International Journal of Pharmaceutical Research and Applications
Volume 10, Issue 2 Mar – Apr 2025, pp: 380-390 www.ijprajournal.com ISSN: 2456-4494

Human Metapneumovirus[Hmpv]

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Date of Submission: 10-03-2025 Date of Acceptance: 20-03-2025

ABSTRACT: Since its discovery in 2001, human metapneumovirus (hMPV) has been found all over the world . A frequent respiratory pathogen particularly in infants and small children, is hMPV. The virus may provoke asthma and is linked to upper and lower respiratory tract infections. During outbreaks in the community, at least two main hMPV genotypes are in circulation. It is still debatable if these genotypes correspond to different serotypes. Comprehending hMPV's pathophysiology sickness and creating a safe and efficient vaccine to prevent infection and illness brought on by this recently identified respiratory virus are the two main issues facing the scientific and medical sectors.

KEYWORDS: HMPV, Pneumonia, etiology, respiratory infections, pathogens, genes.

I .INTRODUCTION:

Among the primary reasons for morbidity and mortality in the world is respiratory tract infections. Regardless of location, respiratory tract infections rank as the second most frequent reason why infants under five die (82). Acute respiratory tract infections are the most common illness, regardless of age or gender (80). With over 45,000 deaths each year, pneumonia, influenza, and influenza-like diseases (ILI) rank as the sixth most common cause of mortality in the US (96). Respiratory tract infections cost $14.6 billion annually in the United States, resulting in over 500,000 hospitalizations and 4 million ambulatory care visits (107). There are 5,445 cases of acute respiratory tract infections for every 10,000 person-years in the Netherlands (124). The etiological agent that causes respiratory tract disease is frequently unknown, despite the fact that the clinical signs of the illness are well recognized. In less over 50% of community-acquired pneumonia cases , a microbiological diagnosis can be made (83, 102, 140). The influenza virus, respiratory syncytial virus (RSV), and parainfluenza viruses are the primary causes of bronchiolitis and lower respiratory tract infections (LRTI) in children. Nevertheless, an infectious agent cannot be found in one-third of these pediatric LRTI cases (27, 135). It is unable to identify an infectious etiology for almost half of pediatric upper respiratory infections (URI) (86). Although the majority of LRTIs are believed to have a viral etiology (39), even with the use of cutting-edge genomic amplification techniques, a viral agent can only be found in 40% of patients (70). These findings raise the possibility that a significant amount of respiratory tract illness may be caused by previously unidentified microorganisms that are already in circulation. The main causes of bronchiolitis and lower respiratory tract infections (LRTI) in children include influenza virus, respiratory syncytial virus (RSV), and parainfluenza viruses. Nevertheless, an infectious agent cannot be found in one-third of these pediatric LRTI cases (27, 135). It is unable to identify an infectious etiology for almost half of pediatric upper respiratory infections (URI) (86). Although the majority of LRTIs are believed to have a viral etiology (39), even with the use of cutting-edge genomic amplification techniques, a viral agent can only be found in 40% of patients (70). These findings raise the possibility that a significant amount of respiratory tract illness may be caused by previously unidentified microorganisms that are already in circulation.

II. DISCOVERY :

The finding of a new virus from children with respiratory tract sickness in the Netherlands was reported by van den Hoogen et al. in 2001 (120). 28 children's respiratory secretions collected over a 20-year period contained this substance. Immunological tests employing virus-specific antibodies and PCR-based techniques using virus genome-specific primers were unable to detect this agent, indicating that it was different from other prevalent respiratory viruses. Until parts of the genomic sequence were identified using molecular biology technologies, the genetic characteristics of this agent was unknown. These Dutch researchers obtained the novel pathogen's genomic sequence

International Journal of Pharmaceutical Research and Applications
Volume 10, Issue 2 Mar – Apr 2025, pp: 380-390 www.ijprajournal.com ISSN: 2456-4494

using a method known as randomly primed PCR. This virus was named human metapneumovirus (hMPV) and, based on limited sequencing data, seems to be closely linked to the avian pneumovirus, which belongs to the Metapneumovirus genus (38, 120). It was suggested by multiple lines of evidence that hMPV was a frequent respiratory infection in humans. Reverse transcription-PCR (RT-PCR) revealed that seven out of 68 respiratory specimens (10%) that were examined during the winter of 2000 were positive for hMPV. Based on viral neutralization assays and immunofluorescence, serological investigations showed that almost everyone exhibited signs of hMPV infection by the age of five. Additionally, hMPV or a similarly comparable virus had been in circulation for at least 50 years, according to screening of banked human sera, indicating that the virus did not "jump" from an animal reservoir, such as birds, to the human population (120).

