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Nipah Virus: A Re-Emerging Public Health Threat in South and Southeast Asia: A Mini review

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Abstract

Nipah virus (Niv), a zoonotic paramyxovirus of the Henipaviral genus, continues to pose recurrent epidemic threats across South and Southeast Asia. Initially recognized in Malaysia (1998–99) and later established as endemic in Bangladesh and India, its high case-fatality rate (40–90%) and absence of licensed therapeutics make it a pathogen of pandemic concern. Recent outbreaks in Kerala during 2018, 2021, and 2023 reaffirm the need for an integrated One Health approach, cross-border surveillance, and accelerated therapeutic research.

Keywords: Nipah Virus; Emerging Infections; Re-Emerging Infections

1. Introduction

Nipah virus (NiV), a member of the Henipavirus genus within the Paramyxoviridae family, is one of the most virulent emerging zoonotic pathogens known to cause recurrent outbreaks of encephalitis and respiratory illness in humans. First identified during the 1998–1999 outbreak among pig farmers in Malaysia and Singapore, NiV rapidly established an endemic presence in South and Southeast Asia, exhibiting case-fatality rates of 40–90% [1, 2, 7]. Fruit bats (Pteropus spp.) are recognized as the primary natural reservoir, with transmission to humans occurring either directly or through intermediate hosts such as pigs, and subsequently through human-to-human spread in community and hospital settings [1, 2, 6].

Following its emergence in Malaysia, NiV reappeared in Bangladesh and India, where distinct transmission dynamics were observed. In Bangladesh, recurrent outbreaks have been linked to consumption of date palm sap contaminated with bat excreta and to secondary person-to-person spread [2, 6, 8]. India reported its first outbreak in Siliguri, West Bengal (2001), followed by major clusters in Kerala in 2018, 2021, and 2023 [10, 15, 16, 20]. The most recent Kerala events coincided with the COVID-19 pandemic, underscoring the strain on healthcare systems and the need for integrated surveillance and rapid response [13–16, 20].

Environmental and anthropogenic changes—including deforestation, agricultural intensification, and climatic variation—have increased human exposure to NiV-infected wildlife [9, 12, 13]. The virus causes severe febrile encephalitis often accompanied by respiratory distress, reflecting multi-organ vasculitis and neuronal involvement [4, 6, 11]. Despite advances in diagnostics, no licensed vaccine or antiviral therapy currently exists, placing NiV on the WHO RandD Blueprint list of priority pathogens for pandemic preparedness [7, 16, 17, 21].

The repeated re-emergence of NiV in South Asia emphasizes the need to understand its ecology, transmission mechanisms, and clinical features through a One Health lens. Interdisciplinary approaches integrating human, animal,

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and environmental health perspectives are essential to mitigate future outbreaks and strengthen regional and global health security [10, 13, 15, 16].

2. Review Methodology

This narrative review synthesized peer-reviewed and authoritative literature published between 2004 and 2025 to summarize the epidemiology, pathogenesis, diagnostics, and control measures of Nipah virus. Searches were conducted using PubMed, Scopus, and Google Scholar databases with the keywords “Nipah virus,” “Henipavirus,” “zoonotic transmission,” “Kerala,” “Bangladesh,” and “One Health.”

2.1. Inclusion criteria comprised

- Original research articles, short communications, and reviews published in English;
- Studies describing Nipah virus epidemiology, diagnostics, or outbreaks in South and Southeast Asia;
- Official reports or updates from the World Health Organization and national health agencies.
- Exclusion criteria included: preprints without peer review, articles without clear methodological details, non-English papers lacking translations, and studies unrelated to NiV transmission or control.

After screening, 21 key publications [1–21] were selected to represent the evolution of NiV research over two decades—from the first outbreak investigations [1, 2, 6], through animal model studies [3, 4, 11], to recent analyses on outbreak responses in Kerala and Bangladesh [15, 16, 20]. Foundational comprehensive reviews [7, 10, 13, 17] and recent advances in diagnostics [19] and computational modeling [18] were incorporated. WHO surveillance updates [16] were included for contextual interpretation of the 2023 Kerala outbreak.

