



CURRENT PERSPECTIVE ON HUMAN METAPNEUMOVIRUS (HMPV) OUTBREAK

**Rajeswar Reddy Kasarla*

Department of Microbiology, Malla Reddy Institute of Medical Sciences, Hyderabad, India

*Corresponding Author

Rajeswar Reddy Kasarla

Email: reddysir4861@gmail.com

ORCID: <https://orcid.org/0000-0001-5422-2328>

CITATION

Kasarla RR, Current Perspective on Human Metapneumovirus (HMPV) Outbreak, MJEN. 2025 December;4(2); (1-3)

A serious global health concern of another health crisis after COVID-19 pandemic is an outbreak of acute respiratory infections with human Metapneumovirus (hMPV) originating in Henan, China and spread rapidly, along with simultaneous circulation of Influenza A, *Mycoplasma pneumoniae* and Covid-19 strains [1]. The hMPV spread from an infected person to others through secretions from coughing and sneezing, close personal contact, such as touching or shaking hands, touching objects or surfaces that have the viruses on them then touching the mouth, nose, or eyes. The infections are usually mild, affecting infants, elderly or immunocompromised, and common in winter and early spring. Early symptoms include runny nose, cough, and sore throat. Good hygiene practices, such as regular hand washing and avoiding close contact with infected individuals are important in prevention [2].

The disease is already globally present and has been around for decades. This means people across the world have "some degree of existing immunity due to previous exposure", with every emerging and re-emerging disease, discussing data and evidence becomes crucial. HMPV has been at the center of significant misinformation recently and there are many myths and misconceptions about hMPV infections [3].

ETIOLOGY

The hMPV was first reported in 2001 by van den Hoogen from nasopharyngeal secretions (swabs) of patients with respiratory disease in Netherlands [4]. It is classified in the Pneumovirinae subfamily of the Paramyxoviridae family (the same viral family that includes RSV, measles, and mumps). In 2016, the genus Metapneumovirus was reclassified within the Pneumoviridae family. The genus Metapneumovirus includes two viral species, human metapneumovirus (hMPV) and avian pneumovirus (aMPV). Avian metapneumovirus (aMPV) causes upper respiratory tract and reproductive tract infections, mainly in poultry, turkeys, and ducks [3].

The hMPV is an enveloped non-segmented single stranded, negative sense, RNA virus, measuring approximately 150 nm to 600 nm in diameter. The nucleocapsid (N) protein surrounds the viral RNA in helical symmetry, forming a ribonucleate complex that protects the genome and serves as a template for transcription and replication. The phosphoprotein (P) acts as a cofactor, linking the N protein with large (L) polymerase protein, facilitating RNA synthesis. The envelope is a lipid bilayer, derived from host cell membrane and contains three surface glycoprotein peplomers: fusion protein (F), glycoprotein (G), and small hydrophobic protein (SH). The RNA genome is of approximately 13.3 kilobases, encoding nine structural proteins: N-P-M-F-M2.1-M2.2-SH-G-L. The hMPV lacks the non-structural proteins NS1 and NS2 found in related viruses like RSV [1,5].



©Authors retain copyright and grant the journal right of first publication. Licensed under Creative Commons Attribution License CC - BY 4.0 which permits others to use, distribute and reproduce in any medium, provided the original work is properly cited.



ARTICLE INFO:

Received Date: 5th August 2025

Accept Date: 3rd November 2025

Published Date: 29th December 2025

The glycoprotein (G) spikes are primarily responsible for attachment by binding to cellular receptors on host cell membrane in the respiratory tract. Thus glycoprotein (G) spikes facilitate the initial contact between the virus and host cell. Studies suggest that the G protein binds to heparan sulfate and other glycosaminoglycans on the surface of target cells, initiating infection. The fusion protein (F) facilitates the fusion of the viral envelope with the host cell membrane, causing viral entry into host cell. The F protein undergoes significant conformational (pre-fusion and post-fusion) changes during this process. Small hydrophobic protein (SH) is believed to function as a viroporin and play a role in modulating the host's immune response, contributing to viral pathogenicity [1,3,5].