Characteristics of Human Metapneumovirus {hMPV}

- **Virus Family:**Respiratory syncytial virus (RSV) and hMPV are both members of the Pneumoviridae family.
- **Structure**:It is an encapsulated single-stranded RNA virus.
- **Transmission**:spreads by contaminated surfaces, direct contact with infected people, or respiratory droplets.
- **Symptoms**:Causes a spectrum of respiratory illnesses, from mild cold-like symptoms to severe conditions like bronchiolitis, pneumonia, and asthma exacerbations
- **Seasonality**:Outbreaks usually follow the seasonal trends of other respiratory viruses, and they are more common in late winter and early spring.Target Groups: Mostly impacts elderly people, young children, and those with compromised immune systems or long-term respiratory disorders.
- **Diagnosis**:For precise diagnosis, laboratory techniques like PCR, antigen detection, or viral culture are employed.
- **Treatment**:Supportive care and symptom management are the main goals of treatment; there is no particular antiviral medication.
- **Prevention**:To lessen the spread, it is crucial to maintain good hygiene and stay away from close contact with infected.
- **HMPV Causes**Although the precise causes of HMPV infections are yet unknown, a number of factors could be involved in their spread:
- **Seasonal patterns:** HMPV infections are more common during winter and early spring.
- **Environmental factors:** Crowded indoor spaces with poor ventilation can facilitate the spread of respiratory viruses like HMPV.
- **Co-circulation with other pathogens:** The simultaneous circulation of HMPV with other respiratory viruses, such as influenza and COVID-19, may complicate diagnosis and treatment.
- **Genetic changes:** Like all viruses, HMPV can mutate over time, potentially leading to more transmissible or virulent strains.

Fig1:Symptoms of HMPV

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Volume 10, Issue 2 Mar – Apr 2025, pp: 380-390 www.ijprajournal.com ISSN: 2456-4494

What are the symptoms of HMPV virus?

The symptoms of HMPV infections can be varied and frequently resemble those of other respiratory conditions such as the flu, the common cold, or even COVID-19. Without specialized testing, this similarity may make the initial diagnosis difficult. Among the most typical symptoms are:

- Fever and Cough
- congestion of the nose
- A sore throat
- Breathlessness

These symptoms are usually modest and go away on their own in a week or two. However, HMPV can result in more severe problems in severe situations,especially in vulnerable populations:

Inflammation of the lungs' tiny airways, known as bronchiolitis, is prevalent in newborns and young children.

A prolonged cough and production of mucus are symptoms of bronchitis, an inflammation of the bigger airways.

Pneumonia: An infection of the lung tissue that, in extreme circumstances, can be fatal.

Flare-ups of asthma or COPD: A worsening of pre-existing respiratory disorders.

Ear infections: Middle ear secondary bacterial infections, especially in children.

It's crucial to remember that a person's age, general health, and immune state can all have a significant impact on how severe and long their symptoms last. Although the majority of people recover without any problems, the elderly, young children, and people withcompromised immune systems or pre-existing lung disorders are most at risk for serious consequences.

III. METHODS

HMPV isolates :-

As previously reported, virus sequences were obtained from specimens gathered in the Vanderbilt Vaccine Clinic over a 20-year period, from 1982 to 2002 [2, 3]. Children under five years old with acute respiratory tract illnesses had nasal wash specimens taken. In order to detect nucleoprotein gene sequences and test for HMPV, we extracted RNA from these samples and using quantitative real-time RT-PCR [2]. As explained below, nested RT-PCR for the F gene was performed on specimens that tested positive for HMPV. The letter code employed in this study's viral nomenclature denotes the geographic location of isolation (for example, "TN" stands for Tennessee), which is followed by the isolate number, year, and month of isolation.

RNA extraction, RT-PCR and sequencing of F genes :-

On a Qiagen BioRobot 9604 Workstation, RNA was extracted using the QIAamp Viral RNA kit (Qiagen) from 220 µl of nasal wash sample, as explained [2]. Following RT-PCR, nested PCR was used to amplify the whole F open reading frame (ORF). FF1 (5'-ATGTCTGTGTACTCCAAA-3') and FR (5'-CCCGYACTTCATATTTGCA-3') were the primers used for RT-PCR, whereas FF2 (5'-AATATGCAAGACTTGGAGCC-3' and 5'-AGGATCTGCAAGAGCTGGAG-3') and FR (5'-CCCGYACTTCATATTTGCA-3') were used for nested PCR. 10 µL of diluted RNA was used as a template in a 50 µL RT-PCR reaction using the Thermoscript/Platinum Taq Polymerase Kit (Invitrogen). Following five cycles of 94°C for 30 seconds, 50°C for 1 minute, and 68°C for 3 minutes, as well as an additional thirty cycles of 94°C for 30 seconds, 55°C for 1 minute, and 68°C for 3 minutes, the RT-PCR was conducted at 50°C for 50 minutes and 95°C for 3 minutes. Using Platinum PCR Supermix (Invitrogen), 2 µL of RT-PCR product was added to a 50 µL reaction for nested PCR. After three minutes of incubation at 95°C, the reaction was subjected to five cycles of 94°C for 30 seconds, 50°C for 30 seconds, and 68°C for 2 minutes. There were then thirty more cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 68°C for 2 minutes. A further extension at 68°C for seven minutes was added for every reaction. The flanking sequences and F ORF were approximately 1.9 kb in size. After RT-PCR and nested PCR, most PCR products were specific and migrated as a single band of the anticipated size (data not shown). When several PCR products were produced, the required ones were purified using an agarose gel. The ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems) was used to perform the sequencing reactions. To guarantee that the open reading frame was covered twice, eight sequencing primers were employed for every fragment. Primers for sequencing can be obtained upon request. Applied Biosystems' ABI 3730 DNA Analyzer was used for capillary electrophoresis, while Gene Codes Corp.'s Sequencher and Applied Biosystems' DNA Sequencing Analysis were used for Strict or relaxed (uncorrelated logarithmic) molecular clocks were used to evaluate data sets under demographic models of constant population size, exponential population growth, and expansion

