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Human Metapneumovirus

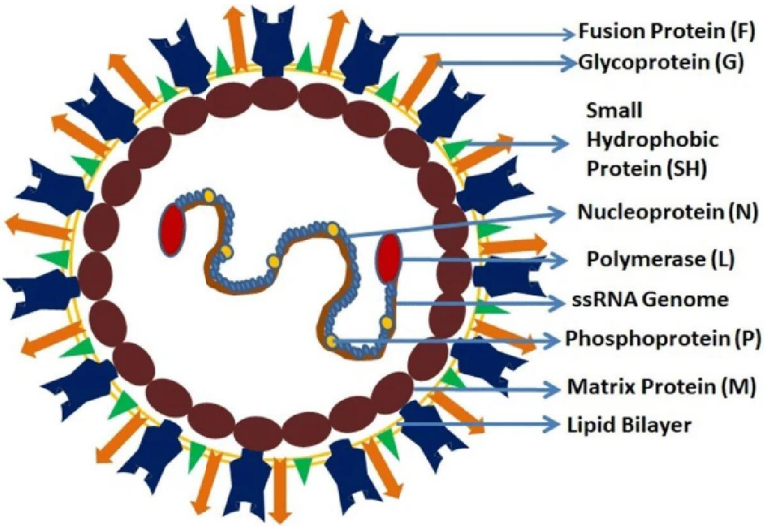
Adil Shah Badshah, Prof. Zameer Shah, Dr. Shivshankar D. Mhaske, Vinayak Bhaskar Chaudhar, Khushi Rajendra Patil
Satyajeet College of Pharmacy, Mehkar, India
aliadils004@gmail.com

Abstract: *First identified in children exhibiting symptoms similar to respiratory syncytial virus (RSV) infection in 2001, human metapneumovirus (HMPV) is a significant respiratory pathogen around the globe.(1) Subsequent research has validated the significance of HMPV, typically ranking it as the second or third most prevalent cause of severe acute upper and lower respiratory tract infection in children. While those with underlying cardiac diseases, the elderly, youngsters and newborns, and those with impaired immune systems are more vulnerable to severe illness caused by this virus, HPV affects people of all ages (2)..*

Keywords: human metapneumovirus, bronchiolitis, pneumonia, upper respiratory infection, lung.

I. INTRODUCTION

Human metapneumovirus is a newly discovered ubiquitous pathogen causing lower respiratory disease in both children and adults (1). Despite being well reported in the infectious disease and pediatric literature, there are no reports of this virus in the Emergency Medicine literature to date (1, 2, 3, 4, 5, 6, 7, 8). More than 11 million patients with respiratory chief complaints account for 10.7% of all patients presenting to US Emergency Departments (9). Therefore, knowledge of the epidemiology, clinical presentation, and complications of human metapneumovirus is essential to the Emergency Physician.



It's interesting to note that, whereas in the Paramyxovirinae subfamily, attachment protein is necessary for viral attachment and subsequent membrane fusion, research has demonstrated that, in the absence of attachment protein, certain members of the Pneumovirinae subfamily can still be infectious. Although RSV without G (G) can proliferate in vitro, it cannot replicate well in vivo (3)Tertiary monkey kidney (tMK), Vero, and A549 cells were shown to multiply hMPV slowly in the initial isolation experiments. However, other cell lines, such as Madin-Darby canine kidney or chicken embryo fibroblasts, did not permit multiplication. Consequently, the majority of isolation attempts have(4)

