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Respiratory Microbiota Imbalance in Children with Mycoplasma pneumoniae Pneumonia

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DESCRIPTION

Mycoplasma pneumoniae, a common cause of community-acquired pneumonia in children, presents a significant health concern globally. While the pathogenesis of Mycoplasma pneumoniae pneumonia (MPP) has been extensively studied, the impact of this infection on the respiratory microbiota remains an emerging area of research. Recent investigations suggest that MPP may lead to alterations in the composition and diversity of the respiratory microbiota, potentially exacerbating disease severity and recovery outcomes. Studies examining the respiratory microbiota in children with MPP have revealed notable shifts in bacterial communities within the respiratory tract. The nasopharynx, a critical site for microbial colonization, experiences a decrease in alpha diversity in MPP patients compared to healthy controls. This reduction in microbial diversity may signify a dysbiosis in the respiratory microbiota, which can influence disease progression. Furthermore, MPP is associated with an increase in relative abundance of potentially pathogenic taxa, including Haemophilus, Moraxella, and Streptococcus. These genera have been linked to respiratory infections and have the potential to contribute to disease severity in MPP. Elevated levels of these microbes may disrupt the delicate balance of the respiratory microbiota, creating an environment conducive to pathogenic overgrowth. The perturbations in respiratory microbiota composition during MPP may also have implications for immune response and host defense mechanisms. Dysbiosis induced by MPP could compromise the competitive exclusion of pathogens, diminishing the microbiota's protective role. This imbalance may render the host more susceptible to secondary infections or prolonged illness. Furthermore, the effects of MPP on the respiratory microbiota appear to extend beyond the acute phase of infection. Longitudinal studies have demonstrated that the dysbiotic state induced by MPP can persist even after clinical recovery. This suggests that MPP may have a lasting impact on the respiratory microbiota, potentially influencing susceptibility to recurrent respiratory infections or other respiratory-related disorders. The mechanisms underlying the alterations in respiratory microbiota during MPP are not fully elucidated but are likely multifaceted. The immune response triggered by Mycoplasma pneumoniae may directly influence the composition of the respiratory microbiota. Additionally, the release of inflammatory mediators and antimicrobial agents in response to infection could inadvertently disrupt microbial communities, contributing to dysbiosis. Antibiotic treatment, a cornerstone of MPP management, may also play a role in shaping the respiratory microbiota. While antibiotics are essential for clearing the pathogen, they can simultaneously disrupt commensal bacteria, potentially exacerbating dysbiosis. This highlights the need for judicious antibiotic use and the exploration of strategies to restore and maintain a healthy respiratory microbiota following MPP. Mycoplasma pneumoniae pneumonia has been associated with significant alterations in the respiratory microbiota of affected children. These changes include reduced diversity, increased relative abundance of potentially pathogenic taxa, and potential long-lasting effects on microbial communities. Understanding the impact of MPP on the respiratory microbiota is crucial for developing targeted interventions to restore and maintain a healthy microbial balance, ultimately improving outcomes for children affected by this common respiratory infection.

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CONFLICT OF INTEREST

The author declares there is no conflict of interest in publishing this article.

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