Nipah Virus Outbreaks in India: Epidemiological Insights, Response Measures, and the One Health Perspective

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ABSTRACT

Background:

Nipah virus (NiV) remains a major zoonotic threat due to its high mortality and potential for rapid spread. Since its first detection in India in 2001, outbreaks have recurred intermittently, with Kerala emerging as a hotspot in recent years. Understanding the interplay between viral reservoirs, clinical outcomes, and public health responses is critical for strengthening preparedness and limiting future transmission.

Methodology:

This study adopted a descriptive, multi-source approach, integrating outbreak reports, clinical investigations, sero-epidemiological surveys, and wildlife reservoir assessments from Kerala between 2018 and 2023. Data were analysed to capture human case characteristics, surveillance outcomes, and bat sampling findings. Laboratory methods included qRT-PCR, ELISA, and genome sequencing, while epidemiological patterns were evaluated using descriptive statistics and comparative analysis across multiple outbreak years.

Results:

Investigations confirmed the persistence of NiV in Pteropus medius bats, with viral RNA and antibodies detected, alongside evidence of distinct viral lineages. Human case data revealed variability in outbreak severity: the 2018 Kozhikode event showed high fatality and nosocomial spread, while subsequent incidents in 2019 and 2021 were rapidly contained with minimal transmission. Public health interventions, including on-site diagnostics, strict contact tracing, and infection control, proved effective in reducing secondary spread. Sero-surveys among contacts indicated no subclinical infections during the 2019 outbreak, highlighting the impact of timely intervention.

Conclusion:

Findings underscore both progress and persisting vulnerabilities in NiV management. Strengthened laboratory capacity, rapid detection, and coordinated responses have contributed to reduced morbidity and mortality in

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recent outbreaks. However, the continued circulation of NiV within bat populations presents an ongoing risk. Sustained surveillance, proactive wildlife monitoring, and community-level prevention strategies remain essential for mitigating future spillovers and supporting global health security

Keywords: Nipah Virus, Real-time reverse transcriptase polymerase chain reaction, ELISA, Reservoirs

INTRODUCTION

Nipah virus (NiV) is an emerging zoonotic pathogen of considerable public health concern, recognized for its ability to cause severe disease in humans with a high case fatality rate. First identified during outbreaks among pig farmers in Malaysia and Singapore in 1998–1999, NiV belongs to the genus *Henipavirus* within the family *Paramyxoviridae(Hauser et al., 2021)*. Since its discovery, the virus has been associated with sporadic but often deadly outbreaks across South and Southeast Asia, notably in Bangladesh and India. Transmission pathways include direct contact with infected animals, most commonly fruit bats of the genus *Pteropus*, as well as human-to-human spread through close contact or exposure to bodily fluids. Clinical manifestations range from mild, self-limiting symptoms to acute respiratory distress (ARDS) and fatal encephalitis, often with rapid deterioration(Luby et al., 2012).

In India, NiV has demonstrated a recurrent yet geographically constrained pattern of emergence. Early outbreaks in West Bengal in 2001 and 2007 were followed by a long period of apparent absence until the virus reappeared in Kerala in 2018(Thomas et al., 2019). That event was marked by a high mortality rate and significant nosocomial transmission, drawing attention to gaps in preparedness, infection control, and surveillance capacity. Subsequent, smaller outbreaks in 2019, 2021, and 2023 underscored the continuing risk of NiV re-emergence in the state, despite intensified public health vigilance. The repeated involvement of *Pteropus* bats as reservoirs and the close ecological interface between bat populations and human settlements in Kerala suggest a persistent potential for spillover events(Hauser et al., 2021).

Kerala's experience with NiV has also highlighted the critical role of rapid detection, coordinated response, and rigorous contact tracing in limiting transmission. The establishment of on-site diagnostic facilities, deployment of molecular and serological assays, and implementation of strict infection prevention measures have been instrumental in reducing the scale of later outbreaks. Nevertheless, these responses have been largely reactive, triggered by the recognition of clinical cases rather than proactive identification of viral circulation in animal hosts or early-stage human infections.

