Nipah Virus: Current Understanding of Epidemiology, Pathogenesis, and Therapeutic Strategies -A Comprehensive Review

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Abstract

Background: Nipah Virus (NiV) is a zoonotic virus with very high pathogenicity. Due to its high death rate, wide host range, and potential to cause epidemic and pandemic spread, it has been acknowledged as a major global health issue. After its initial discovery during the outbreak in Malaysia and Singapore, several re-occurrences in South and Southeast Asia have highlighted the ongoing danger this virus poses. Various factors such as environmental changes, humans invading wildlife habitats, and increased human animal interactions have raised the risk of virus spillover and emergence of diseases.

Objective: The present review was planned to be a summary of the existing knowledge about the epidemiology pathogenesis new developments in diagnostics, and treatments for Nipah virus infection, plus pointing out recent progress and research needs in the future.

Methods: The study was a detailed overview of selected published literature related to Nipah virus research, through which a narrative review was carried out. Incident characteristics of Nipah virus, modes of transmission, viral pathogenicity symptoms diagnostics, genomic monitoring, and treatment options were the main focus areas of research papers published from 2019 to 2026, that have been used in the study. The Chosen findings were rearranged and integrated in a qualitative descriptive manner.

Results: The literature we analyzed showed that the gig virus is still a big virus to humans since it can cause serious brain and lung problems and even death. The spread of the virus has changed from mainly animals carrying the disease to more people passing the disease to each other in the same areas where the virus is mostly found. The virus sticking to the ephrin molecules first is the main thing in the virus harm to the blood vessels, messing up the immune system, and the virus going to the brain effects. Disease monitoring and detection have been enhanced through significant advancements in diagnostic technologies, including molecular testing and genomic sequencing platforms. Currently, the main method of treatment is supportive management. Still, new therapeutic methods like antiviral agents, monoclonal antibodies, vaccine production, and other alternative methods are quite promising.

Conclusion: The Nipah virus continues to be a major concern for public health, given its potential for causing major epidemics. To better prepare ourselves and minimize the effects of any future outbreaks, it is necessary to constantly upgrade our surveillance systems, ensure diagnostics are easily accessible, develop medicines, and carry out researches in various fields. There is no doubt that worldwide cooperation through an integrated One Health approach will are key in devising better strategies for prevention and control.

Keywords: Nipah virus, zoonotic infection, epidemiology, pathogenesis, diagnostics, therapeutics, outbreak preparedness, vaccine development, emerging infectious disease.

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1. Introduction

Zoonotic viral diseases are a persistent threat to global public health as these diseases could cause major outbreaks with high death rates and serious socioeconomic impact. One such pathogen, Nipah virus (NiV), has been recognized as a highly dangerous emerging zoonotic virus with the ability to cause epidemics and pandemics. Nipah virus belongs to the genus Henipavirus, family Paramyxoviridae, and is a negative-sense, single-stranded RNA virus that can infect different mammalian species, including humans. Fruit bats of the Pteropus genus are identified as the natural reservoirs of the virus, enabling transmission between different animal species and infecting humans through zoonotic spillover events and human-to-human transmission (3,5).

Nipah virus was first recognized during an epidemic of pig farmers in Malaysia and Singapore in 1998-1999, where infected pigs acted as the intermediate amplifying hosts. Since then, recurrent outbreaks have been mainly reported in South and Southeast Asian countries, Mainly Bangladesh and India, with different transmission patterns and case fatality rates. The outbreaks in Bangladesh and India, unlike the Malaysian ones, have shown significant human-to-human transmission, raising the worry about the possibility of the virus being spread more widely. Changes in the environment deforestation urbanization, and increased human-animal contacts have also greatly increased the risk of zoonotic spillover and disease emergence (3,5).