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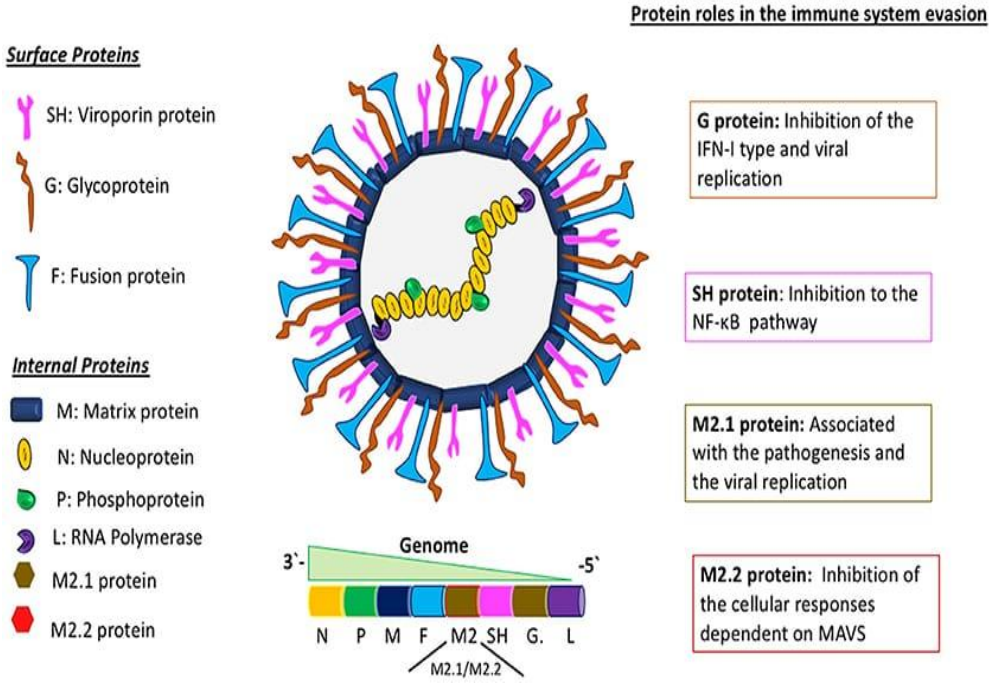
Among the world's leading causes of death and morbidity across all age groups, viral respiratory tract infections (RTIs) are particularly common in young children.(5)

Respiratory syncytial virus (RSV), influenza A and B (Flu-A, Flu-B) viruses, parainfluenza viruses (PIVs), coronaviruses (CoVs), rhinovirus (RV), and human adenoviruses (HAdVs) are the most common viral agents linked to acute respiratory tract infections (RTTIs). Furthermore

In addition to recognized viruses, novel respiratory viruses in humans have been identified that considerably increase the incidence of RTI, such as human metapneumovirus. New human CoVs, boca virus (HBoV), and human MPV(6) Increased illness severity has been linked to the existence of underlying medical disorders, including asthma, cancer, congenital heart disease, chronic lung disease, and chronic obstructive pulmonary disease (COPD).(7)

The identification of human metapneumovirus (HMPV) in Dutch respiratory patients was first documented by van den Hoogen et al. in 2001. The scope of diseases included ranging from moderate upper respiratory tract illness to severe bronchiolitis, pneumonia.

Studies on serology revealed the spread of HMPV for half a century or more (8) We examined 12 throat swab and 15 nasal swab specimens from outpatient clinics, as well as 17 nasopharyngeal aspirate specimens obtained from the pediatric inpatient unit of Sassoon General Hospital, Pune (Maharashtra state), India. departments in July and August of 2003 to look for HMPV via PCR with reverse transcription. They were kept in transit storage. until testing, keep the medium at 70°C. RNA in its entirety was extracted. using the TRIZOL, from 250 l of the respiratory specimens (LS) reagent (Life Technologies, GIBCO BRL) as per as directed by the manufacturer and utilized for nested reverse transcription-PCR in compliance with the guidelines provided and primer sets(9)



The occurrence of ARTIs is caused by a variety of viruses, including the human respiratory syncytial virus (hRSV), coronavirus, and influenza virus. 2001 saw a study team in The human metapneumovirus (HMPV) was the first new virus linked to ARTIs to be identified in the Netherlands.(10) Negroprotein (N), phosphoprotein (P), matrix protein (M), fusion protein (F), matrix-2 proteins (M2-1 and M2-2), small hydrophobic (SH) protein, glycoprotein (G), and large (L) polymerase protein are the nine proteins encoded by the eight genes found in the almost 13 kb HMPV genome.(11)

For example, HMPV infection is linked to around a million outpatient clinic visits with clinical symptoms of antiretroviral drugs (ARTIs), and the illness brought on by HMPV infection presents serious risks to the health of over

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86% of children under the age of five globallyTo avoid this illness, however, a thorough grasp of the epidemiological traits and detection strategies aimed at HMPV would be helpful. Updated data on HMPV in China is presented in this study, with particular attention paid to diagnosis methods, prevalence, and genetic features.(12)