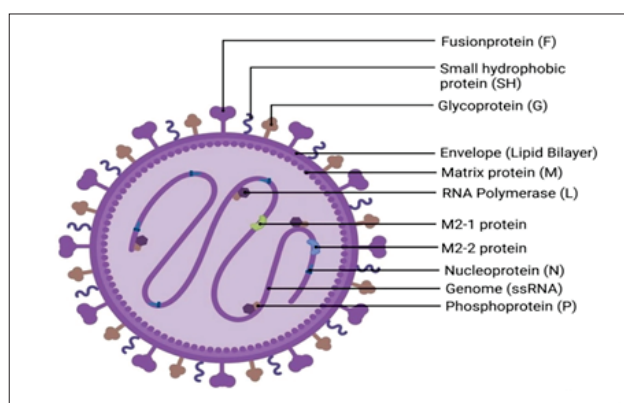


Figure: 1 Structure of human metapneumovirus [3]

The whole genome analysis has shown that hMPV exists as two major genotypes, A and B (hMPV-A and hMPV-B), which are further divided into six subtypes A1, A2a, A2b, A2c, and B1, B2, with A2c and B2 being the most common. The A2c subtype was the predominant variant globally until 2022. A2b (hMPV-A2b) subtype is believed to be responsible for current outbreak in China [6].

Detailed structural knowledge of hMPV proteins, especially G and F proteins is important in vaccine design and developing antiviral strategies. For example, stabilizing the pre-fusion conformation of the protein has been a focus in vaccine development, aiming to elicit a strong neutralizing antibody response [5,6].

EPIDEMIOLOGY

The hMPV is transmitted through inhalation of airborne secretions/droplets released out from coughing or sneezing. Close personal contact such as shaking hands or touching; touching contaminated objects or surfaces such as phones, doorknobs, keyboards, pens, pencils, towels, or toys and then touching the mouth, nose or eyes, making it highly contagious in crowded settings. Most of the infections are mild and only 5% of cases may require hospitalization and the mortality

rate below 1% [1,7].

The hMPV can cause upper and lower respiratory disease including the nose, throat, and lungs. It affects people of all ages, especially among young children under five years old, especially infants, older adults those over 65, immunocompromised people, and people with chronic respiratory conditions like asthma or COPD are at higher risk [1,7].

CLINICAL SYMPTOMS

The incubation period is three to six days. The virus attaches to respiratory epithelium by its glycoprotein (G) spike, and can cause illness ranging from mild cold like symptoms to more severe respiratory conditions. The duration of the illness can vary, depending on the severity of the infection. Symptoms are similar to other viral infections that cause upper and lower respiratory infections, that include cough often with expectoration, hoarseness, runny or stuffy nose (nasal congestion), fever, sore throat, wheezing, difficulty breathing or cyanosis (bluish skin) in severe cases. In some cases, the infection can progress to severe respiratory distress, such as bronchopneumonia, or aggravate chronic obstructive pulmonary disease (COPD), and otitis media [1,3,8].

While many individuals recover from hMPV without complications, infants and younger children, older adults, and individuals with weakened immune systems are at higher risk for severe illness [8].

Those with underlying respiratory conditions, such as asthma or chronic obstructive pulmonary disease (COPD) complications can include broncheolitis, pneumonia, and exacerbation of chronic respiratory disease [8].

DIAGNOSIS

Routine lab testing is very rare unless symptoms are severe or there's an outbreak. Diagnosis involves reviewing the patient's medical history, conducting a physical examination, and from nasopharyngeal secretions (swabs), RNA can be extracted and amplified by RT-PCR. Specific viral antigens can be directly detected in nasopharyngeal secretions using direct immunofluorescence or enzyme immunoassay [9].