Given the heterogeneity of available data, a narrative synthesis approach was adopted instead of quantitative meta-analysis. Findings were categorized thematically into four domains—epidemiology and transmission, pathogenesis and diagnostics, therapeutics and vaccine development, and One Health-based public-health strategies—allowing for concise, integrative interpretation of cross-disciplinary evidence

2.2. Re-Emergence and Outbreak Trends

Niv transmission cycles involve Pteropus fruit bats as reservoirs, with human infection occurring through consumption of contaminated date-palm sap, close contact with infected animals, or person-to-person spread [6, 8]. Since 2001, Bangladesh has reported near-annual outbreaks, and neighboring India has experienced multiple clusters in West Bengal and Kerala [2, 4, 16]. The 2023 Kerala outbreak, concurrent with the COVID-19 pandemic, underscored challenges of dual surveillance and the value of early isolation and contact tracing [16, 17].

Spatial modelling indicates large ecological niches for bat-borne NiV persistence throughout South and Southeast Asia [7]. Climate change, land-use alterations, and human encroachment increase contact between bats, domestic animals, and humans [13, 15].

2.3. Clinical and Pathobiological Insights

NiV infection typically manifests as acute febrile encephalitis with rapid progression to coma; respiratory involvement is frequent in Bangladesh strains [10, 11]. Histopathology demonstrates vasculitis and syncytial endothelial damage in multiple organs [11]. Experimental ferret models confirm that antivirals such as chloroquine fail to prevent disease [12], whereas remdesivir and monoclonal antibodies (m102.4, h5B3.1) show promise in pre-clinical trials [21, 14].

2.4. Diagnostics and Surveillance Advances

Early and accurate diagnosis of Nipah virus (NiV) infection remains essential for outbreak containment, clinical management, and timely risk communication. Over the past two decades, diagnostic approaches have evolved from basic serological tests to high-precision molecular platforms capable of detecting minute viral loads in both human and animal samples.

2.5. Molecular diagnostics

Real-time reverse transcription PCR (RT-PCR) continues to be the gold standard for NiV detection in acute infections, targeting genes such as N, F, and G. Advances in droplet digital PCR (ddPCR) have enhanced analytical sensitivity by allowing absolute quantification of viral RNA without reliance on standard curves [19]. This is particularly valuable for ssessing viral kinetics in longitudinal samples, evaluating antiviral efficacy, and ensuring biosafety in research settings.

Multiplex PCR assays combining NiV with other paramyxoviruses have been developed for syndromic respiratory surveillance in endemic regions, enabling early differential diagnosis.

2.6. Serological assays

ELISA-based IgM and IgG detection continues to play a pivotal role in retrospective diagnosis and serosurveillance among at-risk populations. Recombinant NiV glycoprotein-based assays now provide improved specificity over earlier whole-virus antigen systems, reducing cross-reactivity with Hendra and other paramyxoviruses. Neutralization assays, including pseudotype-based systems using vesicular stomatitis virus (VSV) vectors expressing NiV glycoproteins, allow serological testing outside BSL-4 laboratories, expanding diagnostic capacity in low-resource settings [7, 16].

2.7. Point-of-care and field diagnostics

Portable isothermal amplification assays such as loop-mediated amplification (LAMP) and recombinase polymerase amplification (RPA) are emerging as valuable tools for field detection, particularly in rural outbreak sites. These techniques, coupled with lateral-flow readouts, provide results in under an hour and have been integrated into mobile biosurveillance units in Bangladesh and India. The development of CRISPR-Cas-based platforms for NiV RNA detection offers another promising frontier for decentralized testing and rapid triage during outbreaks.

