



## Editorial

## The surge of human metapneumovirus (hMPV) cases in China and global implications

Recent reports of a rise in human metapneumovirus (hMPV) cases in China have raised public health concerns. The hMPV, a paramyxovirus first identified in 2001, is a significant contributor to respiratory infections, accounting for approximately 10–12% of such cases in children [1]. While hMPV often presents with mild cold- and flu-like symptoms, it can progress to more severe respiratory conditions such as bronchitis, bronchiolitis, and pneumonia. The risk of severe illness is particularly high among young children, the elderly, and immunocompromised individuals [2]. Acute respiratory infections have increased in recent weeks and at the end of the year 2024, as have detections of seasonal influenza, rhinovirus, RSV, and hMPV, especially in northern Chinese provinces, according to data released by China for the period ending December 29, 2024 [3]. The range anticipated for this time of the year during the winter season in the Northern Hemisphere includes the observed rise in the detection of respiratory pathogens. The most frequently detected respiratory pathogen causing acute respiratory infections in China at the specified time is influenza [3].

In 2018, an estimated 14.2 million cases of acute lower respiratory tract infections (ALRTIs) associated with hMPV occurred among children under five years of age worldwide (uncertainty range [UR] 10.2 million to 20.1 million). This included approximately 643,000 hospital admissions (UR 425,000 to 977,000), 7700 in-hospital deaths (2600–48 800), and 16100 total ALRTI deaths (5700–88000) in both hospital and community settings. Specifically, hMPV was estimated to cause 11.1 million ALRTI cases (UR 8.0 million to 15.7 million), 502000 hospital admissions (UR 332000 to 762000), and 11300 ALRI related deaths (UR 4000 to 61600) [4].

News reports indicate a significant surge in hMPV cases in northern provinces of China, leading to overcrowded hospitals and a heightened public concern. Health officials have clarified that there is no evidence to suggest this outbreak is unusual or linked to a new respiratory virus. The rise in hMPV cases aligns with the typical respiratory virus season, adding to public confusion about the situation.

One concern is the potential for hMPV to develop into a pandemic similar to COVID-19. However, hMPV is an established virus, and its recent resurgence is likely due to seasonal patterns rather than representing a novel threat. In the years following COVID-19, there has been an observed increase in cases of various respiratory pathogens at different times. Similar resurgence were seen with Respiratory Syncytial Virus (RSV) and *Mycoplasma pneumoniae* [5–7]. An off-season outbreak of hMPV was also reported in the Netherlands following the lifting of COVID-19 lockdown measures [8]. Despite these patterns, the current spike in hMPV cases calls for a proactive response from health authorities. Phylogenetic analysis of F-gene sequences from 28 hMPV strains indicates that the dominant genotype varies by surveillance year, with

the A1, B1, and B2 genotypes being prevalent in China [9,10].

The rise in hMPV cases highlights the need for greater public awareness and education about respiratory viruses. Limited familiarity with hMPV could result in delays in seeking medical care or adopting preventive measures. Public health campaigns should prioritize educating the public about hMPV, its symptoms, and prevention strategies. Collaboration with healthcare providers, community centers, and schools will be essential to ensure effective outreach and engagement.

The healthcare system must be prepared to manage potential surges in hospitalizations caused by hMPV. This includes ensuring adequate resources, such as staffing and medical supplies, to handle increased patient loads, as with any other emerging or re-emerging respiratory illness [11]. Hospitals and clinics should review their emergency response plans to accommodate a possible rise in respiratory illness cases. These plans should include training employees to identify and manage hMPV cases effectively. Strengthening surveillance systems is crucial to monitor respiratory illnesses, enabling timely interventions and efficient resource allocation. Further research into hMPV and its epidemiology is essential to understand the virus behavior and interaction with other respiratory pathogens. Enhanced surveillance can help identify trends and guide public health responses, reducing the risk of overburdening the healthcare systems. Although no vaccines currently exist for hMPV, prioritizing funding for vaccine development is vital. Preliminary research has shown promise, with a second dose of mRNA-1653 having minimal additional impact on antibody titers, though neutralizing titers remained above baseline for hMPV up to 1 year [12–14].

The World Health Organization (WHO) has developed a framework for preparedness against pathogen X, offering an unprecedented opportunity to guide research on high-threat pathogens [15,16]. While the WHO's priority pathogen includes high, medium and low risk pathogens for potential public health emergencies (Table 1) [17,18]. The hMPV is notably not one of the high risk category. Developing successful preventive strategies will require a deeper understanding of hMPV behavior and its interaction with other respiratory pathogens. The recent surge in hMPV cases in China serves as a reminder of the ongoing challenges posed by respiratory viruses. While the immediate risk of an hMPV pandemic appears low, vigilance and preparedness remain critical. By raising public awareness, strengthening healthcare system, and investing in research, we can better address current and future respiratory virus outbreaks.

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Table 1

A table represents the pathogens considered to have a high risk of causing a Public Health Emergency of International Concern (PHEIC) according to the 2024 WHO list, from the Pathogens Prioritization A Scientific Framework For Epidemic And Pandemic Research Preparedness [18].

Family	Priority Pathogens	PHEIC risk
Arenaviridae	Mammarenavirus lassaense (Lassa Fever virus)	High
Bacteria	Vibrio cholerae serogroup O139	High
Bacteria	Yersinia pestis	High
Bacteria	Shigella dysenteriae serotype 1	High
Bacteria	Salmonella enterica non-typhoidal serovars	High
Bacteria	Klebsiella pneumoniae	High
Coronaviridae	Subgenus Merbecovirus (MERS-CoV)	High
Coronaviridae	Subgenus Sarbecovirus (SARS-CoV)	High
Filoviridae	Orthoebolavirus zairense (Ebola virus)	High
Filoviridae	Orthomarbburgvirus marburgense (Marburg virus)	High
Filoviridae	Orthoebolavirus sudanense	High
Flaviviridae	Ortho flavivirus zikaense (Zika virus)	High
Flaviviridae	Ortho flavivirus denguei	High
Flaviviridae	Ortho flavivirus flavi	High
Flaviviridae	Ortho flavivirus encephalitis	High
Flaviviridae	Ortho flavivirus nilense	High
Hantaviridae	Orthohantavirus sinnombreense	High
Hantaviridae	Orthohantavirus hantanense	High
Nairoviridae	Orthonairovirus haemorrhagiae (Crimean-Congo Hemorrhagic Fever virus)	High
Orthomyxoviridae	Alpha influenza virus Influenzae H1, H2, H3, H5, H6, H7, H10	High
Paramyxoviridae	Henipavirus nipahense (Nipah virus)	High
Phenuiviridae	Bandavirus dabiense (Severe Fever with Thrombocytopenia Syndrome virus)	High
Phenuiviridae	Phlebovirus riftense (Rift Valley Fever virus)	High
Poxviridae	Orthopoxvirus variola	High
Poxviridae	Orthopoxvirus vaccinia	High
Poxviridae	Orthopoxvirus monkeypox virus	High
Togaviridae	Alphavirus chikungunya	High
Togaviridae	Alphavirus venezuelan	High

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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