genomes. The information can be used to do a functional annotation following the gene identification stage by multiplying the aligning target genes against ortholog databases.

Marker gene analysis is a method that uses primers to focus on a particular genomic area and allows for the determination of the phylogenies of different types of microbes. The genetic area is distinguished by a highly variable region that can provide precise identification, it is bordered by conserved sequences that serve as binding sites for PCR primers. The 16S rRNA gene is the primary gene used to define bacteria and archaea, while the internal transcribed spacer is utilized to identify fungi. The method is ideal for samples that can be contaminated by host DNA since it is quick, affordable and allows for the low resolution categorization of microorganisms.

In comparison to the mouth and gut which exhibited the greatest richness, the skin and vaginal locations displayed less diversity. Each person has a unique combination of bacteria at each spot on their body, both in terms of

species and quantity. Numerous subtypes of the same species of bacteria that are distributed throughout the mouth choose to live in distinctly different parts of the mouth. Even previously believed to be well understood enterotypes in the human gut come from a diverse range of communities with hazy taxonomic boundaries.

Pathogenic bacteria are prevented from entering the body by the skin acting as a barrier. Microbes can live in or on the skin of a person and can either be permanent residents or transients. According to the type of skin on a person, different types of resident microbes exist. Most microbes prefer to associate with glands or live on the skin's surface cells. Amino acids, water and fatty acids are given to the bacteria by these glands, such as sweat or oil glands. Additionally, local bacteria found in oil glands are frequently gram-positive and potentially dangerous.

To cling and thrive in the oral environment while being protected from the environment and antimicrobial treatments, bacteria build up on both the hard and soft mouth tissues to form biofilms. By permitting bacterial recolonization for biofilm development and limiting growth by removing biofilm buildup, saliva plays a crucial role in biofilm homeostasis. Additionally, it offers a way to regulate temperature and give nutrients. The kind of exposed nutrients that the biofilm receives depends on where it is. Oral bacteria have developed strategies to sense their surroundings and avoid or alter their hosts. The bacterial colonization is constantly monitored and prevented from invading nearby tissues by a highly effective innate host defense system. When a person dies, the microbiome of the live body disintegrates and a new combination of bacteria known as the necrobiome emerges as an essential active component of the complex physical disintegration process.