Current techniques for HMPV detection using molecular diagnostics Early detection of HMPV infection is essential for the development of effective disease-control strategies, including controlling the spread of the virus and giving patients prompt medical attention. Given that the F protein amino acid sequences of RSV and HMPV are largely conserved(13) a multiplex RT-PCR technique based on the GenomeLab Gene Expression Profler genetic analysis system (GeXP) for the quick and sensitive detection of sixteen ARTIs-related pathogens, including HMPV. When all viral targets were added to the reaction, the detection limit of each virus was 1000 copies/reaction.(14)

Notably, there were notable regional differences in the frequency of HMPV. This variance might be explained by variations in patient ages, sample volumes, and molecular detection techniques, all of which need more research.

Further analysis showed a significant correlation between the age of the patients and the season of sampling and the incidence of HMPV infection. When it came to sample seasons, individuals receiving ARTIs in the spring were almost nine times more likely to get HMPV than those receiving them in the summer or the fall.

Regarding age, younger patients (less than 60 months) had a significantly greater prevalence of HMPV among ARTI users than older patients (more than 60 months) in contrast to patients who are older (>60 months). While senior individuals should not be overlooked, young children are particularly vulnerable to contracting HMPV in the spring. However, the rates of HMPV infection among patients in China were not significantly impacted by the patient's gender or the severity of their condition (inpatients vs outpatients).

HMPV strains may be classified into several genotypes (A1, A2, B1, B2) and lineages (A1, A2a, A2b, A2c, B1, B2) because to their significant genetic heterogeneity.(15) According to our compiled data, at least five HMPV lineages—A1, A2b, A2C, B1, and B2—have been identified as being ubiquitous throughout China; however, the specific lineages and proportions of HMPV differ significantly between provinces and regions. In China, the A2b, B1, and B2 lineages have emerged as the most common strains, but the A1 lineage was infrequently found in the study areas. However, virulence, pathogenicity, and clinical signs are only a few of the traits of several HMPV lineages that have not yet been fully identified.

These problems must be resolved in the future. It should be noted that a number of reasons prevented a thorough analysis of the epidemiological features of HMPV in China in this research. First off, not all reports that are accessible may be covered within the research focus of this review. Second, while 56 representative studies were included in this review to evaluate the prevalence of HMPV in China, some of the papers lacked crucial background data, including the sampling season and year, the disease severity level (inpatients or outpatients), the viral load of the tested sample, and other risk factors. Thirdly, reports on HMPV epidemiological studies have primarily come from Beijing, Jiangsu, and Guangdong. In other provinces or areas, the epidemiological features of HMPV were comparatively restricted, and insufficient. Fourthly, the kinds and proportions of various HMPV lineages in the areas under investigation were compiled in this review. Nevertheless, the majority of the publications lacked crucial details regarding the viral load, clinical manifestations, or severity of the illness in individuals with several HMPV lineages. These constraints make it difficult to conduct a thorough analysis of the epidemiological characteristics of HMPV in China. Therefore, it is recommended that these possible shortcomings be addressed in future HMPV epidemiological surveys. In conclusion, several molecular diagnostic techniques have been created to identify HMPV in China. Multiple RT-qPCR, RT-PCR, and RT-PCR are the most popular methods for treating clinical HMPV identification. Other visual detection techniques should be used as backup choices in clinical trials as soon as feasible, taking into account lower more convenience, greater sensitivity, and higher expense. Te Recapitulated data revealed a comparatively low occurrence. HMPV infection rates among ARTI patients (4.70%) in China.

The frequency was significantly correlated with with the patient's age and the sample seasons. Additionally, There are several HMPV lineages that are common in China. contains significant amounts of the B1, B2, and A2b lineages. Considering the ongoing risk that HMPV poses to public health(16) Two genotypes of HMPV, A and B, have been discovered by phylogenetic research. While both genotypes may co-circulate at the same time, one genotype often predominates during an epidemic [11,12].

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Two clades—designated A1, A2, B1 and B2—are assigned to each of these subgroups [12,13].

The sequence diversity of the attachment (G) and fusion (F) surface glycoproteins serves as the primary basis for this categorization.(17) .. Two more subgroups, A2a and A2b, were identified in 2006; however, this further division was predicated on sparse data and has not

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