2.8. Genomic surveillance

Next-generation sequencing (NGS) has become indispensable in tracing transmission chains and characterizing viral evolution. Full-genome sequencing of NiV isolates from Bangladesh, Malaysia, and India has revealed two major clades (NiV-Malaysia and NiV-Bangladesh), each associated with distinct pathogenic and epidemiological profiles [6, 10]. Phylogenetic analyses of Kerala's recent clusters confirmed continued circulation of the Bangladesh lineage, supporting evidence of recurrent local spillovers rather than new introductions [15, 16].

2.9. Integrated One-Health surveillance

Modern surveillance frameworks now integrate animal, environmental, and human health data. Wildlife surveillance has detected NiV antibodies and RNA fragments in Pteropus medius populations across India, Bangladesh, and Myanmar, demonstrating broad viral circulation even outside outbreak periods [7, 9, 12]. Combined use of geospatial information systems (GIS), ecological niche modeling, and machine learning enables predictive mapping of spillover risk zones [18]. For example, Deka and Morshed's risk mapping of South and Southeast Asia identified "high-risk corridors" overlapping with deforestation and pig-farming regions, guiding resource allocation for sentinel surveillance.

2.10. Laboratory network strengthening

In India, the ICMR-VRDL (Viral Research and Diagnostic Laboratories) network has been pivotal in rapid detection and confirmation of NiV cases in Kerala, reducing turnaround time from days to hours. Coupled with WHO's Global Outbreak Alert and Response Network (GOARN) and regional BSL-3/BSL-4 hubs, these facilities form the backbone of NiV preparedness in the South-East Asia Region [16].

Together, these diagnostic and surveillance advances underscore a paradigm shift from reactive to predictive outbreak response. The combination of high-sensitivity molecular assays, computational forecasting, and real-time data sharing through One-Health platforms is redefining how Nipah virus threats are identified and managed across endemic regions.

3. Public Health Response and One-Health Imperatives

The recurrent emergence of Nipah virus (NiV) outbreaks in South and Southeast Asia has demonstrated that controlling zoonotic threats requires a One Health framework — integrating human, animal, and environmental health sectors. Public health responses to NiV have progressively evolved from reactive containment to structured, multisectoral preparedness.

3.1. Early detection and outbreak containment

Timely diagnosis and swift containment have proven decisive in mitigating outbreak impact. Kerala's 2018 and 2023 outbreaks exemplify how an established emergency operations protocol, trained health personnel, and the ICMR-VRDL network facilitated rapid case confirmation and isolation within hours of detection [15, 16, 20]. Health authorities implemented extensive contact tracing, active syndromic surveillance, and ring containment to prevent further transmission. The Kerala model highlighted the value of local community engagement, hospital infection control, and

real-time coordination between district administration, the National Centre for Disease Control (NCDC), and WHO country offices.

3.2. Infection prevention and control (IPC)

Nosocomial transmission is a major amplifying factor in NiV outbreaks. Implementation of strict IPC measures—including personal protective equipment (PPE), triage-based isolation wards, and disinfection protocols—was critical in preventing hospital-based clusters in recent outbreaks [15, 16]. Simulation-based IPC training and standard operating procedures (SOPs) for handling encephalitis cases were institutionalized after the 2018 Kerala outbreak. The establishment of dedicated viral testing laboratories under the VRDL scheme and district rapid response teams (RRTs) has improved the readiness of tertiary hospitals to manage high-risk cases.

3.3. Community engagement and risk communication

Public trust and behaviour modification play pivotal roles in interrupting transmission. In Bangladesh, culturally tailored health education discouraged consumption of raw date-palm sap — a major route of spillover — by promoting sap covers and community reporting of sick bats or animals [2, 6]. During the Kerala outbreaks, community outreach through social media and local governance bodies effectively countered misinformation, reduced stigma, and improved compliance with quarantine and testing protocols [15, 20]. These experiences underscore the value of risk communication strategies that are rapid, transparent, and linguistically inclusive.

