

The Role of Respiratory Microbiota in the Pathogenesis of Chronic Respiratory Diseases

Abstract

A large number of bacteria, including Firmicutes, Actinobacteria and Bacteroidetes, colonize the respiratory mucosal surfaces of healthy individuals. They interact and coexist with the local mucosal immune system of the human respiratory tract, maintaining immune stability and respiratory system balance. With chronic respiratory diseases, the microbial population in the respiratory tract changes and the proportion of proteobacteria increases in asthmatic patients. The abundance of the microbial population in patients with chronic obstructive pulmonary disease (COPD) decreased and, conversely, the proportion of Firmicutes and Proteobacteria increased. The diversity of the respiratory microbiota in cystic fibrosis (CF) patients is reduced, while pathogenic and conditioned bacteria proliferate in large numbers.

Keywords: Chronic • Immune stability • Proteobacterial • Asthmatic • Asthmatic patients

Introduction

The prevalence of Firmicutes and Proteobacteria was increased in patients with upper respiratory tract cough syndrome (UACS), displacing Streptococcus and Neisseria dominance in the oropharynx of the normal population. Thus, a clear understanding of the airway microbiota immunological pathway and flora immune dysfunction on the pathogenesis of chronic respiratory diseases can yield insights. Novel for the prevention and treatment of respiratory diseases in humans. The human body carries a large group of microbial communities, forming a complex and fragile ecosystem. The complex interaction between bacteria and the human immune system determines the health of the human body. The respiratory tract is an open cavity that connects the human body to the outside world. It is always invaded by external bacteria, so it has a strong local immunity. For example, the respiratory tract contains not only motile cilia, highly secreted goblet cells, and secretory IgA on the mucosal surface, but also abundant submucosa-associated lymphoid tissue sufficient to cope with invasion of foreign pathogens [1]. Once local airway immunity is disrupted, acute and chronic respiratory diseases such as asthma, chronic obstructive pulmonary disease (COPD), cystic fibrosis (CF), and upper respiratory cough syndrome (UACS) is likely to be activated. For a long time, the airways, especially the lower respiratory tract, were considered sterile. The airway is a dynamic ecosystem filled with microbial populations, which are closely related to host immunity and inflammatory response. As in the gut, there are certain types and numbers of microbial populations in the airways of healthy people, i.e. normal flora. Under the influence of external factors, these normal floras are constantly evolving to maintain the dynamic balance of the respiratory micro flora and to resist and avoid invasion and invasion of the respiratory tract. Of pathogens. However, under the influence of external factors, such as environmental pollution and overuse of antibiotics, changes in the respiratory microbiota can lead to pathogenic infections [2]. Even some strains of normal bacteria can turn into conditionally pathogenic bacteria, causing a number of respiratory illnesses. The stability of the respiratory microbiota is greatly influenced by the external environment, affecting the local immune balance of the respiratory tract, even leading to the immune dysfunction of the respiratory system. , thus causing many difficulties for the clinical treatment of respiratory diseases. From a microbiological point of view, it is important to pay attention to local immunity of the respiratory tract in the prevention and treatment of respiratory diseases. In recent years, with the development and

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application of molecular biology techniques, research on the relationship between respiratory microbiota with immunity and respiratory system diseases has been developed. Develop rapidly [3]. Increasing studies have elucidated the role of the complex respiratory microbiota in the course of immune dysfunction in various respiratory diseases, providing new insights to explore disease mechanisms birth and treatment of respiratory diseases. A large number of bacteria reside on the respiratory mucosal surfaces of healthy individuals, the main groups being Firmicutes, Actinobacteria, Bacteroidetes, Proteobacteria and Fusobacteria [4]. Bacteria regulate species and numbers through a quorum sensing system and locally produced antimicrobial peptides to maintain a dynamic balance and achieve peaceful coexistence with the human body [5]. The upper and lower respiratory tract microbiota are very similar, and the upper respiratory tract bacteria population is greater than the lower respiratory tract, which means that there are no specific bacteria in the upper and lower respiratory tract. This is different from the normal gut microbiota [6]. The human airway is mainly protected by the local mucosal immune system. The mucosal epithelial cells act as a physical barrier separating the internal and external environments. They are major structures of the local innate immune system and are major vectors of respiratory flora [7]. There are cilia on the surface of respiratory mucosal epithelial cells, which can transport bacteria of the lower airway upwards, while the mucus secreted by goblet cells and secretory IgA antibodies produced by sub mucosal lymphohistiocytes can further maintain the local chemical immune barrier function of the mucosa and prevent the invasion and colonization of pathogens [8]. However, the local immune system of the airway neither equips with the strong acid and alkali on the surface of alimentary canal mucosa and the powerful germicidal mechanism of excellent enzyme system nor the extremely anaerobic environment, which determines that there is no significant difference in the species but only in the number of bacteria in the upper and lower airway. This is the evolutionary result of the interaction and symbiosis between the airway local immunity and the flora [9]. Asthma is a kind of disease that is well-recognized as immune dysfunction of the respiratory system, which is defined as a clinical syndrome of intermittent respiratory symptoms caused by viral upper respiratory infections, environmental allergens, or other

stimuli, characterized by nonspecific bronchial hyper responsiveness and airway inflammation. Due to the low positive rate of colony culture in sputum in the past and the insignificant effect of antibiotic treatment in the early stage of asthma, it was believed that there was no relationship between bacteria and asthma attacks. An epidemiological study has revealed that bronchial infections may underlie asthma attacks in adults during episodes of bronchitis and pneumonia [10]. This is also consistent with the previously reported efficacy of macrolide antibiotics in the treatment of patients with chronic infectious asthma. With the application of serological tests and PCR-based research methods, he found that *Streptococcus pneumoniae* and *Chlamydia pneumoniae* infections are common in acute asthma attacks. Microbiology analysis of bronchoalveolar lavage (BAL), tracheal brushing, and sputum microbiology revealed that the respiratory microbiota of asthma patients showed a significant increase in airway clearance.

Conclusion

The abundance of proteobacteria in the flora differed significantly from that in healthy subjects. Through culture of respiratory specimens, the rate of bronchial asthma in children caused by bacteria such as *Moraxella catarrhalis*, *Haemophilus influenzae* or *Streptococcus pneumoniae* increased markedly, which is related to the severity of the disease. Severity and exacerbation of asthma. 16S rRNA sequencing results showed that the proportion of proteobacteria, including *Haemophilus influenzae*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and other respiratory pathogens, in respiratory samples of asthma patients was higher than that of the normal population. An increase in these pathogens was also seen in patients on infrequent inhaled hormone therapy, suggesting that this feature of the respiratory microbiota is a feature of asthma itself and not simply result of inhaled hormone immunosuppression. In contrast, the percentage of Bacteroidetes *Prevotella* in the airways of asthmatic patients was lower than that of normal subjects.

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