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population growth. The relaxed clock, exponential population growth model provided the best estimate based on 95% greatest posterior density (HPD), according to a comparison of the output from each model (not shown). Every run was visually inspected to verify convergence and Over 200 is the estimated sample size analysis.

Sequence alignment and phylogenetic analysis : -

The ClustalW method in MEGA version 3.1 and MacVector version 10.0 (Accelrys) were used to align and modify the final sequences [58]. Accession numbers AY145287-AY145301, AY304360-AY304362, AYAY622381, EF051124, EF081369, EF199771-EF199772, EF589610, AF176593, AF187153-AF187154, AF298642-AF298650, AF368170, AF085228, AJ400728, AJ400730, DQ175630-DQ175634, DQ207607, D00850, EU658938, Y14290-Y14294 The sequences found in this investigation have been added to GenBank with accession numbers EU857542–EU857610. Using MacVector version 9.0, percent nucleotide identity computations, pairwise sequence alignment, and multiple sequence alignment were carried out. The Bayesian Markov chain Monte Carlo (MCMC) technique, which is available in the BEAST software http://beast.bio.ed.ac.uk/[37], was used to estimate the time to most recent common ancestor (tMRCA), phylogeny, and overall rates of evolutionary change (nucleotide substitutions per site per year). In each instance, we employed the straightforward HKY85 model of nucleotide substitution since the sequences under analysis were highly linked and showed minimal multiple substitutions at single nucleotide sites; more complicated models occasionally failed to converge (data not shown). Using the Log Combiner tool http://beast.bio.ed.ac.uk/, two independent runs of MCMC chains were combined after 30 million steps at a 10% burn-in rate [37]. The 95% HPD was used to report parameter estimate uncertainty. The Maximum Clade Credibility tree was created by combining output sets of trees using LogCombiner and analyzing them using the TreeAnnotator program. The tree's posterior probability limit was greater than 50%. FigTree was used to create the final tree [37].

Habitat of Human metapneumovirus (HMPV) :-

1. There are no known animal reservoirs for the human metapneumovirus (HMPV), which primarily infects humans.
2. The virus known as HMPV affects the nose, throat, and lungs, as well as the upper and lower respiratory tract
3. They typically impact immunocompromised individuals, older persons, and young children.
4. Like RSV and the flu, HMPV is a seasonal illness that often manifests in the winter and early spring.
5. HMPV may spread indirectly since it can remain on surfaces for several hours.

