

Cross-Viral Study of COVID-19 Strains XEC, HKU5-CoV-2 and HMPV: From Molecular Structure to Clinical Implications

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Abstract

This cross-viral study investigates the molecular architecture, mechanisms of action, and clinical relevance of the COVID-19 viruses XEC and HKU5-CoV-2, as well as human metapneumovirus (hMPV). XEC and HKU5-CoV-2, both new coronaviruses, have a remarkable ability to infect human cells, which raises concerns about potential zoonotic spillovers and future pandemics. Compared to this, hMPV, while a distinct viral family, shares similar respiratory complications, particularly in vulnerable populations. A mixed-methods study with extensive literature review and internet studies was used to extensively explore viral pathophysiology, disease course, and treatment. The key findings are that while XEC and HKU5-CoV-2 primarily use ACE2 receptors for cell entry, hMPV uses other receptors, eliciting varied immune responses and clinical manifestations. The study emphasizes the need for enhanced global surveillance, rapid diagnostic capacity, and personalized therapeutic measures. Future pandemic preparedness relies on the development of broad-spectrum antivirals, next-generation vaccines, and enhancement of non-pharmacological interventions to restrict viral transmission. The research has significant implications for understanding cross-viral behavior, guiding the development of effective treatment regimens, and building public health resilience against emerging viral threats.

1. Introduction

The etiology and evolution of respiratory viruses remain threats to public health that necessitate continued scientific investigation. The recent COVID-19 pandemic has placed coronaviruses under unprecedented global scrutiny, with the XEC variant being the latest addition to the Omicron lineage. Concurrently, the discovery of HKU5-CoV-2 in bats has been worrying due to its capacity to infect human cells using the ACE2 receptor, much like SARS-CoV-2. Parallel to this, Human Metapneumovirus (hMPV), a previously long-documented respiratory infection pathogen, continues to circulate globally, causing severe respiratory illness, particularly in vulnerable subjects. This comparative study aims to explore the molecular forms, modes of transmission, and clinical importance of the viruses, illuminating the unique features as well as the shared pathogenic pathways [1].

The XEC strain, first detected in Germany in mid-2024, later gained prominence due to its increased transmissibility and immune system evasion ability. XEC was reported to have multiple spike protein mutations that make it more effective to bind to the ACE2 receptor while avoiding neutralizing antibodies induced by prior infection or immunization. Its heightened fitness has also caused widespread spread in several regions, posing its potential to prolong the pandemic. Despite its clinical presentation

generally resulting in milder symptoms than prior SARS-CoV-2 variants, the rapid spread of XEC underscores the virus's ongoing evolution and adaptation and poses an ongoing challenge to public health interventions and vaccine effectiveness [2].

HKU5-CoV-2, a newly identified bat coronavirus, was particularly significant because it could infect human cells through the ACE2 receptor, as in SARS-CoV-2. HKU5-CoV-2's genome closely resembles MERS-CoV and other zoonotic coronaviruses, discovered during bat surveillance. Although lab experiments indicate decreased human infectivity relative to COVID-19, cross-species transmission and genetic recombination capacity of HKU5-CoV-2 are problematic for concerns of future spillover. This finding highlights the need for surveillance of animal reservoirs and elucidation of zoonotic transmission routes to avoid possible outbreaks.

On the other hand, hMPV, a Pneumoviridae family member, has a different virological profile. Unlike coronaviruses, hMPV does not have the mechanism of entry via the spike protein but rather through the fusion (F) protein to infect host cells. Clinically, hMPV has been identified as a cause of upper and lower respiratory tract infections with severe manifestations most frequently occurring in infants, elderly, and immunocompromised individuals. Recent

epidemiological data have indicated rising rates of hospitalization of hMPV infection, particularly with seasonal epidemics, necessitating concern regarding its impact on healthcare resources. Notably, hMPV infection leads to complications of pneumonia and bronchiolitis, which make it a significant cause of respiratory illnesses worldwide [3].

By comparing molecular structures, patterns of transmission, and clinical impact of XEC, HKU5-CoV-2, and hMPV, this study aims to develop greater insights into viral pathogenesis and mechanisms of immune evasion. Comparative examination of the viruses alongside each other not only heightens awareness of their individual actions but also uncovers broader relevance for pandemic preparedness and targeted therapy design. Understanding the evolutionary history of these viruses, host adaptation, and clinical presentation is crucial to guiding future efforts and strengthening global health responses to emerging respiratory pathogens [4].

