LETTER TO EDITOR

The growing concern of human metapneumovirus

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Dear Editor,

Human metapneumovirus (hMPV) is a significant yet often overlooked respiratory pathogen belonging to the Pneumoviridae family that is closely related to the respiratory syncytial virus (RSV). Both viruses primarily cause upper respiratory infections that resemble the common cold or flu but can progress to severe conditions, such as bronchiolitis, bronchitis, pneumonia, and chronic obstructive pulmonary disease (COPD). While RSV has received considerable attention, leading to the development of vaccines and prophylactic treatments, hMPV remains underrecognized despite its potential to cause severe illness, hospitalization, and mortality in vulnerable populations. This article aims to highlight the global health implications of hMPV, emphasizing its epidemiology, diagnostic challenges, and potential pandemic threats while addressing gaps in current research and public health policies.

HMPV IN IMMUNOCOMPETENT ADULTS: A GROWING CONCERN

A notable case involves a 68-year-old immunocompetent male diagnosed with severe community-acquired pneumonia (CAP) caused by hMPV. The diagnosis was confirmed using multiplex reverse transcription polymerase chain reaction (RT-PCR), ruling out bacterial and other viral coinfections. Initially mismanaged with empirical antibiotics, the patient showed significant improvement with supportive care alone, reinforcing the importance of rapid molecular diagnostics in preventing unnecessary antibiotic usage. However, rather than suggesting that hMPV is easily treatable, this case underscores the need for heightened clinical awareness and improved diagnostic strategies to effectively distinguish viral from bacterial pneumonia.[1]

Epidemiological insights from the Puducherry Outbreak between November 2022 and March 2023, an outbreak of hMPV in Puducherry, India, revealed crucial epidemiological patterns. A positivity rate of 9.6% was recorded during the outbreak, with the highest prevalence among children under one year of age. Genetic sequencing identified novel lineages A2.2.1 and A2.2.2, highlighting the virus's evolving nature. This outbreak underscores the necessity for robust epidemiological studies and enhanced surveillance strategies to monitor emerging hMPV variants and their potential impact on public health.[2]

AVIAN METAPNEUMOVIRUS (AMPV) AND ITS IMPLICATIONS FOR HMPV

aMPV is another member of the pneumoviridae family that primarily infects poultry, causing respiratory disease and significant economic losses in the poultry industry. While aMPV and hMPV share genetic and structural similarities, their relationship and potential cross-species transmission remain unclear. However, studying aMPV provides valuable insights into pneumovirus evolution, host adaptation mechanisms, and viral recombination. The development of advanced diagnostic tools for aMPV, such as multiplex real-time PCR assays, highlights the importance of rapid detection methods, which could be adapted for improved hMPV diagnostics. Further research into the evolutionary relationship between aMPV and hMPV, particularly regarding the possibility of zoonotic transmission and the emergence of new viral strains, is essential.[3]

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TEMPORAL ASSOCIATIONS BETWEEN RESPIRATORY VIRUSES AND INVASIVE BACTERIAL INFECTIONS

The interplay between viral and bacterial infections is well-documented, with influenza often acting as a precursor to invasive bacterial diseases. However, the specific role of hMPV in predisposing individuals to secondary bacterial infections, such as invasive group A streptococcal (iGAS) disease and invasive pneumococcal disease (IPD), remains underexplored. While a recent study investigated the temporal association between respiratory viruses and bacterial infections, it focused primarily on influenza and rhinoviruses, making it less relevant to hMPV. Future research should examine whether hMPV increases susceptibility to bacterial superinfections, similar to RSV and influenza, to inform better clinical management strategies.[4]

HMPV AND THE PANDEMIC THREAT: A GLOBAL PERSPECTIVE

Recent outbreaks of hMPV in China have raised concerns about its pandemic potential. While hMPV is not currently considered a pandemic-level threat, its high infectivity and genetic variability warrant closer examination. Could hMPV mutate to become more virulent or transmissible among humans If so, what genetic changes would facilitate such a transition Unlike influenza, which undergoes frequent antigenic shifts, hMPV exhibits slower genetic evolution; however, recombination events and immune escape mutations could enhance its pandemic potential. This section emphasizes the need for intensified genomic surveillance, functional virology studies, and predictive modeling to assess the likelihood of hMPV becoming a global public health threat.[5]

THE "IMMUNE DEBT" HYPOTHESIS AND THE RESURGENCE OF HMPV

The post-pandemic surge in hMPV cases may be linked to the "immune debt" hypothesis, which suggests that reduced exposure to common pathogens during COVID-19 lockdowns led to increased susceptibility upon reopening. This phenomenon has been observed with other respiratory viruses, highlighting the importance of maintaining routine viral surveillance and preparedness measures to mitigate future outbreaks.[6]

THERAPEUTIC ADVANCES AND FUTURE DIRECTIONS

Despite its clinical significance, hMPV lacks targeted antiviral treatments or vaccines. While computational studies have identified promising natural compounds, such as epigallocatechin gallate (EGCG), rutin, and quercetin, as potential inhibitors of the hMPV matrix protein, further experimental validation is necessary. Additionally, given the success of RSV monoclonal antibodies and vaccines, similar approaches to Preventing hMPV should be explored. Advancing research into antiviral drug development and vaccine candidates is crucial to reducing the global disease burden associated with hMPV.[7]

hMPV remains an underrecognized yet significant respiratory pathogen with the potential for severe disease outcomes, particularly among vulnerable populations. The increasing incidence of hMPV, its genetic diversity, and its possible role in secondary bacterial infections highlight the need for enhanced surveillance, rapid diagnostics, and vaccine development. By addressing the gaps in our understanding of hMPV and its public health impact, we can develop more effective strategies to mitigate its burden and prevent future outbreaks. Given the evolving landscape of respiratory viral infections, hMPV must be prioritized in research and public health efforts alongside RSV and influenza.

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Use of large language models, AI and machine learning tools

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REFERENCES

1. Costa-Filho RC, Saddy F, Costa JL, Tavares LR, Castro Faria Neto HC. The silent threat of human metapneumovirus: Clinical challenges and diagnostic insights from a severe pneumonia case. *Microorganisms*. 2025;13(1):73.
2. Devanathan N, Philomenadin FS, Panachikuth G, *et al*. Emerging lineages A2. 2.1 and A2. 2.2 of human metapneumovirus (hMPV) in pediatric respiratory infections: Insights from India. *IJID Reg*. 2025;14:100486.
3. Su M, Cheng J, Xu X, *et al*. Establishment and application of a one-step multiplex real-time PCR assay for detection of A, B, and C subtypes of avian metapneumovirus. *Poult Sci*. 2025;104(1):104608.
4. Banerjee A. Outbreak In China due to HMPV: Can "immune debt" explain it. *J Epidemiol Found India*. 2025;3(1):1-2.
5. Teoh Z, Fenchel M, Griffin C, *et al*. Temporal association between respiratory viruses and invasive streptococcal disease. *Pediatr Open Sci*. 2025;1(1):1-9.
6. Dubey A, Kumar M, Tufail A, Dwivedi VD. Harnessing computational insights to identify potent inhibitors for human metapneumovirus (HMPV): A synergistic approach with natural compounds. *bioRxiv*. 2025:2025-01.
7. Zhang L, Wang Y, Zheng Y, *et al*. Epidemiological characteristics of pathogens in bronchoalveolar lavage fluid in children with lower respiratory tract infections: A retrospective analysis. *Pediatr Pulmonol*. 2025;60(1):e27469.