



Nipah Virus Infection and Human Disease

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Mini Review

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Abstract

Nipah virus (NiV) is an important zoonotic pathogen that can cause severe neurological and respiratory disease in humans. The virus belongs to the genus Henipavirus within the family Paramyxoviridae, with fruit bats of the genus *Pteropus* recognized as important natural reservoir hosts. Human infection can occur following exposure to infected animals or contaminated food and, in some settings, through close contact with infected individuals. Since its emergence in Malaysia in 1998–1999, Nipah virus has continued to cause outbreaks, particularly in South and Southeast Asia. The clinical spectrum ranges from nonspecific febrile illness to severe encephalitis, respiratory disease, coma, and death. Despite progress in molecular diagnosis, genomic surveillance, vaccine development, and antibody-based therapeutics, there are currently no widely licensed human vaccines or specific antiviral treatments for Nipah virus. This mini review summarizes the major aspects of Nipah virus infection, including its animal reservoirs, transmission, pathogenesis, clinical manifestations, diagnosis, immune response, prevention, and emerging medical countermeasures. A coordinated One Health strategy integrating human, animal, and environmental surveillance remains essential for reducing the risk of future outbreaks.

Keywords: Nipah virus; zoonotic infection; *Pteropus* bats; viral pathogenesis; encephalitis; immune response; One Health; genomic surveillance; vaccine development

Abbreviations: NIV: Nipah Virus; RT-PCR: Reverse Transcription Polymerase Chain Reaction; NGS: Next-Generation Sequencing; WHO: World Health Organization

Introduction

Nipah virus is a highly pathogenic zoonotic virus that has attracted sustained attention because of its ability to cross the animal–human barrier and cause severe disease. The virus was first recognized during an outbreak of encephalitis and respiratory illness among pig farmers and other exposed individuals in Malaysia and Singapore in 1998–1999. Since then, recurrent outbreaks have been reported in parts of South and Southeast Asia. Recent outbreaks have reinforced the need for continued surveillance and preparedness rather

than treating Nipah virus as an isolated historical threat.

Nipah virus is an enveloped, negative-sense single-stranded RNA virus belonging to the family Paramyxoviridae. Its natural ecology is closely associated with fruit bats, particularly *Pteropus* species. The movement of viruses between wildlife, domestic animals, and humans demonstrates the importance of understanding infectious diseases within their broader ecological setting.

Nipah virus is particularly concerning because human infection can result in severe encephalitis and respiratory disease, while person-to-person transmission can occur during some outbreaks. The combination of zoonotic spillover, severe clinical outcomes, and limited medical

countermeasures makes NiV an important pathogen for pandemic preparedness. Recent reviews continue to identify substantial gaps in diagnostics, therapeutics, vaccines, and surveillance.

Animal Reservoirs and Zoonotic Transmission

Fruit bats of the genus *Pteropus* are considered important natural reservoirs of Nipah virus. These bats can carry the virus without developing the severe disease observed in humans. Viral material may be shed through body fluids, creating opportunities for transmission when bats interact with domestic animals, food sources, or human environments.

The original Malaysian outbreak demonstrated an important role for pigs as an amplifying host. In contrast, outbreaks in Bangladesh and India have involved different transmission patterns, including exposure to food products contaminated by infected bats and subsequent human-to-human transmission. These differences highlight the importance of local ecological and behavioral factors in determining how Nipah virus reaches human populations.

Environmental changes may further influence spillover opportunities. Agricultural expansion, habitat disturbance, changes in food availability, and increasing interactions between wildlife, livestock, and human populations can alter the conditions under which viruses circulate. However, the relationship between environmental change and spillover is complex and requires further investigation.

Human-to-human transmission is an important feature of Nipah virus epidemiology. Close contact with infected patients, particularly within households and healthcare environments, can create secondary transmission. Consequently, early identification, isolation, contact tracing, and appropriate infection-prevention measures are essential components of outbreak control.

Pathogenesis and Human Disease

Nipah virus infection can affect multiple organ systems, with particularly important involvement of the respiratory tract, vascular endothelium, and central nervous system. Viral attachment and entry are mediated by the viral attachment and fusion glycoproteins, allowing infection of susceptible cells. Subsequent viral replication and host responses contribute to tissue injury and disease progression.

The clinical presentation is variable. Early symptoms may include fever, headache, weakness, vomiting, cough, and other nonspecific manifestations. In severe cases, infection may progress to respiratory distress and encephalitis.

Neurological involvement can result in altered consciousness, seizures, coma, and death.

The central nervous system is an important target during severe infection. Damage to the nervous system is believed to involve a combination of viral replication, vascular dysfunction, inflammatory responses, and tissue injury. Survivors of severe disease may experience persistent neurological problems, emphasizing that the impact of Nipah virus extends beyond the acute phase of infection.

The severity of disease is also influenced by host factors and the interaction between viral replication and immune responses. Understanding these interactions may provide opportunities to identify biomarkers associated with disease progression and develop targeted therapies.