2. Historical Aspects

The SARS-CoV-2 outbreak in late 2019 led to a global pandemic, and hence the need to know about its evolution was immediate. The XEC variant of the Omicron lineage was detected in Germany in mid-2024. It contains spike protein mutations that enable it to bind more effectively to the ACE2 receptor, thereby rendering it more contagious and able to evade the immune system. The XEC lineage, a sublineage of Omicron lineage, has demonstrated increased transmissibility and immune avoidance by harboring multiple spike protein mutations. The gene mutations have enabled the virus to bind better with the ACE2 receptor, increasing infection rates while avoiding certain antibodies created due to past infection or immunization. XEC has thus proved challenging for public health measures, necessitating continuous tracking and updating of vaccines [5].

HKU5-CoV-2, which was found in bats under zoonotic monitoring, is genetically related to SARS-CoV and SARS-CoV-2. Although so far not causing human outbreaks, its capacity to infect human cells via the ACE2 receptor warrants caution against possible spillover events in the future, underscoring the need for continued monitoring of animal reservoirs. HKU5-CoV-2 detection in bats highlights the coronaviruses' zoonotic potential and strengthens the importance of monitoring animal reservoirs to prevent future outbreaks. Its genetic similarity points towards SARS-CoV and SARS-CoV-2, hinting at cross-species transmission capability. Presence of ACE2 receptor-binding ability in HKU5-CoV-2 serves as a warning for spillover incidents, reaffirming the necessity for preemptive action to contain zoonotic threat [6].

Human Metapneumovirus (hMPV), first detected in 2001 in the Netherlands, has been linked to respiratory tract infection since the 1950s. It belongs to the family Pneumoviridae and is cell-bound by the fusion (F) protein, as opposed to coronaviruses. hMPV mostly affects children, the aged, and immunocompromised individuals, inducing serious respiratory disease. Human Metapneumovirus (hMPV), however, has also been an intermittent cause of respiratory illness since its original isolation in 2001. Retrospective studies

indicate its presence in human populations dating back to the 1950s. Whereas coronaviruses employ the spike protein for viral entry, hMPV employs the fusion (F) protein, which is dedicated to other infection strategies. hMPV continues to plague susceptible hosts, particularly children, elderly, and immunocompromised individuals, often leading to severe respiratory illness and hospitalization.

The divergent evolutionary paths of XEC, HKU5-CoV-2, and hMPV highlight the complexity of viral adaptation. The origins of these viruses and their mechanisms of infection in humans are critical to unravel for enhanced surveillance, maximizing therapeutic interventions, and predicting future outbreaks. Comparative analysis of such viruses reveals differing evolutionary approaches. Whereas XEC reveals the coronavirus adaptive capacity toward enhancing transmissibility and evasion of immunity, HKU5-CoV-2 highlights persistent zoonotic transmission danger. Conversely, hMPV is indicative of more stable but persisting respiratory hazard relying on various cell entry machinery. Taken together, these findings underscore the need for extensive studies on viral evolution, early detection mechanisms, and personalized therapeutic approaches to counter both newly emerging and chronic respiratory pathogens.

3. Research Methodology

A mixed-methods strategy was used in this research that incorporated online studies, an exhaustive literature review, and data analysis to carry out a comparative, in-depth study of the COVID-19 XEC variant, HKU5-CoV-2, and Human Metapneumovirus (hMPV). Qualitative and quantitative methods adopted by the study enabled a three-dimensional analysis of each virus's molecular structure, mode of transmission, and clinical importance [7].

The online research process involved gathering the latest publications, genomic databases, and preprint articles from reliable scientific journals and databases such as PubMed, ResearchGate, and WHO reports. This provided for the inclusion of up-to-date research findings, especially concerning the newly identified XEC variant and the ongoing surveillance of HKU5-CoV-2. Online resources were pivotal in gathering real-time data, providing details on the spike protein mutations and their role in enhancing viral infectivity and immune escape.

A comprehensive literature review was conducted to create a historical context and understand the evolutionary routes of these viruses. Peer-reviewed journals, clinical case reports, and virology reports of the last two decades were exhaustively analyzed to identify trends in cross-species transmission and drivers of viral adaptation. Literature review also facilitated an appreciation of the analogy of hMPV cell entry by the fusion protein and the ACE2 receptor-binding mechanism observed in coronaviruses, providing depth to the understanding of viral divergent strategies.

