

A Report on Human Metapneumovirus (HMPV)

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Abstract

Human Metapneumovirus (HMPV) is a common respiratory virus that affects people of all ages, especially young children, the elderly, and those with weakened immune systems. It can cause respiratory illnesses, ranging from mild symptoms to serious conditions like bronchiolitis and pneumonia. HMPV is an RNA virus that spreads easily through respiratory droplets, direct contact with infected surfaces, or touching contaminated objects. People at higher risk include infants, the elderly, those with weakened immune systems, and individuals with respiratory issues like asthma or COPD. In severe cases, it can lead to hospitalization or, rarely, death. Coinfections with viruses like RSV or influenza can make symptoms worse. HMPV is diagnosed using advanced molecular tests like RT-PCR, antigen detection methods, such as immunofluorescence and enzyme immunoassays. Treatment focuses on supportive care, while prevention involves good hygiene and infection control. Promising research is underway to develop vaccines and antibody therapies to help reduce its impact. This paper explores the virus, its effects, diagnosis, treatment, and ongoing research efforts.

Keywords: HMPV, Infections, Respiratory, Vaccines.

Introduction

Human Metapneumovirus (HMPV) is a significant respiratory pathogen that primarily affects the respiratory tract and poses a major public health concern (1). It is a leading cause of morbidity across various age groups, particularly in young children, the elderly, and immunocompromised individuals. First identified in 2001 in the Netherlands, HMPV was found in respiratory samples from children presenting with unexplained respiratory illnesses (2). This discovery marked a pivotal moment in the field of virology, revealing a previously unknown contributor to respiratory tract infections (RTIs). HMPV belongs to the Paramyxoviridae family, a group of viruses that includes other respiratory pathogens such as the respiratory syncytial virus (RSV) and parainfluenza viruses. Phylogenetic analysis has shown that HMPV shares a close evolutionary relationship with RSV, though it exhibits unique genomic and antigenic properties. Despite its relatively recent identification, retrospective studies have demonstrated its presence in human populations for several decades, suggesting it has been an unrecognized cause of respiratory diseases worldwide.

HMPV infections typically manifest as upper or lower respiratory tract illnesses, ranging from mild symptoms to severe conditions like bronchiolitis and pneumonia. The virus contributes significantly to the global burden of respiratory illnesses, with seasonal outbreaks observed primarily during late winter and early spring. Epidemiological studies indicate that nearly all individuals are exposed to HMPV by the age of five, emphasizing its widespread prevalence. This report delves into the virology, structure, epidemiology, clinical manifestations, diagnosis, and management of HMPV, highlighting its impact on public health and ongoing research efforts to develop effective vaccines and therapeutic interventions.

Structure of Human Metapneumovirus (HMPV)

HMPV is an enveloped, single-stranded, negative-sense RNA virus with a complex structure that facilitates its ability to infect host cells. Its lipid envelope, the outermost layer, is a lipid bilayer derived from the host cell membrane. It is embedded with surface glycoproteins, including the G glycoprotein, which facilitates viral attachment to

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the host cell by binding to cell surface receptors and the F glycoprotein for membrane fusion, allowing the viral genome to enter the host cell. It is embedded with surface glycoproteins crucial for viral attachment and fusion. Beneath the envelope, the matrix protein provides structural support and aids in virus assembly and budding. The nucleocapsid consists of the single-stranded, negative-sense viral RNA genome, approximately 13 kilobases in length, encapsidated by the nucleoprotein (N). The polymerase complex, consisting of the large polymerase (L) protein and

the phosphoprotein (P), is vital for RNA replication and transcription. Additionally, the small hydrophobic (SH) protein, its precise function remains unclear, but it is thought to play a role in evading the host immune response. This structural organization is critical for the virus's replication cycle, including attachment, entry, replication, and assembly. Understanding these components has been pivotal in developing therapeutic strategies, such as vaccines and monoclonal antibodies. The general structure of HMPV adopted from past research (3) is shown in Figure 1.