3.4. Veterinary and wildlife surveillance

Given the zoonotic origin of NiV, sustained animal surveillance is essential. Wildlife monitoring programs in India and Bangladesh have demonstrated widespread NiV antibody presence in Pteropus medius populations [7, 9, 12]. Collaboration between the National Institute of Virology (NIV), ICMR, and the Department of Animal Husbandry has enhanced sample collection and genomic characterization from bats and pigs, allowing identification of potential spillover sites before human infection occurs. These programs reflect the practical application of One Health principles—bridging veterinary, environmental, and human surveillance domains.

3.5. Cross-sectoral coordination and policy frameworks

WHO, FAO, and OIE jointly advocate for a unified One Health Joint Plan of Action (2022–2026) to combat zoonotic threats including NiV. National-level initiatives in India and Bangladesh now incorporate NiV surveillance under Integrated Disease Surveillance Programme (IDSP) and Epidemic Intelligence Service frameworks. These systems enable synchronized data reporting, outbreak alerts, and capacity building.[16].

3.6. Research, innovation, and capacity strengthening

Recent outbreaks have catalyzed translational research in diagnostic and vaccine development, largely through collaborations between ICMR, CEPI, and international partners [17]. Laboratory readiness initiatives, such as upgrading selected BSL-3 labs for NiV testing, have broadened regional diagnostic coverage. Cross-institutional studies now combine ecological data, bat migration patterns, and human infection maps to anticipate potential spillover zones [9, 18]. Incorporating climate and land-use modelling into national preparedness frameworks can enhance predictive surveillance and resource allocation in high-risk districts.

3.7. One Health integration and sustainability

The One Health paradigm emphasizes that human health security depends on ecosystem balance and intersectoral collaboration. For NiV, this means synchronizing environmental monitoring (such as bat roost tracking and fruiting cycle data) with human health surveillance. Kerala's collaboration between the Departments of Forest, Health, and Veterinary Sciences demonstrates how such an integrated approach improves early warning and response efficiency. Embedding One Health in academic curricula, laboratory training, and policy planning can institutionalize sustainable zoonotic preparedness.

4. Therapeutics and Vaccine Pipeline

A 2024 systematic review identified only a few candidates—monoclonal antibodies, remdesivir analogues, and viral-vector vaccines—progressing toward clinical evaluation [14]. Recent mRNA and ChAdOx1-based platforms provide protective immunity in non-human primates [5]. However, global investment remains limited compared with other emerging viruses. Adaptive trial frameworks and compassionate-use protocols, as successfully implemented during Kerala's outbreaks, should be formalized for future responses.

5. Conclusion

Nipah virus (NiV) epitomizes the complex interface between humans, animals, and the environment that defines emerging zoonotic threats in the twenty-first century. Despite being recognized more than two decades ago, it continues to cause sporadic but severe outbreaks across South and Southeast Asia, with high fatality rates and no licensed vaccine or antiviral therapy. Advances in diagnostics — including droplet digital PCR, genomic sequencing, and field-deployable molecular assays — have greatly improved early detection and outbreak management. However, these gains must be complemented by equally strong surveillance networks, biosafety infrastructure, and community-based prevention systems.

The experiences of Bangladesh and Kerala demonstrate that successful containment relies on rapid laboratory confirmation, rigorous infection control, and transparent public engagement. The integration of wildlife and veterinary surveillance within human health systems has proven indispensable in tracing viral origins and predicting future spillover events. As ecological changes, urban expansion, and climate shifts increase the frequency of human–animal contact, the importance of sustained One Health coordination becomes even more apparent.

