

Potential of Microbiome Research in Respiratory Diseases

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ABSTRACT

The microbial populations have shown to have large effects on human disease and there can be a possible connection between the differences in disease rates among different populations of people and differences in the microbial populations present in the microbiome. The effect of ethnicity and geography on oral, gut and fecal microbiome has studied widely and shows that changing epidemiology and ethnicity has impact on microbiota diversity. However, there are very scanty studies dealing with respiratory diseases.

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Key words: Microbiota diversity; 16S rRNA sequencing; Deep sequencing; Ethnicity; Geography

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REVIEW

The globalization has made world flat, at least, as far as epidemiological profiles are concerned. A revolution is occurring in the way we understand health and disease; the spotlight is now on microbiota: commensal organisms that are an integral part of the

human body. The lung microbiome, like that of other compartments, may be potentially manipulated with an aim to correct dysbiosis and restore “healthy” microbial communities via use of probiotics (extrinsic microbes administered in the interest of health), prebiotics (non-absorbed molecules that promote specific bacterial growth), antibiotics and quorum-sensing molecule inhibitors^[1-6]. Recent studies have revealed associations of some diseases with an imbalance in the microbial community. The understandings suggest that disease phenotypes are more likely to be a result of complex microbial interactions^[5]. This new paradigm will enable the study of host factors enhancing or inhibiting bacterial growth in health and disease.

The bacterial communities of the healthy lung overlap with those found in the mouth but the nasal microbiome, which is distinct from the oral microbiome, appeared to contribute little to the composition of the lung microbiome in healthy subjects. The concept that the entire respiratory tract should be considered a single ecosystem extending from the nasal and oral cavities to the alveoli, which includes gradients and niches that modulate microbiome dispersion, retention, survival, and proliferation have a significant impact on microbiome studies^[2,5,7]. In addition to being strongly influenced by immigration and weakly influenced by the relative reproduction rates of community members, the community membership of the lung microbiome is strongly influenced by selective elimination, which is absent from the gastric microbiome. The empirical evidence normally corroborate with the ecological determinants of known anatomical, physiological, and immunological features of the respiratory tract^[8-10].

During their life cycles, pathogens encounter dramatically different environments to which they must adapt. For certain pathogens, one environmental change is temperature, which can vary widely as organisms alternate between a vector or environmental reservoir and a mammalian host. Pathogens often respond to temperature transitions with increase in the expression of temperature regulated genes that continue as long as it remains at the elevated or low temperature^[11,12].

Quorum sensing plays a major role in the maintenance and survival of bacterium and also modulates physiology of the bacterium such as

biofilm formation, expression of the virulence, and sporulation^[6]. The bacterium senses the environmental changes and induces signaling mechanisms, mediated by a number of soluble signaling molecules, termed as autoinducers. These autoinducers serve like a hormone; the best example is acyl homoserine lactone. These autoinducers are secreted in the external environment of the cells and directly regulate the gene expression of the bacteria. The well understood signaling molecules found in the bacteria are cyclic adenosinmonophosphate, cyclic guanosine monophosphate, and guanosine bis pyrophosphate (ppGpp). The cAMP is known to regulate the carbon metabolism while the ppGpp regulates the bacterial survival during starvation^[12,13]. Cyclic-di-GMP is associated with the regulation of responses relevant to pathogenesis, such as motility, secretion, cytotoxicity, and biofilm formation^[13-15].

High-throughput sequencing technologies have been applied to characterize human microbiota^[1] in various body habitats such as gut (The Human Microbiome Project Consortium, 2012), oral cavity^[11,16], vagina^[17] and respiratory tract^[8]. Human lung microbiota was identified by 16S rRNA sequencing^[9], demonstrating that the lung is not sterile contrary to previous belief. However, there are no reports so far which gives information about the multi drug resistance in microbiome of TB infection.

Besides, complicated bacterial communities associated with respiratory diseases were also identified by analysis of the composition of bacteria by deep sequencing in sputum samples of cystic fibrosis patients, whereas the low-prevalence or fastidious bacteria were not detected by standard clinical culture methods^[15,18]. Deep sequencing also shows higher sensitivity than other detection system like Vitek 2 Compact system in detecting lower respiratory tract infections^[19]. The scarcity of reports from other parts of world indicates that more studies are to be done to understand the local (region specific) microbiome in global perspective. These studies are mainly based on partial 16s rRNA gene analysis. The studies will help to understand not only the mechanism of pathogenesis but also for defense mechanism which will lead to early detection of many respiratory infection.

Metagenomics technique offers a powerful lens for viewing the microbial world that has the potential to revolutionize understanding of the microbiome, bypassing the need for isolation and lab cultivation of individual species. The metagenomic sequencing on Ion torrent platform enhances our understanding on the subject. We are living in fast changing world with path-breaking technological advancements as a norm of the day. In conclusion, microbiome analysis offer exciting promise for future understanding of the respiratory diseases, but significant technical hurdles remain that will only be overcome through years of intensive research. I conclude this write-up with a sense of optimism that our scientific endeavors would make world better place for generations to come.

CONFLICT OF INTERESTS

The author has no conflicts of interest to declar.

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