Structure of Human metapneumovirus (HMPV) :-

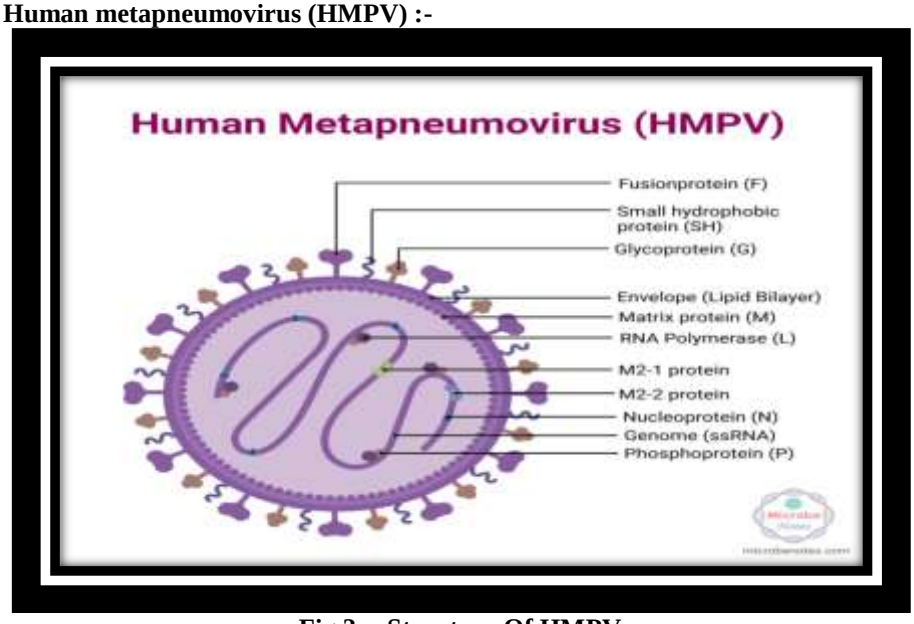

Fig 2 :-Structure Of HMPV

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- The human metapneumovirus, or HMPV, is a pleomorphic, enveloped, negative-sense single-stranded RNA (-ssRNA) virus.
- Their diameter ranges from 150 to 600 nanometers.
- Fusion protein (F), glycoprotein (G), and small hydrophobic protein (SH) are the three membrane surface glycoproteins that make up the outer envelope (lipid bilayer) of HMPV. They resemble spikes that range in size from 13 to 17 nm.
- In order for the virus to enter the host cell membrane and start the infection (replication cycle), the fusion protein (F) and glycoprotein (G) are crucial.
- The inner side of the outer envelope (lipid bilayer) contains the matrix protein (M). The envelope and nucleocapsid are connected by this M protein.

Genome of Human metapneumovirus [HMPV] :-

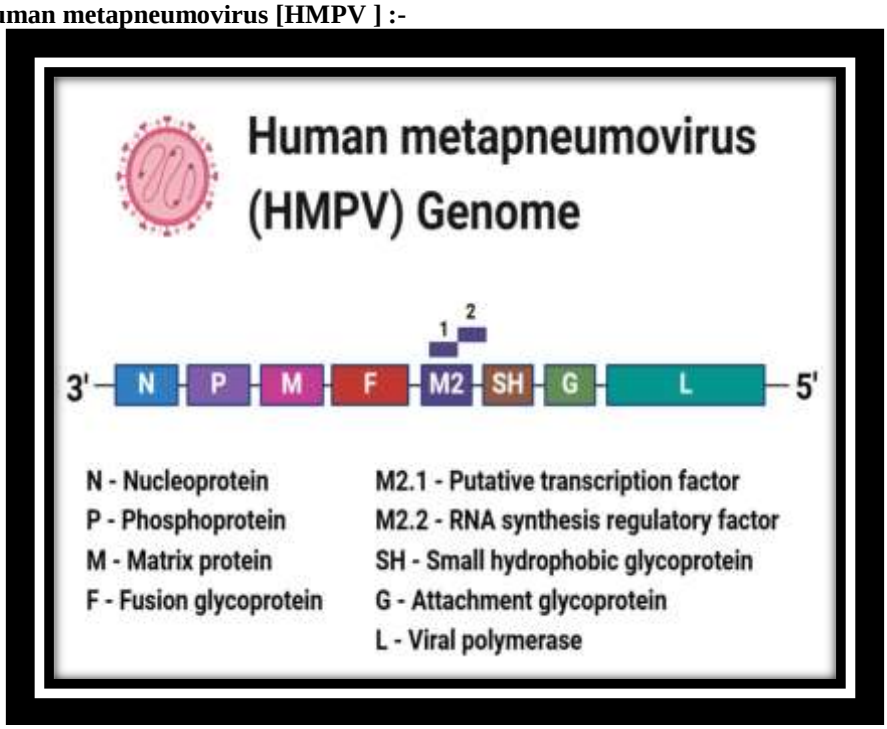

Fig 3 :-Genome Of HMPV

- HMPV's genome is made up of eight genes that code for nine different proteins and negative-sense single-stranded RNA (-ssRNA).
- It has a 13.2 Kb genome.
- From 3′ to 5′ end, the genes in the genome are arranged as follows: N–P–M–F–M2–SH–G–L.
- The proteins are:

1. Nucleoprotein (N protein):N protein, or nucleoprotein, aids in the nucleocapsid's development.
2. Phosphoprotein (P protein):Phosphoprotein, or P protein, aids in transcription and viral replication.
3. Matrix protein (M protein):The matrix protein, or M protein, aids in the assembly and budding of viruses.
4. Fusion glycoprotein (F protein):F protein, also known as fusion glycoprotein, aids in the virus's fusing with the host cell.
5. Putative transcription factor (M2-1 protein):The M2-1 protein, a putative transcription factor, aids in the regulation of transcription.
6. RNA synthesis regulatory factor (the M2-2 protein):The M2-2 protein, also known as the RNA synthesis regulatory factor, aids in transcriptional control.
7. Small hydrophobic glycoprotein (SH protein):The function of the small hydrophobic glycoprotein (SH protein) is unclear, however

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it may aid in the contact between the virus and its host.

8. Attachment glycoprotein (G protein):G protein, or attachment glycoprotein, aids in the virus's attachment to the host cell.
9. Viral polymerase (L protein):L protein, or viral polymerase, aids in transcription and viral replication.