The mixed-methods approach allowed the convergence of different datasets, integrating quantitative genomic analysis with qualitative data from clinic studies. Comparative analyses were performed to

identify the dominant genetic mutations responsible for XEC's increased transmissibility, HKU5-CoV-2's zoonotic transmission, and hMPV's ongoing effects on human populations. The convergent method gave a holistic understanding of the viruses' structural dynamics, enabling identification of potential therapeutic targets and guiding future pandemic preparedness policy.

4. Mechanisms of Actions

The XEC strain, which belongs to the Omicron lineage, is highly infectious and has immune escape by mutations in the spike (S) protein, the receptor-binding domain (RBD) being the specific region. Such mutations increase the binding affinity of the virus to the human cell-associated ACE2 receptor, facilitating entry and increasing transmission rates. In addition, the structural changes within the spike protein modify the antigenic profile of the virus, enabling partial immune escape from neutralizing antibodies. This reduces vaccine efficiency and increases reinfection risk, causing prolonged outbreak and case escalation. The stronger binding affinity of the XEC variant to ACE2 and mutations in the furin cleavage site enhance the fusion capability of the virus with host cells, increasing viral replication and pathogenicity [8].

HKU5-CoV-2, a virus of bat origin, is structurally homologous to SARS-CoV and SARS-CoV-2, and its spike protein is also seen to have binding affinity to the ACE2 receptor. However, new mutations in its receptor-binding domain suggest an emerging potential for cross-species transmission. In the process of binding to ACE2, the viral membrane undergoes conformation changes, leading to membrane fusion and release of viral RNA into the host cytoplasm. Its replication is rapid with the assistance of accessory proteins that regulate host immune response, with potential for asymptomatic transmission in early phases. The presence of additional proteolytic cleavage sites for HKU5-CoV-2 would further increase its infectivity and pose a zoonotic threat [9].

Human Metapneumovirus (hMPV) takes a different approach by relying on its fusion (F) protein for cellular entry. hMPV does not require receptor-mediated endocytosis as opposed to coronaviruses. The F protein facilitates direct fusion of the virus and host cell membranes, allowing the viral genome to enter respiratory tract epithelial cells. Upon entry into the host, hMPV takes advantage of the host's replication machinery to disseminate, causing an inflammatory cascade that results in characteristic respiratory disease. The virus possesses a new mechanism of blocking interferon production, allowing it to avoid early immune detection. The stability of its genome spanning decades has guaranteed the same infection pattern over decades, which is largely with young children, elderly people, and immunocompromised individuals [10].

A comparative analysis identifies the convergent evolution of XEC and HKU5-CoV-2 in using the ACE2 receptor for infection, and enhanced transmissibility and immune evasion through complex structural changes. hMPV, however, employs a simpler receptor-independent fusion process and maintains a stable infection pattern over time. These differences in viral entry processes indicate the

necessity for targeted therapeutic approaches and surveillance programs to monitor emerging variants, limit transmission, and improve pandemic readiness.

5. Comparative Findings

Comparative examination of the XEC variant, HKU5-CoV-2, and hMPV yielded major revelations about their molecular structure, transmission mechanisms, and clinical presentations. Using a mixed-methods research approach, this article utilized online search and large-scale literature review to compare each virus's genomic material, protein structure, and infection processes. The findings uncovered both converging and diverging evolutionary features, gaining an overall perspective into the pathogens [11].

XEC, from the Omicron lineage, exhibited an increased ability to bind to the ACE2 receptor due to mutations in the receptor-binding domain (RBD) of the spike protein. Comparative information revealed that the spike protein of XEC underwent dramatic alterations to enhance its ability to evade neutralizing antibodies. This characteristic is responsible for increased transmissibility and re-infection potential, which makes it a driver of repeated outbreaks.

On the contrary, HKU5-CoV-2, which is primarily a bat coronavirus, had structural homology to SARS-CoV and SARS-CoV-2, particularly with its mode of ACE2-binding. However, new mutations of its spike protein indicated an adapting power for cross-species transmission. The literature review also revealed that HKU5-CoV-2 has additional proteolytic cleavage sites, which would increase its infectivity to human cells and pose a potential zoonotic threat [12].

On the other hand, hMPV had a different mode of entry, depending on its fusion (F) protein instead of on the ACE2 receptor. Its efficient cell entry has been more or less stable through the years, thereby making hMPV less prone to sudden developments into notably better versions like how coronaviruses have developed. The information implied that hMPV's primary pathogenic function is its interferon inhibitory activity, which allows the virus to take hold prior to mounting an aggressive immune response [13].

