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Opinion

Protect Your Microbiome to Stay Healthy and Disease-Free Life

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Abstract

Microbiome greatly influences human physiology and it forms an interface between optimal health and diseases. Humans are colonized with diverse group of microbial communities, which comprised mainly of commensals, symbionts and opportunistic pathogens. Commensals have beneficial effects in humans that may suppress the growth and colonization of incoming as well as opportunistic pathogens. In humans, the overall balance in the structure and composition of microbial communities is important to ensure healthy life. Dysbiosis of the microbiome induced by several risk factors have worsened human health leading to chronic diseases. Recent development and advancement of new OMICS technologies has provided insights into comprehensive structure of microbiome and microbiome-host metabolic signal disruption in humans, which opened up new avenues to gain advance knowledge on the impact of microbial imbalance and the role of microbial communities in human health and diseases. To conclude, microbiome is a key regulator of human health and diseases and it is essentially important for us to protect our microbiome from harmful risk factors to promote disease-free life.

Keywords: *Microbiome; Microbial balance; Dysbiosis; Infectious diseases; Host-Microbiome Interaction*

Humans are colonized by aggregate of microorganisms such as bacteria, fungi and archaea that resides within different parts of body tissues as well as in the gastrointestinal tracts to perform life-sustaining functions. Earlier estimates have revealed that the number of microbial cells in an individual outcompete the number of human cells by a factor of 10 or more [1]. However, the most recent revised estimates have shown that the number of microbial cells in human body is actually of the same order as the number of human cells [2]. Among diverse group of microbial communities existing within humans, some are commensal, while others are symbiotic and a very few populations represent opportunistic pathogens. Commensal microbiota execute task that are known to be beneficial and essential for human development and nutrition. They also boost immunity in humans by suppressing growth and colonization of incoming pathogens as well as opportunistic pathobionts [3].

A healthy or disease-free individual maintain strict balance of their innate body microbe's by keeping trouble-making microbes at the bay. Dysbiosis caused by certain environmental factors such as dietary intake of pesticides, illness, stress, aging, chemical exposures and use of antibiotics can kill beneficial microbes that allows the pathogenic microbes to proliferate and cause life-threatening diseases [4,5]. Subtle changes in microbial balance can cause severe health complications in humans such as diabetes, eczema, allergies, acne, diarrhea, autism, cancer, gastric ulcer, cardiovascular diseases, obesity, rheumatoid arthritis, muscular dystrophy, multiple sclerosis and other medical related illness–suggesting that microbes are the key regulators of human health and diseases [6]. An extensive characterization of human microbiota and their involvement in health and diseases is highly important to eradicate microbiome associated-diseases in humans.

"*Human Microbiome*" represents complete genetic material of all microbes residing within human. The total number of microbial genes within human is 200 times the number of genes in human genome. It shows that microbiome represents the "second genome" of

human, which forms an interface between optimal health and diseases [7]. Microbiome has tremendous potential to alter human physiology in promoting diseases. Changes in microbiome structure can alter host-microbiome interactions, which adversely influence the host physiological state conductive to diseases. Interestingly, new emerging evidence suggests that microbiome can be inherited from parents to offspring. Therefore, it's plausible that the microbiome associated-diseases can also be transferrable from mother to newborn through maternal inheritance of microbiome [8].

Several methods are available to explore the structural and functional composition of microbiome. However, traditional culture-based methods for exploring microbiome have never been successful in the laboratory, due to their inability to mimic specific environmental conditions or nutrients needed for the growth of microbes. Recent advancement in DNA sequencing technologies sheds light on new area of research called 'Metagenomics', which allows comprehensive investigation of microbial communities defying the need for cultivation [9]. Other advanced 'omics technologies' such as transcriptomics, proteomics and metabolomics have also provided effective path in understanding the biological properties of total microbial communities prevailing within human [10]. During recent years, utilization of these advanced technologies have provided important structural and functional insights into host-microbiome interactions that has given rise to new concept for utilizing 'microbiome signatures' as biomarkers. The component of large data profile of individual microbiome is highly valuable for the development of targeted therapies in human. Microbiome information also reflects an individual identity and it can be used for prediction of disease-related risk factors, diagnosis and progression of disease [11].

During recent years, certain important factors such as use of antibiotics and dietary intake of pesticides have been proven to cause tremendous disruption and shift in diversity of human microbiome that serves as major risk factors for infectious diseases. An excess use of antibiotics greatly disrupts the ecology of human microbiome. Unlike innate microbiome, dysbiotic microbiome lose its vital function to afford protection from pathogens, which cause serious health problems associated with metabolic, immunological and developmental disorders leading to high risk for infectious diseases in humans [4]. Certain chemical compounds or persistent organic pollutants (POPs) used in conventional foods were known to decrease beneficial microbes and proportionately increase the number of harmful microbes in human body, which also influences the risk for infectious diseases [5]. Thus, understanding comprehensive structure of microbiome as well as microbiome-host metabolic signal disruption in health and disease will open up new avenues to gain advance knowledge on the consequence of microbial imbalance with the potential to identify a novel drug targets to treat microbiome-associated diseases. To conclude, keeping the microbiome vital by restoring and maintaining healthy microbial balance will help us to stay healthy and disease free life.

Conflict of Interest

Author declare no conflict of interest

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