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Recent Trends in Respiratory Infections

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Editorial

The human microbiome, which is made up of commensal, symbiotic, and pathogenic bacteria that live in the human body, plays a vital role in the health and immunity of the host. The human nasal cavity is home to commensal microorganisms that prevent opportunistic diseases from colonizing. However, nasal microbial dysbiosis is linked to various disorders, including acute respiratory infections like otitis media, sinusitis, bronchitis, and allergic respiratory illnesses like asthma.

While SARS coronavirus 2 (SARS-CoV-2) was recently discovered, other coronaviruses are widespread in humans. The typical seasonal cold is caused by four distinct human coronaviruses (HCoV-OC43, HCoV-HKU1, HCoVNL63, and HCoV-229E). SARS-CoV-2–induced sickness, also known as coronavirus disease 2019 (COVID-19), can range from asymptomatic to requiring mechanical ventilation or resulting in death.

Acute lower respiratory infections (ALRIs) are caused by various pathogens, including bacteria, viruses, and fungi. Most respiratory viruses cause ALRIs, such as a respiratory syncytial virus (RSV), influenza viruses, human parainfluenza virus, adenovirus, human metapneumovirus, human rhinovirus, human coronavirus, and human bocavirus, have been discovered for the first time in recent years. RSV is the most common viral cause of hospital admissions, especially in newborns, accounting for over 65 percent of all hospitalized cases.

The birth season has a significant impact on early postnatal bacterial colonization of the upper airways, highlighting the need for future models of the effects of early dynamic changes in airway bacterial populations on later disease development to include the seasonality factor. Although bacterial species and strains are temporary, especially with antibiotic use and pneumococcal immunization protocols, nasopharyngeal colonization commences early in life and is regularly present after that.

Streptococcus pneumonia, non-typeable *Haemophilus influenzae*, and *Moraxella catarrhalis*, which make up most OM's bacterial nasopharyngeal microbiota, are the most prone to undergo virulence shifts. Microbial interactions, microbial carrying load, mucosal integrity, demographic and environmental factors, and host immunity are all factors that impact. In fact, influenza A infections caused an increase in *S. pneumoniae* and *S. aureus* nasal carriage in adults and changes in nasal microbiota between healthy people and influenza–A infected patients. Other viruses, such as adenovirus and rhinovirus, can boost *S. pneumoniae* colonization in the nasal and respiratory tract, raising the risk of pneumococcal illness. After many viral infections in neonates, such as respiratory syncytial virus or rhinovirus, high *H. influenza* or *Moraxella* nasal carriages were detected.

The most common consequences in children with complex disorders are acute and chronic rhinosinusitis. As a result, substantial research has been carried out. Several of them have shed light on various microbiological features of rhinosinusitis, such as epidemiology and the involvement of bacterial biofilm makers. The microbiota of the nasal sinus has recently been studied in healthy children and adults. However, no definite bacterial or viral etiology has been identified, and information is still limited. According to a few research, microbial diversity rises dramatically with age.

Pneumococcus co-colonization and polymicrobial interactions with other respiratory colonizers, primarily non-typeable *H. influenza* and *M. catarrhalis* result in various hazards for the development of OM. Numerous pneumococcal serotypes show decreased progression rates to OM in children with non-tippable *H. influenza* and *S. pneumonia* in the nasopharynx, and non-typeable *H. influenza* is likely the etiology in up to 75% of cases.

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