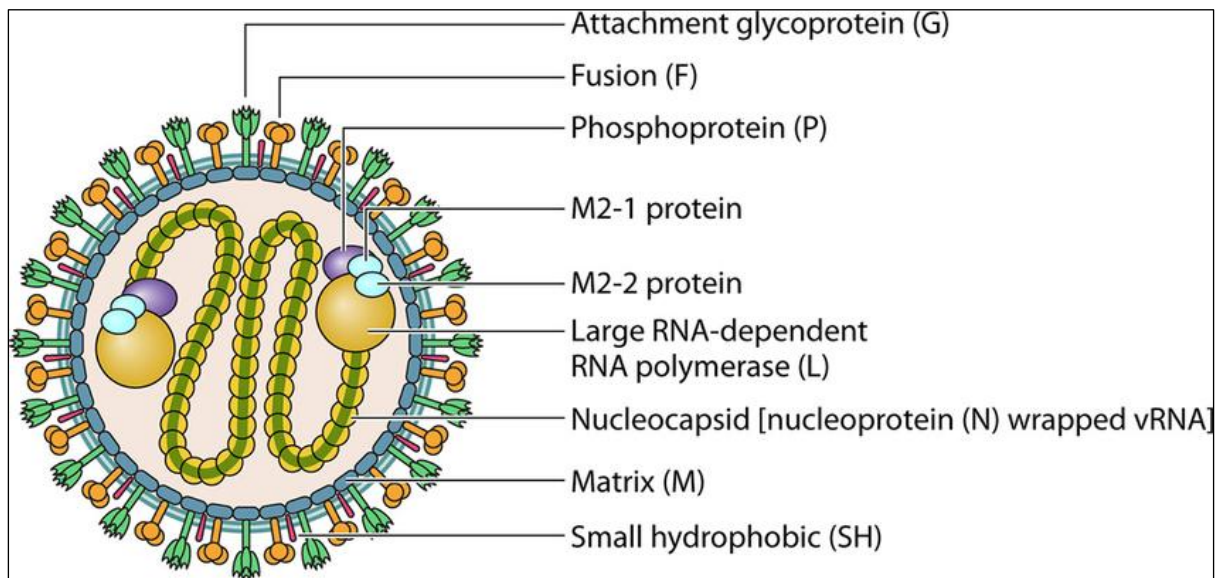


Figure 1: General Structure of the HMPV (3)

Virology and Transmission

HMPV is an enveloped, single-stranded, negative-sense RNA virus with two major subgroups, A and B, each further divided into genotypes. The virus primarily spreads via respiratory droplets, direct contact with infected secretions, or fomites. Like other respiratory viruses, HMPV is highly contagious, with an incubation period of approximately 4-6 days.

Epidemiology

HMPV infections occur globally, with nearly universal exposure by the age of 5 years (4, 5). Seasonal patterns mimic those of RSV and influenza, peaking during colder months. The virus contributes significantly to respiratory infections in young children, ranking as the second most common cause of lower respiratory tract infections (LRTIs) after RSV. Populations at higher risk of HMPV infection include infants and young children, particularly those under 2 years of age, as their immune systems are still developing. Elderly

individuals are also vulnerable due to decline in immunity. Immunocompromised patients, such as organ transplant recipients and those undergoing chemotherapy, face increased risk due to weakened immune defenses. Additionally, patients with underlying respiratory conditions such as asthma or chronic obstructive pulmonary disease (COPD) are also susceptible to severe complications from the infection.

Since its discovery, HMPV has been extensively studied to understand its epidemiological significance and clinical impact. Early research identified its genetic similarity to RSV and its role in causing lower respiratory tract infections (LRTIs), particularly in young children. Epidemiological studies estimate that HMPV accounts for 5-15% of annual respiratory infections globally (6), with a disproportionate burden on vulnerable groups, including infants, the elderly, and immunocompromised individuals. Clinical studies have demonstrated a wide spectrum of disease severity, ranging from mild

upper respiratory symptoms to severe LRTIs such as bronchiolitis and pneumonia. Coinfections with other respiratory viruses, such as RSV and influenza, often lead to worsened outcomes. Advances in molecular diagnostics, particularly the use of RT-PCR, have greatly improved the detection and surveillance of HMPV. However, challenges remain in distinguishing HMPV infections from those caused by other respiratory pathogens based on clinical presentation alone. Efforts to develop vaccines and antiviral therapies are ongoing. Experimental vaccines and monoclonal antibodies targeting HMPV have shown promise in preclinical trials, though no licensed products are currently available. Research emphasizes the importance of preventive measures, such as hand hygiene and infection control practices, to limit the spread of HMPV, particularly in healthcare and community settings.

