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REVIEW ARTICLE

A Comprehensive Review on Human Metapneumovirus (HMPV)

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ABSTRACT

Human Metapneumovirus (HMPV) is a globally prevalent respiratory pathogen that primarily affects children, immunocompromised individuals, and the elderly. Since its discovery in 2001 in the Netherlands, HMPV has been implicated in a range of respiratory illnesses, from mild upper respiratory tract infections to severe bronchiolitis and pneumonia. This review provides a detailed examination of HMPV, including its discovery, virology, epidemiology, clinical manifestations, diagnostic methodologies, treatment, and prevention strategies. Additionally, we discuss the origin of the virus and its first reported case in India, emphasizing the importance of ongoing research to understand its pathogenic mechanisms and epidemiological patterns.

Keywords: Human Metapneumovirus, Respiratory infections, Virology, Epidemiology, India, Bronchiolitis, Pneumonia.

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INTRODUCTION

Respiratory tract infections (RTIs) represent a significant global health burden, particularly in pediatric populations. Among the plethora of respiratory viruses, Human Metapneumovirus (HMPV) has emerged as a critical pathogen since its discovery in 2001 by van den Hoogen and colleagues in the Netherlands. Belonging to the Pneumoviridae family, HMPV is closely related to Respiratory Syncytial Virus (RSV) and shares a similar clinical and epidemiological profile.

This review delves into the comprehensive understanding of HMPV, from its molecular structure and pathogenesis to its clinical significance and epidemiological trends. Additionally, the review highlights the first recorded case of HMPV in India and discusses its implications in the context of public health.

Discovery and Origin of HMPV

Historical background

HMPV was first isolated in 2001 from nasopharyngeal aspirates of children presenting with RTIs in the Netherlands. Genetic analysis revealed that the virus shared approximately 80% amino acid sequence identity with Avian Metapneumovirus (AMPV), suggesting a zoonotic origin. Phylogenetic studies further indicated that HMPV diverged from AMPV approximately 200 years ago, likely through a series of genetic mutations and adaptations to human hosts.

First reported case in india

The first documented case of HMPV infection in India was reported in 2009. A study conducted in Vellore, Tamil Nadu, identified HMPV in children hospitalized with acute respiratory infections (ARIs). Subsequent surveillance studies across various Indian states have confirmed the widespread circulation of HMPV, with seasonal peaks during winter and early spring.

Virology

Genetic structure

HMPV is an enveloped, negative-sense, single-stranded RNA virus with a genome approximately 13 kb in length. The genome encodes eight proteins:

- Nucleoprotein (N): Encapsulates the RNA genome.
- Phosphoprotein (P): Functions as a polymerase cofactor.
- Matrix protein (M): Plays a role in virion assembly.
- Fusion protein (F): Mediates viral entry by facilitating membrane fusion.
- Glycoprotein (G): Involved in host cell attachment.

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- Small hydrophobic protein (SH): Potentially modulates host immune responses.
- Large polymerase protein (L): Responsible for RNA synthesis.
- M2 protein: Regulates transcription and replication.

Pathogenesis

HMPV primarily targets the epithelial cells of the upper and lower respiratory tract. Following attachment and entry mediated by the G and F proteins, the virus induces a cascade of immune responses, including the production of pro-inflammatory cytokines and chemokines. Severe infections are often associated with an exaggerated immune response, leading to tissue damage and impaired gas exchange.

Epidemiology

Global prevalence

HMPV is estimated to account for 5-10% of hospitalizations due to RTIs worldwide. The virus exhibits a seasonal pattern, with increased activity during winter and early spring in temperate regions and year-round circulation in tropical climates.

Epidemiology in india

In India, HMPV has been detected in 2-10% of children presenting with ARIs. Surveillance studies indicate that HMPV co-circulates with other respiratory viruses such as RSV, influenza, and parainfluenza, complicating diagnosis and management. The highest burden of disease is observed in children under five years, particularly those with underlying comorbidities.

Clinical Manifestations

Spectrum of disease

HMPV infection manifests as a wide spectrum of clinical syndromes, including:
Mild Symptoms: Rhinorrhea, cough, and fever.
Moderate Symptoms: Wheezing and tachypnea.
Severe Symptoms: Bronchiolitis, pneumonia, and acute respiratory distress syndrome (ARDS).

Risk Factors

The severity of HMPV infection is influenced by several factors, including:
Age (infants and elderly at higher risk)
Immunocompromised status
Presence of chronic lung or heart diseases

Diagnosis

Laboratory techniques

- Reverse Transcription Polymerase Chain Reaction (RT-PCR): The gold standard for HMPV detection.
- Immunofluorescence Assay (IFA): Used for rapid antigen detection.
- Viral Culture: Less commonly employed due to its time-consuming nature.

Challenges

Co-infection with other respiratory viruses and the genetic diversity of HMPV strains pose significant challenges to accurate diagnosis.

Treatment and Management

Current therapeutics

- Supportive Care: Oxygen therapy, hydration, and antipyretics.
- Antiviral Agents: Ribavirin has shown in vitro efficacy but lacks robust clinical evidence.

Emerging Therapies

Research is ongoing to develop monoclonal antibodies targeting the F protein and small-molecule inhibitors of viral replication.

Prevention

Vaccination

Despite extensive research, there is currently no licensed vaccine for HMPV. Experimental vaccines based on recombinant F protein and live-attenuated virus platforms are under development.

Public health strategies

- Hygiene Practices: Handwashing and respiratory etiquette.
- Surveillance: Continuous monitoring of HMPV activity to guide intervention strategies.

CONCLUSION

HMPV remains a significant cause of respiratory morbidity and mortality, particularly among vulnerable populations. The absence of a licensed vaccine and effective antivirals underscores the need for enhanced research efforts. Strengthened surveillance systems, along with multidisciplinary approaches combining clinical, molecular, and epidemiological studies, are essential to mitigate its impact. Future research should prioritize the development of targeted therapeutics and preventive measures to reduce the global burden of HMPV. Furthermore, collaborative efforts across countries are required to understand its transmission dynamics, especially in resource-limited settings, to formulate effective global intervention strategies.

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