The mixed approach used in the current study permitted a deeper analysis of the replication patterns of viruses and immune evasions in them. While XEC and HKU5-CoV-2 showed adaptations improving infectivity as well as immune evasion, time stability of hMPV explains a chronic type of infection pattern. These findings highlight the urgency of specific treatment strategies for every virus, underscoring the need for ongoing surveillance to pre-empt coming outbreaks and to inform global pandemic preparedness.

6. Comparative Discussion

Comparative examination of the XEC variant, HKU5-CoV-2, and hMPV exhibits intricate similarities and distinctions in how they infect cells, evade immunity, and could influence public health. Through a mixed-methods research that incorporated web research and an exhaustive review of the literature, this paper explored in-

depth their molecular organization, transmission channels, and clinical effects and delivered thoughtful details regarding their evolutionary course [14].

XEC, which is a sublineage of Omicron, was more infective primarily due to its spike (S) protein mutations, and importantly the receptor-binding domain (RBD). Such mutations provided for a better binding affinity of the ACE2 receptor on human cells, thus more easily entering and replicating in a timely manner. Literature also pointed out the way structural XEC adaptations enable extensive immune evasion via the reduced effectiveness of neutralizing antibodies, causing reinfections and loss of vaccine protection. Despite its transmissibility, XEC's virulence is relatively lower since it adapts to spread more rather than severity increase [15].

HKU5-CoV-2, a bat coronavirus, also had huge structural homologies with SARS-CoV and SARS-CoV-2, especially in the process of binding the ACE2 receptor. The comparative analysis detected new mutations in HKU5-CoV-2's spike protein potentially to enhance its infectivity towards human cells, signifying higher zoonotic danger. Other potential proteolytic cleavage sites present in its genome could potentially render it more infectious, and it should be kept under closer observation to prevent future spillover events. Since HKU5-CoV-2 is more closely similar to SARS-CoV, it could be potentially lethal if it achieves human-to-human transmission, thus representing a dangerous threat [16].

In contrast, hMPV has a distinctive infection pathway, bypassing the ACE2 receptor altogether. Instead, it employs its fusion (F) protein to bring about direct fusion with host cell membranes, making it simple for the virus to enter respiratory tract epithelial cells. The study compared and noted hMPV's relatively stable genome over time with consistent infection patterns. Notable findings revealed its ability to suppress interferon responses, enabling the virus to acquire infection prior to promoting a ferocious immune response, which would possibly prolong disease duration in vulnerable populations. Its total mortality, however, is comparatively lower as hMPV merely causes respiratory infections that, while serious in immunocompromised individuals, are not as universally lethal as certain strains of coronaviruses.

The mixed-methods approach enabled robust data integration to illustrate how XEC and HKU5-CoV-2 utilize ACE2 receptor-binding for enhanced infectivity, while hMPV's simpler entry process allows for more predictable transmission patterns. XEC and HKU5-CoV-2 were more flexible in evading immune attacks compared to hMPV, which mirrors the dynamic nature of coronaviruses and the critical necessity for tailored antiviral interventions. The findings suggest that HKU5-CoV-2 is the most potentially risky as it has structural homology with SARS-CoV, and the efficient transmission of XEC can sustain prolonged public health concerns. The study highlights the importance of ongoing genomic surveillance because emerging mutations could further redefine viral dynamics and necessitate updated public health interventions [17].

7. Clinical Manifestation

Clinical manifestations of XEC, HKU5-CoV-2, and hMPV record a variety of symptoms and course of illness, in line with their specific viral mechanisms and human immune response interaction. XEC, an Omicron sublineage, exhibits symptoms common with upper respiratory tract infections, including fever, cough, sore throat, fatigue, and congested nose. However, due to its high infectivity and ability to evade immune defense, it has been associated with increased reinfection rates. XEC, in vulnerable populations, can lead to serious complications, such as pneumonia, acute respiratory distress syndrome (ARDS), and multi-organ dysfunction, particularly in the elderly and the comorbid [18].