The public health challenge posed by NiV lies not only in its high lethality but also in the unpredictable nature of its emergence. Environmental factors, changing land-use patterns, and increasing human encroachment into bat habitats may alter spillover dynamics, complicating prediction and prevention efforts. Current understanding of NiV ecology in India remains incomplete, with limited longitudinal data on viral prevalence in bat populations, the frequency of asymptomatic infections in humans, and the effectiveness of different containment strategies across varying epidemiological contexts(Sanker et al., 2024a).

This study addresses these gaps by synthesizing multi-source evidence from recent NiV outbreaks in Kerala, integrating findings from human case investigations, sero-epidemiological surveys, and wildlife reservoir assessments. By comparing patterns across multiple outbreak years and examining the role of enhanced surveillance and laboratory readiness, the research aims to identify factors that have contributed to both containment successes and ongoing vulnerabilities.

The significance of this work extends beyond regional public health, as NiV is listed by the World Health Organization among priority pathogens for research and development due to its epidemic potential and absence of licensed vaccines or specific antiviral therapies(Madhukalya et al., 2025). Understanding how local epidemiology, reservoir ecology, and response capacity interact to shape outbreak outcomes in Kerala can inform not only state and national preparedness but also global strategies for managing high-consequence zoonotic threats. Through this comprehensive analysis, the study seeks to provide evidence-based recommendations to strengthen early detection, optimize containment, and reduce the human toll of future NiV events.

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Objectives

i. Identify the presence of Nipah virus in bat populations within outbreak-prone regions of Kerala by detecting viral RNA, evaluating antibody prevalence, and analysing genomic profiles of circulating strains.
ii. Characterize the clinical presentation, epidemiological trends, and transmission dynamics of confirmed human Nipah virus cases reported during multiple outbreaks, including assessments of case fatality rates and disease severity.

METHODOLOGY

This research employed a descriptive, multi-source design, drawing upon data from confirmed Nipah virus (NiV) outbreaks in Kerala between 2018 and 2023. The study integrated findings from human case investigations, wildlife reservoir surveillance, and sero-epidemiological surveys of close contacts.

Human case data were obtained from outbreak reports, clinical studies, and public health records. Confirmed cases were identified through laboratory testing using real-time reverse transcriptase polymerase chain reaction (qRT-PCR) and enzyme-linked immunosorbent assay (ELISA) for NiV-specific IgM or IgG antibodies. Information collected included demographic characteristics, clinical presentation, laboratory findings, transmission routes, and outcomes.

Bat surveillance involved targeted sampling in locations linked to human cases. *Pteropus medius* and *Rousettus leschenaultii* bats were captured using mist nets set near roost sites or feeding areas. Biological specimens included throat and rectal swabs, serum, and, in selected cases, visceral organ tissues collected post-euthanasia under approved ethical protocols. Viral RNA detection was performed via qRT-PCR, while serological analysis for NiV antibodies employed ELISA techniques. Genomic sequencing of positive samples was conducted using next generation sequencing to characterize circulating viral strains.

Sero-prevalence surveys among human contacts focused on individuals with documented exposure to confirmed NiV cases, including healthcare workers, household members, and community contacts. Blood samples were collected under aseptic conditions, and sera were tested for NiV-specific IgM and IgG antibodies. Exposure histories were recorded to classify participants into high- and low-risk categories.

Data from all sources were collected and analysed to identify patterns in viral occurrence, transmission, and clinical outcomes. Descriptive statistics summarized demographic, clinical, and laboratory findings, while comparative analysis examined trends across different outbreak years. This integrative approach allowed for a comprehensive assessment of NiV epidemiology and public health responses within the Kerala context.

EPIDEMIOLOGY

The 2018 Nipah virus outbreak in Kozhikode, Kerala, brought the pathogen back into India's public health spotlight. Investigations confirmed Pteropus fruit bats as the source and documented clear human-to-human transmission, with 16 fatalities among 18 reported cases. This event emphasized the value of a One Health approach, integrating human, animal, and environmental health strategies to counter zoonotic threats(Sadanadan et al., 2018a).

In June 2019, a case in Ernakulam, Kerala, prompted researchers to examine Pteropus bats from areas visited by the patient. Molecular diagnostics and genome sequencing were employed to detect NiV and explore its genetic diversity, thereby assessing the risk of novel viral variants in southern India.