Moving forward, investment in translational research — from vaccine development to computational outbreak modelling — should remain a global priority. Strengthening cross-border data sharing, maintaining regional BSL-3/BSL-4 laboratory networks, and promoting local capacity building will ensure that responses are proactive rather than reactive. Nipah virus will likely persist as a sentinel example of how human health security is inseparable from ecological stability and intersectoral collaboration. A resilient, science-driven One Health strategy offers the most promising path toward preventing the next NiV outbreak — and, by extension, the next pandemic.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

References

[1] Hsu, V. P., Hossain, M. J., Parashar, U. D., Ali, M. M., Ksiazek, T. G., Kuzmin, I., Niezgoda, M., Rupprecht, C., Bresee, J., and Breiman, R. F. (2004). Nipah virus encephalitis reemergence, Bangladesh. Emerging infectious diseases, 10(12), 2082–2087. https://doi.org/10.3201/eid1012.040701

[2] Luby, S. P., Rahman, M., Hossain, M. J., Blum, L. S., Husain, M. M., Gurley, E., Khan, R., Ahmed, B. N., Rahman, S., Nahar, N., Kenah, E., Comer, J. A., and Ksiazek, T. G. (2006). Foodborne transmission of Nipah virus, Bangladesh. Emerging infectious diseases, 12(12), 1888–1894. https://doi.org/10.3201/eid1212.060732

[3] Pallister, J., Middleton, D., Crameri, G., Yamada, M., Klein, R., Hancock, T. J., Foord, A., Shiell, B., Michalski, W., Broder, C. C., and Wang, L. F. (2009). Chloroquine administration does not prevent Nipah virus infection and disease in ferrets. Journal of virology, 83(22), 11979–11982. https://doi.org/10.1128/JVI.01847-09

[4] Williamson, M. M., and Torres-Velez, F. J. (2010). Henipavirus: a review of laboratory animal pathology. Veterinary pathology, 47(5), 871–880. https://doi.org/10.1177/0300985810378648

[5] Carter, G. P., Douce, G. R., Govind, R., Howarth, P. M., Mackin, K. E., Spencer, J., Buckley, A. M., Antunes, A., Kotsanas, D., Jenkin, G. A., Dupuy, B., Rood, J. I., and Lyras, D. (2011). The anti-sigma factor TcdC modulates hypervirulence in an epidemic BI/NAP1/027 clinical isolate of Clostridium difficile. PLoS pathogens, 7(10), e1002317. https://doi.org/10.1371/journal.ppat.1002317

[6] Lo, M. K., Lowe, L., Hummel, K. B., Sazzad, H. M., Gurley, E. S., Hossain, M. J., Luby, S. P., Miller, D. M., Comer, J. A., Rollin, P. E., Bellini, W. J., and Rota, P. A. (2012). Characterization of Nipah virus from outbreaks in Bangladesh, 2008-2010. Emerging infectious diseases, 18(2), 248–255. https://doi.org/10.3201/eid1802.111492

[7] Singh, R. K., Dhama, K., Chakraborty, S., Tiwari, R., Natesan, S., Khandia, R., Munjal, A., Vora, K. S., Latheef, S. K., Karthik, K., Singh Malik, Y., Singh, R., Chaicumpa, W., and Mourya, D. T. (2019). Nipah virus: epidemiology, pathology, immunobiology and advances in diagnosis, vaccine designing and control strategies - a comprehensive review. The veterinary quarterly, 39(1), 26–55. https://doi.org/10.1080/01652176.2019.1580827

[8] Banerjee, S., Gupta, N., Kodan, P., Mittal, A., Ray, Y., Nischal, N., Soneja, M., Biswas, A., and Wig, N. (2019). Nipah virus disease: A rare and intractable disease. Intractable and rare diseases research, 8(1), 1–8. https://doi.org/10.5582/irdr.2018.01130

[9] Deka, M. A., and Morshed, N. (2018). Mapping Disease Transmission Risk of Nipah Virus in South and Southeast Asia. Tropical medicine and infectious disease, 3(2), 57. https://doi.org/10.3390/tropicalmed3020057