Past Researches on HMPV

HMPV was first identified by Van den Hoogen *et al.* in 2001, their work described the virus's genetic similarity to RSV and highlighted its role in respiratory illnesses (2). Subsequent epidemiological studies in the early 2000s revealed its global prevalence and seasonal distribution, with other researchers demonstrated a high incidence of HMPV among hospitalized elderly patients and those with chronic cardiopulmonary diseases (7). Some findings emphasized HMPV's significant contribution to pediatric hospitalizations for lower respiratory tract infections (LRTIs) (8). Their findings showed that children under the age of two were particularly vulnerable, while other researchers documented cases of severe respiratory infections in immunocompromised patients, underscoring the virus's clinical severity (9). Advances in diagnostics, such as the development of sensitive RT-PCR assays by Mackay *et al.*, revolutionized the detection of HMPV, enabling more accurate epidemiological and clinical studies (10). Some study explored the impact of HMPV coinfections with other respiratory viruses, such as RSV and influenza, finding increased disease severity in such cases (11). Efforts to combat HMPV have included the development of live-attenuated vaccines, with promising immunogenicity observed in animal models (12) and the exploration of monoclonal antibodies as potential therapies, as investigated (13).

Clinical Manifestations

HMPV infections can range from mild upper respiratory tract symptoms, such as cough, nasal congestion, fever, and sore throat, to severe lower respiratory tract infections (LRTIs), including bronchiolitis and pneumonia. Severe cases may present with wheezing, difficulty breathing, hypoxia, and dehydration. In high-risk groups, HMPV can lead to hospitalization and, in rare cases, death. Coinfections with other pathogens, such as RSV or influenza, can exacerbate disease severity.

Diagnosis

HMPV infection requires clinical suspicion based on symptoms and confirmation through laboratory tests. Molecular assays, particularly reverse transcription polymerase chain reaction (RT-PCR), are the gold standard for detecting HMPV RNA due to their high sensitivity and specificity. Antigen detection methods, such as immunofluorescence and enzyme immunoassays, are also used for rapid diagnosis. Serological tests measuring HMPV-specific antibodies can provide evidence of past infection but less commonly used in acute settings.

Treatment and Prevention

There is no specific antiviral therapy for HMPV, and management is primarily supportive. This includes oxygen therapy for patients with hypoxia, hydration through oral or intravenous fluids, and symptom relief with antipyretics and analgesics. Preventive measures are similar to those for other respiratory viruses and include regular handwashing, avoiding close contact with infected individuals, and implementing infection control practices, such as isolating infected patients in healthcare settings. Research is ongoing to develop effective vaccines and antiviral agents targeting HMPV. Experimental vaccines and monoclonal antibodies have shown promise in preclinical and early clinical trials.

Public Health Implications

HMPV represents a significant burden on healthcare systems due to its contribution to respiratory illnesses, particularly during peak seasons. Increased awareness among healthcare providers and the public is crucial to improve diagnosis, management, and prevention. Surveillance programs play a vital role in understanding epidemiological trends and guiding vaccine development efforts.