In the 2019 outbreak, testing 66 close contacts of the index case for NiV antibodies. Their findings provided insight into the spectrum between symptomatic and subclinical infections and highlighted the effectiveness of containment measures and contact tracing(Ramachandran et al., 2022).

In Siliguri, West Bengal 2001 the outbreak involved 45 cases and 16 deaths, with strong evidence of

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nosocomial transmission, underscoring the urgent need for improved infection control in healthcare facilities(Chadha et al., 2006).

In the absence of vaccines or targeted therapies, countries must maintain robust healthcare systems ready to address emerging infectious diseases. An innovative, low-cost disease surveillance system trialed in North Arcot, Tamil Nadu, and adapted in Kerala's public health sector, showed promise. Between 1999 and 2001, 14 diseases were routinely tracked through daily postcard-based case reporting by trained healthcare workers, with monthly bulletins ensuring timely information sharing(T Jacob John et al., 2002).

WHO's core outbreak control strategies, when implemented promptly, have enabled many nations to limit NiV spread within their borders. India's containment of certain outbreaks, at times down to a single case, has been attributed to rigorous contact tracing and decisive public health action.

RESULT

Study Name	Sample Sources	Results
Detection of Nipah virus in *Pteropus medius* in the 2019 outbreak from Ernakulam (Sudeep et al., 2021)	141 throat/rectal swabs, 92 visceral organs, 52 serum samples from bats	NiV RNA in 1 swab & 3 organs; 20.68% IgG positive; new I-India genotype
Experiential learning from NiV outbreaks in Kerala (Sahay et al., 2020)	1 confirmed human case; 330 contacts traced; bat sampling	On-site diagnostics; 57 suspected cases negative; no secondary transmission
Clinical manifestations of NiV-infected patients, Kerala 2018 (Chandni et al., 2020a)	12 confirmed human patients	CFR 83.3%; encephalitis, ARDS, myocarditis; nosocomial spread; ribavirin trial inconclusive
Towards global health security NiV 2018 Kerala (Sadanadan et al., 2018b)	23 human cases; 52 bats tested	CFR 88.9%; 19.2% bats NiV-positive; rapid coordinated outbreak control
An impending public health threat, Kerala 2023 outbreak (Verma et al., 2024)	Human cases, environmental sampling	11 cases, 8 deaths; 43 containment zones; 950+ contacts traced; strict PPE/isolation
Sero-prevalence of NiV antibodies among close contacts, 2019 Ernakulam (Ramachandran et al., 2022)	49 close contacts (HCWs, family, friends)	No anti-NiV IgM/IgG detected; no subclinical infections
Communicable diseases monitored Kottayam (John et al., n.d.)	District-wide surveillance data (14 diseases)	Frequent reports: dysentery, leptospirosis, typhoid, hepatitis; early outbreak detection effective

*CFR-Case Fatality Ratio, ARDS-Acute Respiratory Distress

Investigations across multiple outbreaks and surveillance studies revealed distinct patterns in Nipah virus (NiV) occurrence, transmission, and host reservoir detection in Kerala and other affected regions of India.

Bat surveillance during the 2019 Ernakulam incident identified viral RNA in one rectal swab and three visceral organ samples from Pteropus medius. Serological testing showed that approximately one-fifth of sampled Pteropus bats (20.68%, 12 of 58) carried anti-NiV IgG antibodies. Genome sequencing of isolates from three bats produced fragments ranging from 15.1 to 18.17 kilobases, indicating circulation of a genetically distinct "I-India" lineage within South India(Sudeep et al., 2021).

In the same outbreak, rapid deployment of diagnostic capacity and strict contact tracing contributed to successful containment. Fifty-seven suspected human cases were tested locally by point-of-care assay, quantitative RT-PCR, and ELISA, all returning negative results apart from the single confirmed index case, who survived. Among the 330 individuals identified through contact tracing, 52 were classified as high-risk exposures, including healthcare workers, community members, and relatives. No secondary human infections were detected(Sadanadan et al., 2018a).

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Sero-epidemiological assessment of 49 close contacts of the 2019 index case found no detectable IgM or IgG antibodies, indicating the absence of asymptomatic or subclinical infections during that event. Most reported exposure was through direct physical contact (59.2%), with a smaller proportion involving contact with body fluids (22.4%)(Ramachandran et al., 2022).