- HMPV has two genotypes, A and B, according to whole genome study (Barbara Huck et al. 2006).
- These two genotypes are further separated into subgroups A1, A2, B1, and B2 according to the sequence variability of the attachment (G) and fusion (F) surface glycoproteins.
- Once more, subgroup A2 is separated into A2a and A2b.
- Unique HMPV variants have recently been found that have a 180 nt duplication (nt-dup) in the G gene and a 111 nt-dup in the G gene (Zhibo Xie et al. 2021).

Replication of Human metapneumovirus (HMPV) :-

Human metapneumovirus (HMPV) replicates in the cytoplasm of host cells, mainly in the respiratory tract's epithelial cells.

1. Attachment: Glycoprotein (G) aids in the virus's attachment to the host cell. The hydrophobic portion of the glycoprotein (G) serves as a membrane anchor and an uncleaved signal peptide, aiding in the binding of the virus.
2. Fusion and Entry :Fusion protein (F) facilitates the fusion of HMPV with the host plasma membrane. Using an arginine-glycine-aspartate (RGD) pattern, the fusion protein (F) can attach to host cells through integrin αvβ1. At pH values that are acidic, HMPV fusion takes place. After then, the host's cytoplasm receives the viral ribonucleoprotein (RNP), which contains the negative-sense viral RNA (vRNA genome).
3. Transcription and Translation:The polymerase complex is created when the viral polymerase (L protein), phosphoprotein (P protein), and nucleoprotein (N protein) split out from the vRNA and attach to one another. The negative-sense viral RNA (vRNA) is converted into messenger RNA (mRNA) by the viral RNA-dependent RNA polymerase. The host's ribosome machinery subsequently translates these mRNAs to create the viral proteins required for assembly and replication.
4. Replication:The viral genome replicates when enough viral proteins are produced.
5. Assembly:Nucleoproteins encapsidate newly generated viral genomes from replication, forming ribonucleoprotein complexes. The matrix protein (M) beneath the host's plasma membrane, where viral glycoproteins (F, G, and SH) are carried and embedded, interacts with the ribonucleocapsid.
6. Budding and Release:Virion release occurs when the completed virions sprout from the host cell membrane through the ESCRT complex.

IV. EPIDEMILOGY:-

- Worldwide, HMPV affects people of all ages, but it is more severe in small children, the elderly, and those with weakened immune systems.
- By the age of five, the majority of children have contracted HMPV.
- Most HMPV infections happen in the winter and early spring.
- As one gets farther away from the equator, the incidence of HMPV is said to rise (Medscape).
- According to a study conducted at the primary care Vanderbilt Vaccine Clinic in Nashville, HMPV caused 12% of acute respiratory tract illness cases in children in good health who visited an outpatient clinic in the United States (John V. Williams et al. 2007).
- A childhood infection increases the likelihood of re-infections throughout adulthood.

V. SYMPTOMS OF HMPV INFECTION :-

After being exposed to the virus, symptoms usually appear 3–6 days later (the incubation phase) and persist for 2–5 days. The symptoms resemble those of a cold**.**

Common Symptoms of HMPV Infection :-

- Fever,
- Runny nose,
- Cough
  - Fatigue
  - Rash
  - Sore Throat
  - Nasal Congestion

Severe Symptoms of HMPV Infection ;-

- Breathing Issues
- Wheezing

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- Bronchiolitis
- Both pneumonia and bronchitis
- Flare-ups of COPD or asthma
- Infections of ears
- Croups

VI. TRANSMISSION OF HMPV :-

HMPV is spread from one person to another through:

- Direct and intimate contact with an infected person's droplets or aerosols.
- coughing, sneezing, splitting.
- physical contact, such as caressing, kissing, embracing, or shaking hands with an infected individual.
- contacting items or surfaces that contain viruses, such as door handles, tissues, cutlery, phones, toys, etc., and coming into contact with the mouth, nose, or eyes.

VII. RISK FACTORS OF HMPV :-

Some groups are more vulnerable to HMPV because of the following**:**

- Young children under the age of five**.**
- people over 65 who are older adults.
- people with compromised immune systems, such as those suffering with HIV/AIDS, cancer, organ transplants, or long-term diseases.
- People with chronic respiratory conditions like Asthma and Chronic obstructive pulmonary disease (COPD).
- Premature babies are particularly susceptible to HMPV infections because their immune systems and lungs may not be fully formed.

VIII. PATHOGENESIS OF HMPV :-

- HMPV interferes with the host's innate immune system using specific mechanisms.
- By controlling pattern recognition receptors, including toll-like receptors, retinoic acid-inducible gene-like receptors, and other signaling molecules, the virus counteracts cellular reactions.
- A weak and delayed immune response, delayed cytotoxic T-lymphocyte activity, and poor virus clearance during the initial infection are all possible outcomes of HMPV infections.
- Infection decreases antigen-specific T-cell activation and disrupts dendritic cell function.
- As a result, the virus cannot be completely eradicated, and the risk of re-infection rises.
- Long-term immunity generation is hindered, and antigen-specific CD4+ T cell proliferation is limited.
- Cellular signaling that is dependent on toll-like receptors is induced by HMPV infection.
- Type I and type III interferons, which are essential for antiviral defense, are inhibited by HMPV infection.