The range of clinical symptoms in Nipah virus infection is very broad and includes asymptomatic infection, mild febrile illness, severe respiratory disease, and fatal encephalitis. Neurological manifestation is one of the most critical features of the infection and in many cases, survivors of the infection suffer from long term neurological sequelae. The mortality rate of Nipah infection is very high and has been reported to be between 40% - 75% based on the outbreak situation and availability of healthcare facilities. This is indicative of the significant threat this pathogen poses. Besides this, the virus is also considered a potential candidate for a future "Disease X" scenario by the WHO due to its high pathogenicity, wide host range and the lack of effective therapeutics and vaccines. (2,7).

The pathogenesis of Nipah virus (NiV) is the result of various interactions between the host and virus that allow the virus to enter cells, escape the immune system, spread through the body, and cause severe damage to organs. Mechanisms of viral attachment and entry hinge mainly on the binding of viral glycoproteins to the ephrin-B2 and ephrin-B3 receptors, which are highly located in endothelial and neuronal tissues. This explains why the virus causes extensive vascular injury, endothelial dysfunction, inflammation, and CNS involvement, the primary characteristics of severely ill patients. Progresses in molecular biology and virological research have led mostly understanding these pathogenic mechanisms; But, there are certain aspects that are not fully known to date (1,2).

Quick and precise identification is critical to successfully prevent the spread of the outbreak and properly treat the patients with Nipah virus infection. In recent times diagnostic methods have improved A lot. For example, reverse transcription polymerase chain reaction (RT-PCR) is a method that detects virus particles by amplifying their genetic material directly; serological assays help identify whether a person has developed antibodies against the virus; next-generation sequencing technologies facilitate extensive genomic analysis; portable genomic platforms can be carried on the site of the outbreak. Developments like culture-independent whole-genome sequencing by nanopore-based technologies have not only become a method for the estimation and monitoring of real-time evolution during outbreaks but also have the power to facilitate the enhancement of epidemiological studies as well as health-related decisions (4,8).

Although more and more scientists are focusing on it, the number of therapeutic options available for Nipah virus infection is still quite limited. At the moment, patients are mainly treated by support measures; several antiviral drugs, monoclonal antibodies, immune therapy techniques, and different vaccine candidates are being tested. Also, new studies on other ways of treating by herbal medicine are attracting attention as possible extra measures in managing the disease. Research that is presently being carried out shows that there is a dire need for effective drugs and preventive measures to reduce the risk of new outbreaks and global spread (1, 6, 7).

So, this in-depth review essentially intends to present a summary of existing knowledge about Nipah virus epidemiology pathogenesis diagnostic improvements, and treatment approaches. At the same time, it focuses on recent developments and

outlines potential research areas that are crucial for enhancing preparedness against this emerging global health threat.

2. Material and Methods

2.1 Study Design

The objective of this work is a detailed narrative review, focusing mainly on combining up-to-date information about Nipah virus epidemiology pathogenesis diagnostics, and therapeutic interventions. The purpose of the review was to offer a coherent overview of the existing knowledge on Nipah virus infection as well as to highlight the latest discoveries and new research areas. Since the topic is very wide and involves different disciplines, a narrative style was chosen to be able to bring together epidemiological virological clinical, diagnostic, and therapeutic results in one comprehensive document.

2.2 Literature Search Strategy

To collect the literature for this review, we carried out a comprehensive study of published research papers and gathered updated virology related to Nipah virus infection. The current review mainly made use of eight carefully chosen articles that came out from 2019 to 2026, discussing significant features of Nipah virus biology and disease in detail. These pieces of works were review articles, epidemiological studies, diagnostic problems, treatment researches, and genomic surveillance studies. The chosen literature samples offered both basic and up-to-date information to cover the subject thoroughly.

2.3 Selection of Relevant Literature

Studies that was part of this review were picked based on their relevance to the main points and goals of the article. The main criteria for selecting studies were publications about the epidemiological distribution of Nipah virus, transmission modes, pathogenesis mechanisms, clinical features, diagnostic methods, and therapeutic options, including new and potential treatments. Great emphasis was laid on getting the most recent publications to capture the latest developments in diagnostics, genomic sequencing, and therapeutic possibilities. Overlapping material was carefully reviewed to ensure the truthfulness of evidence and to avoid unnecessary duplication.

