

Microbiome Research: A Change of Mentality

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Microbial communities are ubiquitous and occupy almost all known ecological niches. These communities are dynamic, highly complex and diverse. The microbial components of these communities are usually communicating and interacting mutually, synergistically and in many time competitively. Despite these conflicting relationships, microbial communities usually reach balanced relationship among its constituents that ensure their stability and survival. Any imbalance in these communities can be harmful to them, their niches or their hosts. The term microbiome usually refers to any microbial community that resides in a definite habitat such as a type of soil, plant roots, and the human gut. In the last decade, there is a change of mentality within the microbiological community into the global understanding microbial community level instead of pinpointing of an individual or few microorganisms try to link that to the outcome of a specific relationship. Recent advances in next-generation sequencing, metagenomics, meta-transcriptomics and metabolomics methods facilitated this global approach toward better understanding microbial communities. One important question when dealing with a microbiome is to identify the taxonomic profile of its microbial community both qualitatively and quantitatively. Metagenomics can satisfy this question by either targeting 16S ribosomal RNA genes or even whole-metagenome sequencing (WMS). Nevertheless, WMS can also provide an additional fractional functional profile of the investigated microbiome. However, a better insight into the full functionality of the microbiome can be achieved through Meta-transcriptomics, in which we can acquire information about all expressed genes in the community under investigation. Utilizing bioinformatics tools will aid in annotating these expressed genes and thus we can build a functional profile of the community in question. Comparative metagenomics and meta-transcriptomics are very important approaches to understanding the effect of variable condition on the composition and the function of a certain microbiome. In addition, metabolomics, which is the whole byproducts produced by a microbiome under a specific condition, is very important since it can affect the well-being of the ecological niche it resides. For example, it was proposed bacterial cellular components and products such as lipopolysaccharide (LPS) and endotoxin as well play a role in aggravating an inflammatory response in the host cells through the Toll-like protein receptors (TLRs) and thus can induce an inflammatory cascade that may lead to many inflammatory diseases such as diabetes. There are several global initiatives that have been launched such as human microbiome initiative launched and funded by the National Institute of Health that aims to understand the impact of the gut, oral and skin microbiome on the human health. One more global initiative is the Earth Microbiome Project that aims to investigate the microbial communities' diversity, distribution, and structure all over the planet that led to the creation of the new database that includes data from 27,000 samples collected at sites ranging from Alaskan permafrost to the ocean floor. In conclusion, I believe that there is a change in the microbiological mentality toward the global functional network approaches that will lead to a more comprehensive in-depth understanding of microbiomes and relations with their habitats.

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