TREATMENT

Most cases are mild and can be managed at home with rest and hydration and taking paracetamol for fever. Currently, there is no specific antiviral therapy or vaccine to prevent hMPV. Symptomatic treatment and supportive care can be given. Severe cases may require hospitalization, oxygen therapy, intravenous fluids help maintain hydration or corticosteroids to reduce inflammation and to manage symptoms [10].

PREVENTION

Since there is no specific antiviral treatment, prevention is a key to control hMPV spread. It is recommended to follow basic standard preventive measures precautions to prevent the spread of infection [1,7].

- Washing hands regularly and thoroughly, with soap and water or an alcohol-based hand rub
- Avoiding touching eyes, nose, mouth, and face with unwashed hands
- Maintaining good respiratory hygiene
- Covering mouth and nose while coughing and sneezing with handkerchief or towel
- Avoiding crowded places and maintaining distance from infected people
- Wear masks while stepping out or while sneezing or coughing and in crowded places
- Avoiding sharing utensils, cups or other personal items to reduce the chances of infecting others
- Avoid kissing others
- Staying home and self-isolation during illness, and
- Take nutritious food and improve gut health with fruits, vegetables, and fermented foods

- Improving ventilation where possible (such as by opening a window for air flow)

CONCLUSION

The hMPV is not a newly discovered virus, does not pose a pandemic threat, although the incidence of hMPV respiratory infections have increased recently due to winter occurrence as seasonal surges are typical. The current hMPV outbreak in China is not new and occurring for the last eight years. Covid-19 lockdown and reduced social interaction had limited the spread of many viruses, leaving people, especially children less exposed to common pathogens and increasing the susceptibility among them. Once lockdown was lifted, social interactions returned, many are encountering these viruses for the first time causing a surge in respiratory infections.

The growing respiratory infections of hMPV demands enhanced surveillance, targeted research, and awareness to this challenge. Research should be focused on developing vaccines, understanding virus behavior, and improving treatment protocols to better manage hMPV infections.

REFERENCES

1. Ji wangquan, et al. Clinical and epidemiological characteristics of 96 pediatric human metapneumovirus infections in Henan, China after covid-19 pandemic: a retrospective analysis. *Virology Journal*. 2024;21:100.
2. Chan WS, Yau SK, To MY, Leung SM, Wong KP, Lai KC, et al. The seasonality of respiratory viruses in a Hong Kong hospital, 2014–2023. *Viruses*. 2023;15(9):1820.
3. Vinci A, Lee PJ, Krilov LR. Human Metapneumovirus Infection. *Pediatr Rev*. 2018 Dec;39(12):623–624.
4. van den Hoogen BG, de Jong JC, Groen J, Kuiken T, de Groot R, Fouchier RA, et al. A newly discovered human pneumovirus isolated from young children with respiratory tract disease. *Nat Med*. 2001;7(6):719–24.
5. Leyrat C, Paesen GC, Charleston J, Renner M, Grimes JM. Structural insights into the human metapneumovirus glycoprotein ectodomain. *J Virol*. 2014 Oct;88(19):11611–6.
6. Zhu R, Guo C, Zhao L, Deng J, Wang F, Sun Y, et al. Epidemiological and genetic characteristics of human metapneumovirus in pediatric patients across six consecutive seasons in Beijing, China. *Int J Infect Dis*. 2020;91:137–42.
7. Feng, Y., He, T., Zhang, B. *et al*. Epidemiology and diagnosis technologies of human metapneumovirus in China: a mini review. *Viol J*. 2024;21:59.
8. Wei HY, Tsao KC, Huang CG, Huang YC, Lin TY. Clinical features of different genotypes/genogroups of human metapneumovirus in hospitalized children. *J Microbiol Immunol Infect*. 2013;46(5):352–357.
9. Jeong S, Park MJ, Song W, Kim HS. Advances in laboratory assays for detecting human metapneumovirus. *Ann Transl Med*. 2020;8(9):608.
10. Van Den Bergh A, Bailly B, Guillon P, von Itzstein M, Dirr L. Antiviral strategies against human metapneumovirus: Targeting the fusion protein. *Antiviral Res*. 2022;207:105405.