Research Gaps and Future Scope

The research gap on HMPV lies in several critical areas that hinder the complete understanding and effective management of this pathogen. Despite notable advancements since its discovery in 2001, gaps persist in vaccine development, with no approved vaccines available and ongoing difficulties in eliciting long-lasting immunity across diverse populations. Therapeutic options are also limited. No specific antiviral therapies for HMPV are available, and current treatment remains supportive. Research into antiviral agents, such as small molecules targeting the F glycoprotein or replication machinery, is still in experimental stages. The lack of therapeutic interventions leaves high-risk populations, including the immunocompromised, without targeted treatment options. The pathogenesis and immune evasion mechanisms by which HMPV causes disease and evades the host immune response are not fully understood. Studies on the role of the SH protein, immune modulation, and interactions with the host cellular machinery are sparse, limiting insights into how the virus establishes infection and persists. Most epidemiological studies on HMPV have been conducted in high-income countries. Data from low- and middle-income countries (LMICs), where the burden of respiratory infections is high, are limited. This lack of information hampers the global understanding of HMPV's impact and its contribution to respiratory diseases in these regions. Additionally, the impact of coinfections with other respiratory viruses on disease severity and outcomes is poorly understood. The long-term consequences of severe HMPV infections, particularly in children who experience bronchiolitis or pneumonia, are not well-documented. Whether these infections predispose individuals to chronic respiratory conditions later in life remains an area of active investigation. Finally, Variations among HMPV subgroups and genotypes, and their implications for disease severity and immune response, require further study. Such knowledge is essential for designing broad-spectrum vaccines and therapies. Addressing these gaps through multidisciplinary research efforts will enhance our understanding of HMPV and lead to more effective preventive and therapeutic strategies.

The future scope of research on HMPV is vast and includes several promising areas that could significantly improve our understanding and management of this pathogen. A top priority is the development of effective vaccines, for eliciting robust and long-lasting immunity research should focus on identifying optimal antigens, such as the F and G glycoproteins. Advances in mRNA vaccine technology and other novel platforms could accelerate this process. Parallel efforts in antiviral therapies, including small-molecule inhibitors, RNA-based treatments, and monoclonal antibodies targeting on the F glycoprotein and polymerase complex hold significant potential, offer potential breakthroughs. A deeper understanding of the immune response, particularly immune evasion mechanisms like the SH protein, is essential for advancing therapeutic and vaccine design. Elucidating the molecular mechanisms of HMPV-induced disease, including how the virus triggers inflammation and tissue damage, is vital. Studies should investigate the roles of viral proteins in modulating host cell signaling and immune responses.

More comprehensive data on the global burden of HMPV, particularly in resource-limited settings, is needed. Research should also explore regional variations in HMPV genotypes and their clinical impact to inform vaccine and therapeutic design. Investigating HMPV's role in coinfections with other respiratory pathogens and its impact on disease severity can improve clinical management strategies. Understanding these interactions may help guide treatment protocols and prioritize vaccine development.

Studies on the long-term consequences of severe HMPV infections, especially in children, are necessary to determine whether these infections predispose individuals to chronic respiratory conditions like asthma or reduced lung function. Developing rapid, point-of-care diagnostic methods that are cost-effective and widely accessible will enhance early detection, reduce misdiagnosis, and enable timely interventions. Research into HMPV's evolutionary dynamics and its potential to jump between species is crucial for understanding its emergence and preventing potential zoonotic outbreaks. Finally, robust public health strategies, including cost-effectiveness analyses of vaccines and antivirals, will guide policies to mitigate HMPV's impact globally. By

addressing these areas, future research will not only advance the scientific understanding of HMPV but also contribute to the development of effective preventive and therapeutic measures, ultimately reducing its global health burden.

Conclusion

HMPV is a pervasive and clinically significant respiratory pathogen that poses challenges to public health systems worldwide. Since its discovery in 2001, substantial progress has been made in understanding its virology, epidemiology, and clinical impact. HMPV is now recognized as a leading cause of respiratory infections, especially in vulnerable populations such as young children, the elderly, and immunocompromised individuals. The virus's ability to cause mild to severe respiratory illnesses underscores its clinical significance, while its global prevalence highlights the need for ongoing research and public health interventions.

Despite advances in diagnostic methods, such as RT-PCR and antigen detection, the lack of specific antiviral treatments and vaccines remains a major challenge. Current management strategies rely on supportive care, emphasizing the importance of preventive measures like hygiene practices and infection control protocols. Encouragingly, recent research into vaccine development and monoclonal antibody therapies shows promise, offering hope for targeted interventions to reduce the burden of HMPV in the future.

HMPV's seasonal patterns and its role in coinfections with other respiratory pathogens underscore the importance of robust surveillance systems. These systems are crucial for tracking epidemiological trends, guiding clinical management, and informing vaccine development.

Abbreviations

HMPV: Human Metapneumovirus, RTIs: Respiratory Tract Infections, RSV: Respiratory Syncytial Virus, COPD: Chronic obstructive pulmonary disease, LRTIs: Lower respiratory tract infections.