2.4 Data Extraction and Organization

We systematically extracted relevant information from the selected documents and categorized it as the main thematic areas connected to Nipah virus research. The data we obtained involved viral features, reservoir hosts, modes of transmission, outbreak patterns, molecular mechanisms responsible for disease pathogenesis, diagnostic tools, and treatment options. We also discussed the latest progress in genomic sequencing and new ways of therapy, to give a fresh view of the continuing research trends. We then divided the extracted data into different parts to help the clear presentation and understanding.

2.5 Data Synthesis and Interpretation

We used a qualitative descriptive approach to merge and synthesize the evidence gathered into one comprehensive narrative. Different studies reporting similar findings were compared and integrated to draw a general picture of knowledge on the topic. By critically analyzing the differences and new insights in the various studies, we were able to pinpoint changes in the concepts of Nipah virus infection. More attention was given to highlighting the areas of ongoing research, diagnosing difficulties and drug therapy shortages that might be the main factors for future Nipah virus readiness and E disease control.

2.6 Ethical Considerations

This review was an analysis of previously published literature only. No human participants, animal experiments, or patient confidential data were handled. That means, no ethical approval or informed consent was necessary. To ensure academic integrity and prevent plagiarism, all the source materials used were properly recognized and referenced.

3. Results

In-depth study of the chosen articles revealed that Nipah virus still a major hazardous emerging zoonotic disease from virus with a growing public health threat due to its very high death rate, possibility of transmission between different species, and potential to cause worldwide epidemic. The articles examined together provided evidence that analysis patterns of Nipah virus infection had changed over time, and transmission variations existed in different regions. First outbreaks mainly involved animals as transmission media like pigs Though the latest outbreaks have shown more human-to-human transmissions Mostly in the South Asian countries. Besides, the research showed great strides in unraveling the molecular mechanism of Nipah virus disease and the latest development in the field of diagnostics and therapeutics.

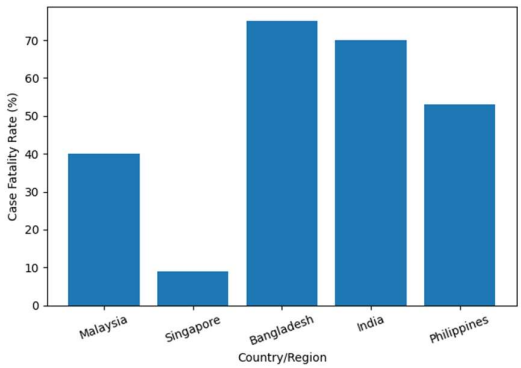
According to the published works, the severity of diseases depends on the viral tropism, immune response, and the host factors that are involved. When the virus spreads to the brain and the lungs, these are the most common symptoms in the cases of severe infections. Presently supportive treatment is the main approach to dealing with the disease. Though, new antiviral drugs, monoclonal antibodies, and advanced genomic methods for tracking diseases hold the potential to make us well-prepared for disease outbreaks and may help in controlling the diseases.

Table 1. Summary of Epidemiological Characteristics of Nipah Virus Outbreaks

Region /Country	Approximate	Dominant Trans	Estimated	Major Reservoir/

	Period of Major Outbreaks	mission Route	Case Fatality Rate (%)	Intermediate Host
Malaysia	1998–1999	Pig-to-human	40	Fruit bats/Pigs
Singapore	1999	Pig-to-human	9	Fruit bats/Pigs
Bangladesh	2001–Present	Human-to-human, contaminated food	70–75	Fruit bats
India	2001–Present	Human-to-human, bat exposure	65–75	Fruit bats
Philippines	2014	Animal-to-human	53	Horses
Southeast Asia (Potential risk areas)	Recent surveillance reports	Spillover transmission	Variable	Fruit bats

The epidemiological evidence indicates that alterations in environmental conditions and enhanced human contacts with wildlife reservoirs could be key factors leading to the emergence of new outbreaks. Areas having high densities of fruit bat populations and with frequent human-animal interactions could be the ones at a higher risk of virus transmission.