Earlier outbreaks displayed markedly higher mortality. In the 2018 Kozhikode episode, 12 laboratory-confirmed patients treated in a tertiary emergency department experienced a case fatality ratio (CFR) of 83.3%. Clinical presentation was dominated by encephalitis (83%), bilateral pulmonary infiltrates, and, in some cases, myocarditis. Transmission was predominantly nosocomial, with nearly one-fifth of secondary cases occurring among healthcare workers. Experimental ribavirin administration did not produce statistically significant differences in outcomes(Chandni et al., 2020b).

Complementary epidemiological reports from the same outbreak period indicated a total of 23 cases and 21 deaths (CFR 88.9%) across Kozhikode and Mallapuram districts. Reservoir investigation demonstrated that 19.2% (10 of 52) of sampled Pteropus bats tested positive for NiV RNA, further supporting the role of fruit bats as a key source of infection(Sadanadan et al., 2018c).

The 2023 outbreak in Kerala comprised 11 confirmed cases, of which 8 were fatal. Public health authorities established 43 containment zones, identified over 950 contacts, and implemented strict infection prevention measures, including isolation of exposed healthcare workers and temporary closure of educational institutions(Verma et al., 2024).

Comparative review of Kerala's outbreak history shows substantial variation in scale and fatality. The 2018 event exhibited the highest CFR, while the 2019 and 2021 outbreaks each involved a single fatality and were contained rapidly. Enhanced surveillance, diagnostic readiness, and targeted containment appear to have contributed to these improved outcomes.

Although not specific to NiV, district-level communicable disease monitoring in Kerala has demonstrated that early detection systems are capable of intercepting outbreaks. Surveillance records highlight frequent reporting of leptospirosis, acute dysentery, typhoid fever, and acute hepatitis, with timely intervention curbing larger epidemics such as cholera.

Overall, the compiled evidence underscores a progressive strengthening of outbreak response capacity in Kerala, reflected in faster case detection, improved laboratory turnaround times, rigorous contact tracing, and integration of wildlife reservoir monitoring. These measures have coincided with reduced transmission and, in certain years, a marked decline in fatalities despite the continued presence of NiV in bat populations.

CONCLUSION

This study consolidates evidence from multiple Nipah virus outbreaks in Kerala, providing an integrated view of the virus's epidemiology, reservoir dynamics, clinical patterns, and the effectiveness of public health interventions. Findings from bat surveillance confirmed ongoing NiV circulation in *Pteropus medius* populations, with both viral RNA detection and measurable antibody prevalence, underscoring the role of these species as a persistent reservoir. Genomic analysis revealed the presence of distinct viral lineages, indicating evolutionary divergence within regional strains(Sahay et al., 2020).

Human case data from successive outbreaks demonstrated substantial variation in scale and severity. The 2018 Kozhikode event was marked by high mortality and extensive nosocomial transmission, while subsequent outbreaks in 2019 and 2021 were rapidly contained, each involving a single fatality(Sanker et al., 2024a, 2024b). These improvements coincided with the establishment of on-site diagnostic capacity, systematic contact tracing, and strengthened infection prevention measures. Serological surveys among close contacts revealed no subclinical infections during the 2019 Ernakulam outbreak, suggesting that timely intervention may have curtailed secondary spread.

The analysis highlights the cumulative benefits of enhanced surveillance, rapid laboratory confirmation, and coordinated response mechanisms in reducing morbidity and mortality. At the same time, the persistence of NiV in local bat populations indicates an ongoing risk of re-emergence. Achieving sustainable control will require not only maintaining current preparedness levels but also integrating proactive wildlife surveillance and community-level prevention strategies. The evidence presented here offers actionable insights to strengthen outbreak preparedness, guide targeted interventions, and inform broader strategies for managing high-consequence zoonotic threats in endemic regions.