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Author Contributions

All authors contributed equally.

Conflict of Interest

Authors declare no conflict of interest.

Ethics Approval

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References

- Schuster JE, Williams JV. Human metapneumovirus. *Pediatrics in review*. 2013 Dec 1;34(12):558-65.
- Van den Hoogen BG, de Jong JC, Groen J, Kuiken T, de Groot R, Fouchier RA, Osterhaus AD. A newly discovered human pneumovirus isolated from young children with respiratory tract disease. *Nature medicine*. 2001 Jun;7(6):719-24.
- Céspedes PF, Palavecino CE, Kaleris AM, Bueno SM. Modulation of host immunity by the human metapneumovirus. *Clinical Microbiology Reviews*. 2016 Oct;29(4):795-818.
- Panda S, Mohakud NK, Pena L, Kumar S. Human metapneumovirus: review of an important respiratory pathogen. *International journal of infectious diseases*. 2014 Aug 1;25:45-52.
- Lefebvre A, Manoha C, Bour JB, Abbas R, Fournel I, Tiv M, Pothier P, Astruc K, Aho-Glélé LS. Human metapneumovirus in patients hospitalized with acute respiratory infections: a meta-analysis. *Journal of Clinical Virology*. 2016 Aug 1;81:68-77.
- Miyakawa R, Zhang H, Brooks WA, Prosperi C, Baggett HC, Feikin DR, Hammitt LL, Howie SR, Kotloff KL, Levine OS, Madhi SA. Epidemiology of human metapneumovirus among children with severe or very severe pneumonia in high pneumonia burden settings: the Pneumonia Etiology Research for Child Health (PERCH) study experience. *Clinical Microbiology and Infection*. 2024 Nov 1. <https://www.sciencedirect.com/science/article/abs/pii/S1198743X24005056>
- Falsey AR, Erdman D, Anderson LJ, Walsh EE. Human metapneumovirus infections in young and elderly adults. *The Journal of infectious diseases*. 2003 Mar 1;187(5):785-90.
- Parks OB, Eddens T, Zhang Y, Oury TD, McElroy A, Williams JV. Human metapneumovirus reinfection in aged mice recapitulates increased disease severity in elderly humans infected with human metapneumovirus. *ImmunoHorizons*. 2023 Jun 1;7(6):398-411.
- Boivin G, Abed Y, Pelletier G, Ruel L, Moisan D, Côté S, Peret TC, Erdman DD, Anderson LJ. Virological features and clinical manifestations associated with human metapneumovirus: a new paramyxovirus responsible for acute respiratory-tract infections in all age groups. *The Journal of infectious diseases*. 2002 Nov 1;186(9):1330-4.
- Mackay IM, Jacob KC, Woolhouse D, Waller K, Symmis MW, Whitley DM, Siebert DJ, Nissen M, Sloots TP. Molecular assays for detection of human metapneumovirus. *Journal of clinical microbiology*. 2003 Jan;41(1):100-5.
- Semple MG, Cowell A, Dove W, Greensill J, McNamara PS, Halfhide C, Shears P, Smyth RL, Hart CA. Dual infection of infants by human metapneumovirus and human respiratory syncytial virus is strongly

- associated with severe bronchiolitis. The Journal of infectious diseases. 2005 Feb 1;191(3):382-6.
12. Goutagny N, Jiang Z, Tian J, Parroche P, Schickli J, Monks BG, Ulbrandt N, Ji H, Kiener PA, Coyle AJ, Fitzgerald KA. Cell type-specific recognition of human metapneumoviruses (HMPVs) by retinoic acid-inducible gene I (RIG-I) and TLR7 and viral interference of RIG-I ligand recognition by HMPV-B1 phosphoprotein. The journal of immunology. 2010 Feb 1;184(3):1168-79.
13. Ulbrandt ND, Ji H, Patel NK, Riggs JM, Brewah YA, Ready S, Donacki NE, Folliot K, Barnes AS, Senthil K, Wilson S. Isolation and characterization of monoclonal antibodies which neutralize human metapneumovirus in vitro and in vivo. Journal of virology. 2006 Aug 15;80(16):7799-806.