



## **Microbiome and Human Health**

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Advances in proteomic and sequencing technologies coupled with new bioinformatic developments have allowed the scientific community to deeply investigate the microbes that inhabit the human body. Microbes associated with the human body include eukaryotes, archaea, bacteria and viruses, with bacteria alone estimated to outnumber human cells within an individual by an order of magnitude. Our knowledge of these communities and their genes content, referred to collectively as the human microbiome, has until now been limited by a lack of population-scale data detailing their composition and function. It is now well established that the human microbiota as a whole encode 150 times more genes in their collective metagenome than are present in the human host genome. Human microbiota functions are crucial for human health and its alteration have been associated multiple human diseases such as metabolic, cardiovascular, neurological and immuno-inflammatory diseases.

The prevention of microbiota alteration, the identification of pathologic microbiota and the development of new therapy that restore healthy microbiota offer a unique approach for human diseases prevention and treatment.