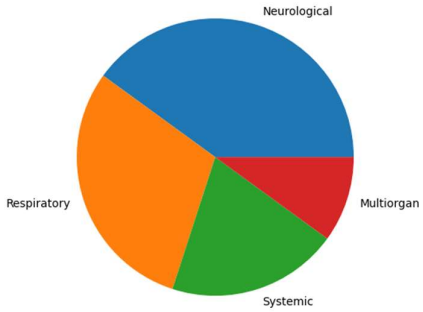
Graph 1. Geographical Distribution and Approximate Case Fatality Rates of Major Nipah Virus Outbreak Regions

Neuronal cells and endothelial tissues are infected early, mostly where ephrin-B2 and ephrin-B3 receptors are found. These receptors spread throughout the body, making both cell types major targets. Once infected, they trigger widespread inflammation, harm blood vessels, and cause serious nerve-related symptoms.

Table 2. Major Pathogenic Mechanisms and Clinical Manifestations of Nipah Virus Infection

Pathogenic Mechanism	Target Tissue/Cells	Biological Consequence	Common Clinical Manifestations
Viral attachment through ephrin receptors	Endothelial cells	Viral entry and dissemination	Fever, malaise
Endothelial dysfunction	Blood vessels	Vasculitis and vascular injury	Headache, dizziness
Blood-brain barrier disruption	Central nervous system	Neurological involvement	Encephalitis, seizures
Pulmonary tissue infection	Respiratory epithelium	Respiratory distress	Cough, dyspnea
Immune activation and inflammation	Multiple organs	Cytokine-mediated tissue injury	Multiorgan dysfunction

From what we saw, how sick people get ties back to both virus damage in tissues and the body's own immune reaction kicking in. Looking at the research, trouble breathing plus serious nerve issues kept showing up when patients did badly.



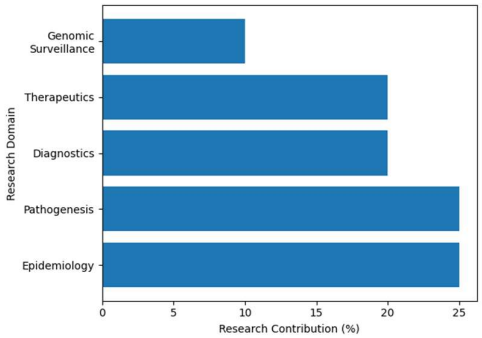
Graph 2. Distribution of Major Clinical Manifestations in Severe Nipah Virus Infection

One more main point of the review was that we have made progress in diagnostic technologies and therapeutic investigations. Traditional molecular diagnostic methods are still mainly used for case identification, but recent genomic technologies and experimental treatments have shown a lot of promise for managing outbreaks in the future.

Table 3. Emerging Diagnostic and Therapeutic Approaches for Nipah Virus Infection

Category	Method/Approach	Current Status	Potential Advantages
Molecular diagnosis	RT-PCR	Established	High sensitivity and specificity
Serological diagnosis	ELISA-based antibody testing	Established	Useful for surveillance
Genomic surveillance	Nanopore whole-genome sequencing	Emerging	Rapid outbreak tracking
Antiviral therapy	Ribavirin	Investigational use	Potential reduction of disease severity
Monoclonal antibody therapy	Human monoclonal antibodies	Experimental	Targeted viral neutralization
Phytomedicine-based therapeutics	Plant-derived compounds	Preclinical investigation	Potential alternative treatment approach
Vaccine development	Recombinant vaccine platforms	Clinical development stage	Long-term prevention

Results indicate that diagnostic improvements in particular through genomics sequencing may increase the effectiveness of outbreak surveillance and allow the identification of transmission patterns to be done swiftly. At the same time, therapeutic studies are still growing, but more clinical proof is needed to decide on the official treatment guidelines.