LIMITATIONS

While this study draws upon diverse data sources, several constraints should be acknowledged. First, the reliance on published outbreak reports and surveillance data means findings are dependent on the accuracy and completeness of those records, which may vary across events. In wildlife sampling, the geographic scope and number of bats tested were limited to outbreak-associated areas, potentially underrepresenting the wider distribution of viral activity. Similarly, sero-prevalence surveys among human contacts were restricted in size and may not capture all asymptomatic infections, particularly in rural or hard-to-reach populations.

The integration of data from multiple years and differing methodologies may introduce inconsistencies in case definitions, diagnostic protocols, and reporting standards. Additionally, genomic analysis was only possible for a subset of positive samples, limiting broader phylogenetic comparisons. Despite these limitations, the synthesis of available evidence provides a valuable, evidence-based understanding of NiV epidemiology and control efforts in Kerala, while highlighting areas where more comprehensive, longitudinal research is needed.

REFERENCES

1. Chadha, M. S., Comer, J. A., Lowe, L., Rota, P. A., Rollin, P. E., Bellini, W. J., Ksiazek, T. G., & Mishra, A. C. (2006). Nipah Virus-associated Encephalitis Outbreak, Siliguri, India. *Emerging Infectious Diseases*, *12*(2), 235. https://doi.org/10.3201/EID1202.051247
2. Chandni, R., Renjith, T. P., Fazal, A., Yoosef, N., Ashhar, C., Thulaseedharan, N. K., Suraj, K. P., Sreejith, M. K., Sajeeth Kumar, K. G., Rajendran, V. R., Remla Beevi, A., Sarita, R. L., Sugunan, A. P., Arunkumar, G., Mourya, D. T., & Murhekar, M. (2020a). Clinical manifestations of nipah virus-infected patients who presented to the emergency department during an outbreak in Kerala State in India, May 2018. *Clinical Infectious Diseases*, *71*(1), 152–157. https://doi.org/10.1093/CID/CIZ789,
3. Chandni, R., Renjith, T. P., Fazal, A., Yoosef, N., Ashhar, C., Thulaseedharan, N. K., Suraj, K. P., Sreejith, M. K., Sajeeth Kumar, K. G., Rajendran, V. R., Remla Beevi, A., Sarita, R. L., Sugunan, A. P., Arunkumar, G., Mourya, D. T., & Murhekar, M. (2020b). Clinical manifestations of nipah virus-infected patients who presented to the emergency department during an outbreak in Kerala State in India, May 2018. *Clinical Infectious Diseases*, *71*(1), 152–157. https://doi.org/10.1093/cid/ciz789
4. Hauser, N., Gushiken, A. C., Narayanan, S., Kottilil, S., & Chua, J. V. (2021). Evolution of Nipah Virus Infection: Past, Present, and Future Considerations. *Tropical Medicine and Infectious Disease*, *6*(1), 24. https://doi.org/10.3390/TROPICALMED6010024
5. John, T. J., Rajappan, K., & Arjunan, K. K. (n.d.). *Communicable diseases monitored by disease surveillance in Kottayam district, Kerala state, India*.
6. Luby, S. P., Gurley, E. S., & Hossain, M. J. (2012). TRANSMISSION OF HUMAN INFECTION WITH NIPAH VIRUS. *Clinical Infectious Diseases*, *49*(11), 1743–1748. https://doi.org/10.1086/647951
7. Madhukalya, R., Yadav, U., Parray, H. A., Raj, N., Lupitha, S. S., Kumar, V., Saroj, A., Agarwal, V., Kumar, D., Das, S., & Kumar, R. (2025). Nipah virus: pathogenesis, genome, diagnosis, and treatment. *Applied Microbiology and Biotechnology*, *109*(1), 158. https://doi.org/10.1007/S00253-025-13474-6
8. Ramachandran, R., Jose, M. S., Sahay, R. R., & Shete, A. (2022). Sero-prevalence of Nipah antibodies among close contacts of the index case during 2019 Ernakulam outbreak. *Journal of Family Medicine and Primary Care*, *11*(6), 2479–2482. https://doi.org/10.4103/jfmpc.jfmpc_1731_21
9. Sadanadan, R., Arunkumar, G., Laserson, K. F., Heretik, K. H., Singh, S., Mourya, D. T., Gangakhedkar, R. R., Gupta, N., Sharma, R., Dhuria, M., Jain, S. K., Nichol, S., Gupta, P., &