Immune Response to Nipah Virus

The immune response to Nipah virus is an important area of current research. Innate immune mechanisms provide the first line of defense following infection, while adaptive immunity contributes to viral clearance and longer-term protection. However, Nipah virus possesses mechanisms that interfere with antiviral immune signaling, allowing it to replicate efficiently within susceptible hosts.

Antibodies directed against viral surface glycoproteins are particularly important because they can interfere with viral attachment and membrane fusion. The viral G and F glycoproteins have therefore become major targets for vaccine and monoclonal antibody research.

Recent immunological research has examined innate immune responses, T-cell activity, B-cell responses, cytokine signaling, and mechanisms of immune evasion. Better understanding of these processes may help explain differences in disease severity and support the development of more effective medical countermeasures.

Diagnosis and Genomic Surveillance

Rapid diagnosis is essential because early recognition allows appropriate clinical management and infection-control measures to be implemented. Molecular detection using reverse-transcription polymerase chain reaction (RT-PCR) is an important approach for confirming acute infection, while serological methods can provide evidence of previous or recent infection.

However, Nipah virus diagnosis remains challenging in areas without specialized laboratory facilities. Strengthening diagnostic networks in regions at risk of Nipah virus emergence should therefore remain a priority.

Genomic surveillance can provide additional information during outbreaks. Viral genome sequencing can help investigators understand transmission patterns, identify genetic relationships between cases, and monitor viral evolution. When genomic information is combined with epidemiological and clinical data, it can provide a more complete picture of how an outbreak develops.

Surveillance should also extend beyond human populations. Monitoring wildlife reservoirs, domestic animals, and environmental conditions can help identify changes in viral circulation and improve early-warning systems. This integrated approach is consistent with the One Health framework.

Prevention and One Health

Because Nipah virus is maintained within an animal-environment system, prevention cannot depend exclusively on human healthcare interventions. A One Health strategy brings together human health, veterinary medicine, wildlife surveillance, environmental science, and public health.

At the community level, reducing exposure to potentially contaminated food and infected animals may lower spillover risk. In healthcare settings, early recognition of suspected infection, appropriate personal protective equipment, isolation, and contact tracing are important for limiting person-to-person transmission.

Community engagement should be a central component of prevention programs. Public health recommendations are more likely to succeed when they are practical, culturally appropriate, and developed with affected communities.

A particularly important priority is maintaining surveillance between outbreaks. If surveillance capacity is established only after human cases appear, opportunities for early intervention may already have been lost. Continuous monitoring of high-risk areas can provide a stronger foundation for outbreak preparedness.

Vaccines and Therapeutic Development

The absence of widely licensed human vaccines or specific antiviral therapies remains a major limitation in Nipah virus preparedness. Current clinical management is primarily supportive, making prevention and early outbreak control particularly important.

Several vaccine strategies are under investigation, including approaches targeting the viral attachment and fusion glycoproteins. These proteins are attractive targets because they are exposed on the viral surface and play

essential roles in viral entry.

Monoclonal antibody research has produced encouraging experimental findings. In a 2024 study, an antibody targeting the Nipah virus fusion glycoprotein provided complete protection against disease in a hamster model, supporting continued investigation of antibody-based approaches.

Other antiviral candidates and vaccine platforms are also being investigated. However, clinical development remains challenging because Nipah outbreaks are relatively sporadic, making conventional large-scale efficacy trials difficult. Sustained research networks, appropriate animal models, coordinated preparedness studies, and international collaboration will therefore be important for advancing promising candidates.

Future Perspectives

Future Nipah virus preparedness should focus on connecting surveillance, research, and public health response. Genomic sequencing should increasingly be incorporated into outbreak investigations, while wildlife and animal surveillance should complement human disease monitoring.

Another important priority is maintaining research capacity during periods without major outbreaks. Laboratories, trained personnel, diagnostic systems, and research networks require long-term support. Waiting for an outbreak before rebuilding these capabilities is likely to delay response.

Greater attention should also be given to the interface between environmental change and zoonotic disease emergence. Understanding how changes in land use, agriculture, wildlife habitats, and human behavior influence spillover could improve risk assessment and guide targeted prevention.

The development of vaccines and therapeutic antibodies remains equally important. Future interventions should ideally be safe, effective, rapidly deployable, scalable, and accessible to populations living in areas where Nipah virus outbreaks occur.

Conclusion

Nipah virus infection represents a continuing challenge in zoonotic and emerging infectious disease research. Its association with animal reservoirs, ability to cross species barriers, potential for human-to-human transmission, and capacity to cause severe neurological disease make it an important pathogen for global health preparedness.

Considerable progress has been made in understanding Nipah virus biology, pathogenesis, immune responses, diagnostics, and potential medical countermeasures. Nevertheless, the absence of widely licensed human vaccines and specific treatments highlights the need for continued research.

A sustained One Health approach that integrates wildlife surveillance, veterinary medicine, human healthcare, genomic technologies, community engagement, and international collaboration offers the strongest pathway toward reducing Nipah virus risk. Preparing before the next outbreak, rather than responding only after human transmission has begun, should remain the central objective of future Nipah virus research and public health planning.

References

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