Graph 3. Relative Research Focus Across Nipah Virus Domains

Overall, the studies reviewed together point out that the Nipah virus is still an emerging pathogen that is highly prioritized by the world because of its possible large-scale epidemic potential. Combining epidemiological monitoring, better diagnostic methods, genomic technologies, and drug discovery for specific targets may be the key to advancing preparedness for the future and lowering the impact of the disease.

4. Discussion

Nipah virus remains one of the most significant emerging zoonotic pathogens due to its high pathogenicity, wide host range, potential for recurrent outbreaks, and high mortality rates. This article reviews work done in the past as well as very recent discoveries and reveals that, despite the improved understanding of the epidemiology and biology of Nipah virus, a lot still needs to be done for disease surveillance diagnosis drug development, and preparedness strategies. For the last twenty years, the virus has been causing outbreaks in South and Southeast Asia, which clearly shows the ongoing threat to public health and the need for international coordinated actions (3,9,12).

The results of this review show that epidemiological patterns of Nipah virus have changed a lot since the Malaysia outbreak in 19981999, when the virus was first recognized. The first outbreaks were mainly linked to transmission through animal hosts like pigs, which served as intermediaries. But, the latest outbreaks in Bangladesh and India have revealed a significant human-to-human transmission. Variations in transmission patterns not only point to the possibility of the virus changing its behavior but also to its increasing adaptation to human populations. In fact, factors like deforestation, agricultural expansion, urbanization, and climate-related ecological disturbances have increased, among others, human contacts with wildlife, which are reservoirs of the virus and as such, have given rise to zoonotic spillover events. Other researchers have made similar remarks when they identified human-induced environmental changes as a leading

factor for the emergence and persistence of henipavirus infections (5, 10, 12).

Fruit bats in the genus Pteropus are still the main natural reservoirs of the virus that keep the viral circulation in nature. Usually, people get the virus by touching food, animals or persons infected directly or indirectly. Infected bats are known to contaminate raw date palm sap which is a common source of infection among humans. Besides, intimate contact with infected persons also constitute as a major risk factors in endemic regions. Since the virus is not easily removed from the animal host then one of the reason why future outbreaks may be is because of viral circulation in wildlife populations. For that matter, animal and environmental monitoring are among the vital preventive measures which are gaining recognition day by day [10 ,11, 13].

The development of Nipah virus infection is mainly responsible for the severity of the disorder and the high mortality rates. The literature examined showed that the viral attachment via ephrin-B2 and ephrin-B3 receptors results in the virus being distributed widely into endothelial and neuronal tissues. The presence of such receptors explains the widespread vascular injury, respiratory affection, and severe neurological symptoms of infected people. Neurological issues such as acute encephalitis and neurocognitive impairment being some of the sequelae of infection are two quite serious effects. But, immune system failure and inflammatory reactions seem to be major factors in disease evolution and multiorgan failure. The host-pathogen interaction with the Nipah virus has been commonly used as a model to describe similar pathogenic mechanisms in the field (1, 2, 14).

Advances in diagnostic technologies have drastically enhanced the capability to identify and keep track of Nipah virus infection during outbreaks. Reverse transcription polymerase chain reaction is still the preferred diagnostic method due to its very high sensitivity and specificity. Then again, portable whole-genome sequencing platforms and nanopore-based diagnostic methods, among other genomic technologies, have been recently developed that can be utilized for rapid outbreak investigation and real-time surveillance. Combining genomic epidemiology with conventional diagnostic methods can Quite a bit help in outbreak control efforts and provide better insights into viral changes and transmission routes. But, the availability of high-end diagnostic technologies is still quite limited in areas with fewer resources, where cases of outbreaks are frequently reported (4, 8, 14).