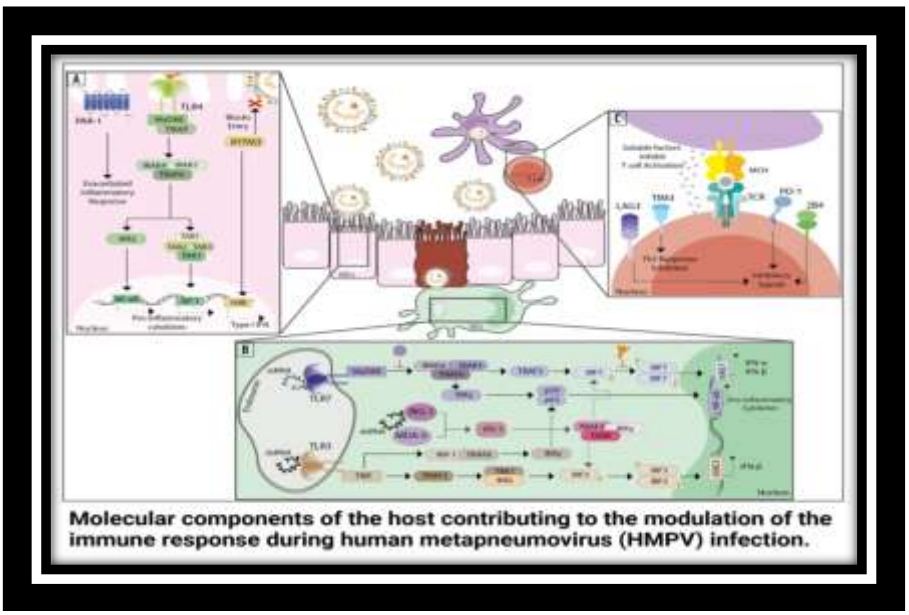

Fig 4:-Host Immune Response during HMPV Infection

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HMPV infects the respiratory tract, causing infections, inflammation, and damage to the airway epithelium.

Host Immune Response :-

- HMPV uses certain mechanisms to disrupt the host's innate immune system.
- The virus inhibits cellular reactions by controlling pattern recognition receptors, including retinoic acid-inducible gene-like receptors, toll-like receptors, and other signaling molecules..
- A weak and delayed immune response, delayed cytotoxic T-lymphocyte activity, and poor virus clearance during the initial infection are all possible outcomes of HMPV infections.
  - Infection decreases antigen-specific T-cell activation and disrupts dendritic cell function.
  - As a result, the virus cannot be completely eradicated, and the risk of re-infection rises.
  - Long-term immunity generation is hindered, and antigen-specific CD4+ T cell proliferation is limited.
  - Cellular signaling that is dependent on toll-like receptors is induced by HMPV infection.
- Type I and type III interferons, which are essential for antiviral defense, are inhibited by HMPV infection.

Mucin 19 :-

- mucus formation is a typical aspect of HMPV infection, little is known about how it affects the pathogenesis and immune response caused by HMPV**.**
- Mucins are a major component of mucus and could impact how the host responds to Although infections**.**
- Mucin 19 is predominantly expressed in the respiratory tract when infected with HMPV.
- The immunological response to HMPV and HMPV-induced pathogenesis is triggered by mucin 19.

Inflammation :-

- Chemokines and cytokines are released when an HMPV infection occurs, which results in inflammation and immune cell infiltration.
- In cotton rats and BALB/c mice, HMPV infection causes pulmonary inflammatory alterations and raises the levels of monocyte chemotactic proteins, interleukins (IL-2, IL-8, and IL-4), interferon (IFN-α), and macrophage inflammatory protein 1α in the lungs and bronchoalveolar lavage fluid.
- These changes further lead to perivascular and peribronchiolar infiltration and inflammation.

Tissue Damage :-

- The respiratory epithelium is harmed by viral cytopathic effects**.**
- HMPV infection is characterized by smudge cells, alveolar damage, hyaline membrane disease, and intra-alveolar foamy and hemosiderin-loaded macrophages**.**

IX. RECOVERY :-

- The infection is finally managed and eradicated by the body's immune system.
- People with risk characteristics may occasionally have a more serious infection. In this situation, recuperation can take longer.