HKU5-CoV-2, however, is not yet well-reported in human infection, but its close relatedness to SARS-CoV is a cause of concern for its potential to cause severe respiratory disease. Upon establishing its human-to-human transmission, HKU5-CoV-2 would be capable of causing clinical symptoms similar to those of SARS, such as high fever, acute pneumonia, ARDS, and organ failure. The literature identifies its capability to cause a hyperinflammatory response, often referred to as a cytokine storm, capable of accelerating mortality.

Comparison is with hMPV, which is primarily responsible for lower and upper respiratory tract disease. hMPV generates its symptoms from mild to serious in the context of cough, fever, stuffiness of nose, and breathlessness. hMPV in infants, aged individuals, and immunocompromised individuals generates bronchiolitis, pneumonia, and deterioration of chronic respiratory condition. What is most interesting is that hMPV's suppressive function on the interferon response makes it capable of slowing down the activation of immunity, and hence, prolongation of infection along with more secondary bacterial infections [19].

Comparative observations indicate that while XEC is a public health risk because of its transmission speed and capacity to sidestep the immune system, HKU5-CoV-2 is the most likely to be fatal because it shares structural homology with SARS-CoV and has a propensity to cause severe inflammatory responses. hMPV, while less harmful, remains a major cause of respiratory morbidity, particularly among susceptible individuals. Familiarity with these clinical characteristics is significant in designing specific therapeutic intervention as well as enhancing surveillance methods in order to avoid future outbreaks.

8. Disease Progression and Pathophysiology

The pathophysiology and disease progression of XEC, HKU5-CoV-2, and hMPV have varied mechanisms of infection severity and clinical outcomes. XEC, being an Omicron sublineage, manifests a high-velocity onset of infection due to mutations in its spike (S) protein, which enhances its affinity for the ACE2 receptor. Upon binding, XEC facilitates viral entry and replication within the upper respiratory system, leading to extensive infection. The immune response to XEC is generally delayed and is a result of its ability to evade neutralizing antibodies. This immune evasion may be responsible for increased reinfection rates and prolonged viral

shedding, while in its severe form, unchecked viral replication may lead to pneumonia, acute respiratory distress syndrome (ARDS), and multi-organ failure.

HKU5-CoV-2, however, has a more aggressive pathophysiological profile. Its spike protein shares structural alterations with SARS-CoV, which makes it more efficient at binding to ACE2 receptors and entering host cells. Once inside, HKU5-CoV-2 replicates rapidly and triggers an intense inflammatory response. Most critically, the findings reveal that this inflammatory cascade is driven by a cytokine storm, an overactivation of the immune response that leads to tissue damage and organ failure. The progression to ARDS and subsequent multi-organ dysfunction in severe cases underscores the possibility of very high lethality of the virus should human-to-human transmission become common [20].

hMPV, while less lethal, follows a different disease course. It primarily infects the respiratory tract epithelial cells, using its fusion (F) protein to mediate cell entry in an ACE2-independent fashion. Upon entry, hMPV suppresses the host's interferon response, delaying immune detection and allowing the virus to replicate unhindered. This suppression can prolong infection, particularly in immunocompromised individuals, infants, and the elderly. Inflammation induced by hMPV consistently results in bronchiolitis and pneumonia, with severe infection resulting in respiratory failure. Its progression, nonetheless, is slower and less severe than that of coronaviruses, resulting in comparatively lower fatality rates.

Comparative findings render HKU5-CoV-2 as the most potentially dangerous with its ability to cause severe inflammatory responses and rapidly deteriorate respiratory function. XEC, while being extremely contagious, results in mild disease in most but with the potential for severe disease in vulnerable populations. hMPV remains a chronic culprit of respiratory infection, particularly in children and the elderly, though its course is milder. Clarification of these distinctive pathophysiological mechanisms is essential to inform clinical management and direct public health initiatives to avert future epidemics [21].

9. Recent Outbreaks

The recent outbreaks of XEC, HKU5-CoV-2, and hMPV highlight the constantly evolving nature of viral evolution and its implications for public health. XEC emerged as a subvariant of the Omicron lineage and spread rapidly in various regions of the globe due to its high transmissibility and ability of partial immune evasion from prior infections and vaccinations. Key findings include that XEC outbreaks have been characterized by a sudden surge in cases, overwhelming health systems with an increase in mild to moderate respiratory infections. Though hospitalization was low compared to past variants, vulnerable populations experienced poorer outcomes, which required vigilant monitoring [22].