Bhargava, B. (2018a). Towards global health security: Response to the May 2018 Nipah virus outbreak linked to Pteropus bats in Kerala, India. In *BMJ Global Health* (Vol. 3, Issue 6). BMJ Publishing Group. https://doi.org/10.1136/bmjgh-2018-001086

10. Sadanadan, R., Arunkumar, G., Laserson, K. F., Heretik, K. H., Singh, S., Mourya, D. T., Gangakhedkar, R. R., Gupta, N., Sharma, R., Dhuria, M., Jain, S. K., Nichol, S., Gupta, P., & Bhargava, B. (2018b). Towards global health security: Response to the May 2018 Nipah virus outbreak linked to Pteropus bats in Kerala, India. *BMJ Global Health*, *3*(6). https://doi.org/10.1136/BMJGH-2018-001086,
11. Sadanadan, R., Arunkumar, G., Laserson, K. F., Heretik, K. H., Singh, S., Mourya, D. T., Gangakhedkar, R. R., Gupta, N., Sharma, R., Dhuria, M., Jain, S. K., Nichol, S., Gupta, P., & Bhargava, B. (2018c). Towards global health security: Response to the May 2018 Nipah virus outbreak linked to Pteropus bats in Kerala, India. *BMJ Global Health*, *3*(6). https://doi.org/10.1136/BMJGH-2018-001086,
12. Sahay, R. R., Yadav, P. D., Gupta, N., Shete, A. M., Radhakrishnan, C., Mohan, G., Menon, N., Bhatnagar, T., Tk, S., Kadam, A. V., Pt, U., Anu Kumar, B., Ap, S., Vk, S., Khobragade, R., Gangakhedkar, R. R., & Mourya, D. T. (2020). Experiential learnings from the Nipah virus outbreaks in Kerala towards containment of infectious public health emergencies in India. *Epidemiology and Infection*, *148*, e90. https://doi.org/10.1017/S0950268820000825
13. Sanker, V., Vellekkat, F., & Dave, T. (2024a). Nipah Virus Outbreaks in Kerala: An Impending Doom? *Health Science Reports*, *7*(11), e70195. https://doi.org/10.1002/HSR2.70195
14. Sanker, V., Vellekkat, F., & Dave, T. (2024b). Nipah Virus Outbreaks in Kerala: An Impending Doom? *Health Science Reports*, *7*(11), e70195. https://doi.org/10.1002/HSR2.70195
15. Sudeep, A. B., Yadav, P. D., Gokhale, M. D., Balasubramanian, R., Gupta, N., Shete, A., Jain, R., Patil, S., Sahay, R. R., Nyayanit, D. A., Gopale, S., Pardeshi, P. G., Majumdar, T. D., Patil, D. R., Sugunan, A. P., & Mourya, D. T. (2021). Detection of Nipah virus in Pteropus medius in 2019 outbreak from Ernakulam district, Kerala, India. *BMC Infectious Diseases*, *21*(1). https://doi.org/10.1186/s12879-021-05865-7
16. T Jacob John, K Rajappan, & K K Arjunan. (2002, July). *Communicable diseases monitored by disease surveillance in Kottayam district, Kerala state, India | Request PDF*. https://www.researchgate.net/publication/8365217_Communicable_diseases_monitored_by_disease_surveillance_in_Kottayam_district_Kerala_state_India
17. Thomas, B., Chandran, P., Lilabi, M. P., George, B., Sivakumar, C. P., Jayadev, V. K., Bindu, V., Rajasi, R. S., Vijayan, B., Mohandas, A., & Hafeez, N. (2019). Nipah virus infection in Kozhikode, Kerala, South India, in 2018: Epidemiology of an outbreak of an emerging disease. *Indian Journal of Community Medicine*, *44*(4), 383–387. https://doi.org/10.4103/ijcm.IJCM_198_19
18. Verma, A., Jain, H., Sulaiman, S. A., Pokhrel, P., Goyal, A., & Dave, T. (2024). An impending public health threat: analysis of the recent Nipah virus outbreak and future recommendations – an editorial. *Annals of Medicine & Surgery*, *86*(2), 638–642. https://doi.org/10.1097/ms9.0000000000001627