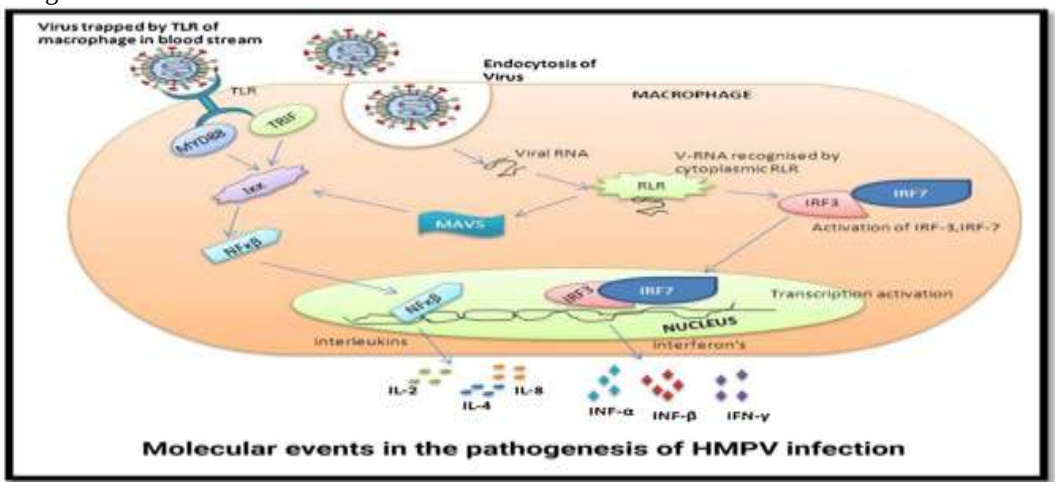

Fig 5:- Molecular events in the pathogenesis of HMPV infection

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- When you're sick, stay at home.
- In order to treat patients with suspected or proven HMPV, healthcare facilities should adhere to infection prevention and control protocols.

Public health officials should keep an eye on HMPV activity

Clinical Manifestation of HMPV Infection :-

Both upper and lower respiratory tract infections are caused by the human metapneumovirus (HMPV), and the clinical presentation of HMPV varies depending on a person's age, health, and immune state.

Upper Respiratory Tract Infections :-

- Persistent cough along with mucus production
- Runny or stuffy nose
- Throat pain
- Mild to moderate fever, Headache
- Sense of tiredness or malaise

Lower Respiratory Tract Infections :-

- Wheezing: high pitch whistling sound while breathing
- Breathing difficulties or shortness of breath
- Pulling Back the Chest
- COPD and asthma flare-ups: HMPV exacerbates asthma and COPD symptoms.

Severe Clinical Manifestations :-

- **Bronchiolitis :-**It is a frequent viral lung illness that affects both infants and toddlers. Breathing becomes difficult due to inflammation of the lungs' bronchioles, which are tiny airways. It makes the bronchioles expand and produce mucus.
- **Bronchitis :-**It is an inflammation of the lining of the bronchial tubes, which are the lungs' airways. It could be chronic or acute.
- **Pneumonia :-**It is a lung inflammation that affects the alveoli, which are tiny air sacs. Mucus or pus fills the air sacs.

Secondary Infections

- **Central nervous system diseases: -**Some studies have shown that HMPV infection may cause diseases of the central nervous system (CNS) like seizures and encephalitis (John C Arnold et al. 2009).
- **Otitis Media :-**According to one study, otitis media was diagnosed in 50% of children infected with HMPV (John V. Williams et al. 2007).

X. DIAGNOSIS :-

Diagnosis is typically done through a physical examination, patient history, and lab tests. Laboratory tests are done to confirm the presence of Human metapneumovirus (HMPV) in the body.

1. Clinical Evaluations :-

- **Risk Factor Assessments :-**Taking health history
- **Symptoms Assessments :-**For initial purposes, a few symptoms are examined, including fever, cough, congestion of the nose, and dyspnea.

2. Laboratory Test :-

A. Sample:-:- Aspirates are used to get samples from the upper respiratory system, which is typically the throat or nose. Bronchoalveolar lavage or bronchoscopy may be used in cases of severe illness.

B. Virus Culture :-HMPV is grown and isolated using a variety of cell lines, including Vero cells, HEp-2 cells, Hep G2 cells, 293 cells, and LLC-MK2 cells.

C. Antigen Detection :-HMPV antigen is detected utilizing the anti-hMPV antibody in direct immunofluorescence or ELISA-based techniques. It is less sensitive than molecular approaches like PCR.

D. Molecular Diagnosis :-Reverse transcription polymerase chain reaction (RT-PCR), real-time RT-PCR, and multiplex RT-PCR (mRT-PCR) are PCR techniques that can be used to accurately diagnose HMPV. mRT-PCR has an advantage over immunofluorescence tests because it can detect undetectable co-infections, even with lowviral loads**.**

E. Chest Radiography :-Chest X-rays may aid to discover hyperinflation, peribronchial thickening, or infiltrates, suggesting bronchiolitis or pneumonia.