Despite major breakthroughs, the range of possible treatments for Nipah virus infections has not greatly expanded. Present therapeutic methods still depend heavily on symptomatic therapy since no drugs have yet been universally approved for this purpose. Studies of Ribavirin and other antiviral medicines have produced inconsistent results, while monoclonal antibodies and other immune-based methods have given promising preliminary data. At the same time, vaccine production through recombinant viral vectors or subunit formulations has made significant advancements in the last few years. new research indicates that therapies derived from herbal medicines as well as new antiviral drugs may open up extra avenues for intervention in the future. Yet, most of the experimental drugs are still in the animal testing or phase I clinical trial stages and need more thorough testing before they can be used regularly in clinical practice (6, 14, 15).

Another significant point raised in this review is the alarming rise of Nipah virus as a potential cause of future pandemic or a "Disease X" scenario. Some key elements that fuel these worries are the high fatality rates of cases, ability of the virus to spread from one person to another, susceptibility to diverse animals, and lack of vaccines or treatment options on a large scale. Covering preparedness in a recent public health review the critical elements included early warning through surveillance strengthening laboratories ample and rapid diagnosis of pathogens effective communication and partnerships within a multidisciplinary including One Health concept. Such vulnerability planning measures become fundamentally relevant mainly in endemic and at risk areas where natural and human factors through the changing conditions will allow the virus to emerge (2, 7, 9, 11).

Over the years, the research work done on understanding Nipah virus infection has been massive Though a number of challenges still exist. The interpretation of the findings might be affected by factors like changes in the features of outbreaks, disparity in the level of diagnostics among different areas, and scarcity of large clinical trials. Besides that, most of the data on therapeutic effectiveness come from lab experiments or studies on animals rather than from large randomized clinical trials. In consequence, more studies are necessary to shed light on the ways the virus changes, immune responses by hosts, long-term conditions of those who have survived, and the potential of new treatments and preventive methods (7, 14, 15).

This review's results align with those of previous studies in emphasizing that the global threat posed by Nipah virus remains unresolved and calls for relentless scientific exploration and worldwide cooperation. Enhancing surveillance capabilities, raising the level of diagnostic availability, the discovery of new vaccines and therapies as well as

the execution of impactful preventive measures are still the crucial aspects to be focused on for mitigating disease impact and being ready for the next outbreak even better (9, 11, 12).

5. Conclusion

Nipa virus is a serious emerging zoonotic pathogen which remains a major threat to public health worldwide due to its high mortality rate, wide host range, potential for repeated outbreaks, and ability to transmit from human to human. The review here shows that a lot of work has been done to understand the epidemiological features, transmission patterns, pathogenesis at molecular level, diagnostic methods, and the therapeutic possibilities of Nipah virus infection. Still, even with the progress in scientific understanding, there are key issues that remain unresolved such as early detection, good treatment methods, and outbreak preparedness. The epidemiological evidence suggests that shifting environmental situations, more human-animal contacts, and ecological imbalances should cause further emergence and re-emergence of Nipah virus outbreaks. The intricate pathogenesis of the virus involving damage to the endothelium, nervous system, and immune response is responsible for severe disease and adverse clinical outcomes. Upgrades in molecular diagnostic methods and viral genomic surveillance have made it easier to track outbreaks and characterize viral changes, allowing more efficient health responses. At the moment most treatment methods are supportive, simply managing symptoms since there is no specific antiviral remedy recognized as universally effective. Still, many studies with monoclonal antibodies, antiviral drugs, vaccines, and also new ways of treatment gave hope that getting an actual drug into the market is just the matter of time. What is more, combining high-tech diagnostics, modern therapy, and the use of genomics could result in major leaps forward in managing diseases and controlling epidemics. Going forward, it will be important to improve the effectiveness of surveillance systems, support research in different fields, increase vaccine and drug development, and adopt prevention measures through a One Health approach. Working together at the international level and continued funding of science will be key to enhancing the ability to respond to Nipah virus outbreaks and lessening their effects. Altogether, these steps might help lessen the extent of the disease and increase the world's preparedness for this ongoing and possibly pandemic infectious threat.

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