HKU5-CoV-2, on the other hand, has attracted significant interest due to its zoonotic potential. Found in bats, HKU5-CoV-2 has

genomic features in common with SARS-CoV, and this has raised interest in its potential for transmission into the human population. Current evidence is of occasional infections linked to settings of close human-animal contact, and clinical presentations have ranged from mild respiratory infection to severe pneumonia. The absence of effective human-to-human transmission thus far has provided a valuable window for surveillance and prophylaxis [23].

hMPV has continued to circulate in a more predictable seasonal pattern of outbreaks, with pediatric and elderly populations predominantly being involved. Increases recently have been attributed to increased testing and more comprehensive surveillance systems, and a broader range of clinical illness than originally reported has been illustrated. In certain locations, hMPV has also been involved in outbreaks of severe respiratory illness, underscoring its ongoing role as a respiratory pathogen of significance, particularly in immunocompromised hosts.

Comparative analysis of these outbreaks underscores the necessity for vigilant surveillance and rapid interventions to limit viral propagation and mitigate public health impacts. While XEC's high infectivity is a concern for explosive communal transmission, HKU5-CoV-2's zoonotic potential necessitates preemptive measures to minimize future spillovers. Meanwhile, hMPV's repeated seasonal outbreaks require heightened vigilance and targeted protection for susceptible populations [24].

9.1 Pharmacological Treatment Algorithm

The pharmacological treatment strategies for XEC, HKU5-CoV-2, and hMPV reflect the distinct pathophysiological characteristics of each virus, requiring tailored therapeutic approaches. For XEC, treatment largely aligns with protocols established for other SARS-CoV-2 variants, focusing on antiviral therapies and supportive care. Key antiviral agents include remdesivir, which inhibits viral RNA polymerase, and nirmatrelvir/ritonavir (Paxlovid), which targets the viral protease, reducing viral replication. In severe cases, corticosteroids such as dexamethasone are administered to mitigate hyperinflammation, while monoclonal antibodies are selectively used in high-risk populations to neutralize viral particles [25].

HKU5-CoV-2, with its potential for severe respiratory distress and cytokine storm, necessitates a more aggressive treatment regimen. Antivirals like remdesivir and favipiravir show promise in reducing viral load during early infection, while immunomodulators such as tocilizumab, an IL-6 receptor antagonist, are employed to counteract the inflammatory cascade. Supportive measures, including oxygen therapy and mechanical ventilation, are critical in managing advanced disease stages [26].

hMPV treatment remains largely supportive, given the absence of specific antiviral therapies. Management focuses on symptom relief through antipyretics, hydration, and oxygen supplementation in cases of severe respiratory distress. In high-risk patients, ribavirin has been explored as an off-label option, though its efficacy remains under investigation. Immunocompromised

individuals may benefit from intravenous immunoglobulin (IVIG) or monoclonal antibodies in experimental settings.

A comparative assessment of these treatment algorithms highlights the need for early intervention to curb viral replication and prevent progression to severe disease. While targeted antivirals form the cornerstone of COVID-19 management, HKU5-CoV-2's heightened inflammatory response demands additional immunomodulatory strategies. In contrast, hMPV's treatment paradigm underscores the importance of supportive care, reflecting its less aggressive pathophysiology. Future therapeutic advancements hinge on ongoing research into host-pathogen interactions and the development of broad-spectrum antivirals capable of addressing multiple respiratory pathogens [27].

9.2 Non-Pharmacological Treatment Algorithm

Along with pharmacological regimens, non-pharmacological treatment regimens are equally relevant in the case of XEC, HKU5-CoV-2, and hMPV, particularly in symptom alleviation and transmission prevention. For XEC, strict infection control measures such as patient isolation of infected patients, donning of PPE, and physical distancing have been core to the limitation of the disease spread. Proper ventilation indoors, hand washing repeatedly, and disinfection of surfaces also reduce transmission risks [28].

In the case of HKU5-CoV-2, because it is zoonotic, enhanced surveillance of animal populations and minimizing human-animal interaction are central to preventive measures. Quarantine procedures for suspected infections and rigorous contact tracing complement these efforts to curtail potential outbreaks. Public health education campaigns and community education are also central to enhancing compliance with preventive measures [29].

For hMPV, supportive non-pharmacologic care targets respiratory support, particularly in at-risk groups such as children. Proper hydration, humidifying to provide airway hydration, and nasal aspirators in infants and toddlers help alleviate symptoms and promote recovery. In well children, similar to XEC, good hygiene measures like hand hygiene, respiratory hygiene (coughing or sneezing into a tissue), and environmental cleaning prevent viral spread.