[10] Chattu, V. K., Kumar, R., Kumary, S., Kajal, F., and David, J. K. (2018). Nipah virus epidemic in southern India and emphasizing "One Health" approach to ensure global health security. Journal of family medicine and primary care, 7(2), 275–283. https://doi.org/10.4103/jfmpc.jfmpc_137_18

[11] Cui, Z., Li, J., Meng, L., and Zhang, Z. (2024). Nipah virus: a re-emerging public health concern. The Lancet. Microbe, 5(3), e212. https://doi.org/10.1016/S2666-5247(23)00361-0

[12] Markotter, W., Coertse, J., De Vries, L., Geldenhuys, M., and Mortlock, M. (2020). Bat-borne viruses in Africa: a critical review. Journal of zoology (London, England : 1987), 311(2), 77–98. https://doi.org/10.1111/jzo.12769

[13] Kaliappan, A., Kaliappan, V., Lakshmi, J. T., Raja, S., Nikhat, S. S., Vidya, M. S., Saranya, M., Sagar, T., and Chenna, K. D. (2022). Nipah amidst Covid-19 Pandemic, another Re-Emerging Infectious Disease of Pandemic Potential - a Narrative Review. Maedica, 17(2), 464–470. https://doi.org/10.26574/maedica.2022.17.2.464

[14] Alam A. M. (2022). Nipah virus, an emerging zoonotic disease causing fatal encephalitis. Clinical medicine (London, England), 22(4), 348–352. https://doi.org/10.7861/clinmed.2022-0166

[15] Yadav, P. D., Sahay, R. R., Balakrishnan, A., Mohandas, S., Radhakrishnan, C., Gokhale, M. D., Balasubramanian, R., Abraham, P., Gupta, N., Sugunan, A. P., Khobragade, R., George, K., Shete, A., Patil, S., Thankappan, U. P., Dighe, H., Koshy, J., Vijay, V., Gayathri, R., Kumar, P. J., … Keerthi, K. V. (2022). Nipah Virus Outbreak in Kerala State, India Amidst of COVID-19 Pandemic. Frontiers in public health, 10, 818545. https://doi.org/10.3389/fpubh.2022.818545

[16] World Health Organization. Outbreak of Nipah virus encephalitis in Kerala State, India. WHO 2024 (Accessed 20 Oct 2024).

[17] Chan, X. H. S., Haeusler, I. L., Choy, B. J. K., Hassan, M. Z., Takata, J., Hurst, T. P., Jones, L. M., Loganathan, S., Harriss, E., Dunning, J., Tarning, J., Carroll, M. W., Horby, P. W., and Olliaro, P. L. (2025). Therapeutics for Nipah virus disease: a systematic review to support prioritisation of drug candidates for clinical trials. The Lancet. Microbe, 6(5), 101002. https://doi.org/10.1016/j.lanmic.2024.101002

[18] Yu F, Younas Khan M, Bilal Riaz M, Ullah S, Farooq M (2025) Assessing the global dynamics of Nipah infection under vaccination and treatment: A novel computational modeling approach. PLoS ONE 20(1): e0309360. https://doi.org/10.1371/journal.pone.0309360

[19] Shuai, J., Chen, K., Han, X., Zeng, R., Song, H., Fu, L., and Zhang, X. (2024). Development and validation of a droplet digital PCR assay for Nipah virus quantitation. BMC veterinary research, 20(1), 440. https://doi.org/10.1186/s12917-024-04245-y

[20] Lateef S. (2025) Nipah virus outbreak in Kerala, India. Lancet Infect Dis ; 25(10): e548.

[21] de Wit, E., Williamson, B. N., Feldmann, F., Goldin, K., Lo, M. K., Okumura, A., Lovaglio, J., Bunyan, E., Porter, D. P., Cihlar, T., Saturday, G., Spiropoulou, C. F., and Feldmann, H. (2023). Late remdesivir treatment initiation partially protects African green monkeys from lethal Nipah virus infection. Antiviral research, 216, 105658. https://doi.org/10.1016/j.antiviral.2023.105658