XI. TREATMENT OF HMPV INFECTION:-

- Currently, there is no specific antiviral therapy to treat HMPV.
- Relieving symptoms and offering supportive care are the main goals of treatment.
- Over-the-counter drugs including cough suppressants, decongestants, and pain relievers can be taken by infectious patients.
- Drugs like ibuprofen or acetaminophen can be used to treat body aches and lower fever
- If we have trouble breathing, oxygen therapy may be administered.

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Volume 10, Issue 2 Mar – Apr 2025, pp: 380-390 www.ijprajournal.com ISSN: 2456-4494

- We can use a room humidifier or take a hot shower to assist soothe a sore throat and cough and drink plenty of liquids to stay hydrated.
- To stay hydrated, intravenous fluids can be administered.
- Steroids may alleviate some of the symptoms and reduce inflammation
- After contracting HMPV, most people recover in 7–10 days.
- Nonetheless, some research has examined the potential use of immunoglobulin, fusion inhibitors, ribavirin, and small interfering ribonucleic acids for the treatment and management of HMPV infection (Swagatika Panda et al. 2014).

Does an HMPV infection require antibiotics? :-
Antibiotics are not necessary to treat HMPV infection. Antibiotics are ineffective against human metapneumovirus because they only operate against bacteria. However, if the patient also develops bacterial pneumonia (a secondary infection), doctors and physicians may prescribe medicines to treat any secondary infection, including bacterial pneumonia.

HMPV Infection Vaccines :-

- Currently, as of January 2025, there are no specific vaccines to prevent HMPV.
- Rodent and non-human primate models have been used to evaluate a number of HMPV vaccine candidates (Marie-Ève Hamelin et al. 2007).
- The following are a few vaccines and clinical trials currently in development:
- Moderna's mRNA-1653 genetically modified vaccination (https://trials.modernatx.com/study/?id=mRNA-1653-P102)
- (https://trials.modernatx.com/study/?id=mRNA-1365-P101) Moderna's mRNA-1345 and mRNA-1365
- ALVR106: AlloVir's multi-virus T cell treatment (https://clinicaltrials.gov/study/NCT04933968)

XII. PREVENTION AND CONTROL OF HMPV INFECTION :-

- Frequent and appropriate hand washing.
- Refrain from using unwashed hands to contact your mouth, nose, or eyes.
- Steer clear of intimate contact with sick people.
- When sneezing or coughing, cover your mouth and nose.
- Put on a mouth and nose mask.
- Steer clear of sharing utensils and glasses.
- Scrubbing and disinfecting surfaces and promptly inform the public .

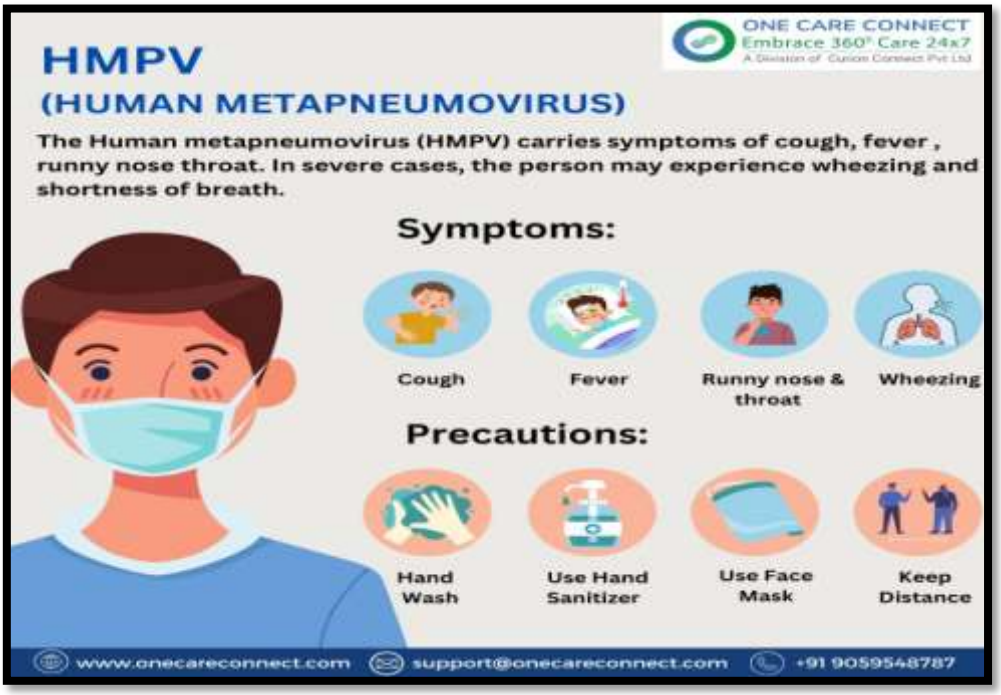

Fig 6 :- Symptoms and Precaution Of HMPV

International Journal of Pharmaceutical Research and Applications
Volume 10, Issue 2 Mar – Apr 2025, pp: 380-390 www.ijprajournal.com ISSN: 2456-4494

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