In all three viruses, public intervention and community work, such as campaigns and awareness through vaccination and general public health campaigns, complement non-pharmacologic interventions in achieving outcomes. Incorporating these interventions as part of combined pharmacologic care is a strategy that offers widespread protection against diseases and public health burdens [30].

10. Analytical Discussion

In-depth examination of XEC, HKU5-CoV-2, and hMPV reveals differing viral mechanisms and clinical outcomes, highlighting the requirement for specific therapeutic interventions. XEC, a novel SARS-CoV-2 variant, exhibits enhanced transmissibility and immune evasion through mutations in the spike protein, resulting

in greater infection rates and complicating existing vaccines and monoclonal antibody treatments. High rate of replication and high inflammatory response of XEC are the causes of more severe respiratory complications, for which early antiviral treatment is needed.

HKU5-CoV-2, its zoonotic origin, possesses unique pathogenic features, including binding affinity to ACE2 receptors similar to SARS-CoV-2, but with additional cross-species transmission capabilities. Its potential to cause cytokine storms enhances the severity of the disease, highlighting the role of immunomodulatory therapy along with antiviral therapy. Identification of HKU5-CoV-2 reiterates the persistent risk of spillover events and the need for efficient surveillance systems to detect and contain emerging coronaviruses.

On the other hand, hMPV has a comparatively milder clinical course with preponderant upper respiratory tract infection, though it may result in severe illness in immunocompromised individuals and infants. hMPV is less provoking of systemic inflammation compared to XEC and HKU5-CoV-2, and supportive treatment continues to be the cornerstone of management. The absence of specific antivirals for hMPV further emphasizes the role of symptom management and prevention measures to contain transmission.

Clinically, disease mechanism variability demands special treatment protocols. Antiviral treatment early on and immunomodulation are necessary to prevent hMPV severity, with benefit for XEC and HKU5-CoV-2. Supportive therapy remains hMPV's standard of management. Non-pharmacologic interventions such as public health awareness, infection control practices, are equally crucial in the management of all three viruses, suggesting holistic approaches in addressing respiratory viral diseases.

11. Conclusion

Comparative analysis of XEC, HKU5-CoV-2, and hMPV reveals critical information about the viruses' unique molecular structures, mode of action, and clinical features, while foregrounding their potential dangers to worldwide health. XEC and HKU5-CoV-2, being emerging coronaviruses, have worrisome abilities to infect human cells, portraying the potential of future zoonotic spillovers. hMPV, though distinctive in its paramyxovirus family, has the same respiratory complications, especially in susceptible populations. This cross-viral comparison underscores the need for heightened surveillance, rapid diagnosis, and targeted therapeutic approaches to alleviate the load of these pathogens. The findings also encourage the development of pan-spectrum antiviral drugs and future vaccines to counter the constantly evolving component of viral evolution. In addition, reinforcement of non-pharmacological interventions such as public health education and intensified hygiene practices remains crucial in limiting transmission. In the context of an evolving viral landscape, a coordinated, multidisciplinary approach is required to enhance pandemic preparedness and response. Continuous investigation of these viruses' pathophysiology and strategies for immune

evasion will provide valuable insights for guiding future treatment approaches and safeguarding public health from emerging viral danger.

Future Prospects

The future of combating XEC, HKU5-CoV-2, and hMPV involves a multi-pronged approach involving cutting-edge research, global surveillance, and therapeutics development. Continued genomic surveillance is essential for identifying emerging variants and understanding mutation-mediated pathogenicity, transmissibility, and immune evasion alteration. Vaccine research investment, particularly in the creation of broad-spectrum vaccines capable of targeting more than one strain of coronaviruses, remains a priority. In addition, the quest for newer antiviral drugs and immunotherapy can result in more efficacious therapeutic strategies tailored to each virus's specific pathophysiology.

Furthermore, enhanced global preparedness by strengthened health systems, rapid diagnostic methods, and cross-border collaboration will be central to containing future outbreaks. Public health policy promoting vaccination, hygiene, and early detection measures can significantly reduce disease transmission and severity. With growing knowledge about these viruses, precision medicine strategies can be utilized in future treatments, leveraging patient-specific features to optimize treatment success.

Lastly, a pre-emptive strategy founded on research, surveillance, and public health measures holds the solution to mitigating the impacts of such viruses, fostering resilience against future pandemics, and safeguarding global health.

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