

“NIPAH VIRUS: A DEADLY ZOONOTIC VIRUS”

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Abstract:

Nipah virus is emerging zoonotic virus from HENIPAVIRUS genus that poses a serious threat to public health due to its high fatality rate and lack of specific treatment or vaccines. First identified in Malaysia in 1998 it has since caused outbreak in countries like Bangladesh, India and Philippines, often linked to fruit bats as natural reservoirs. Human to human-transmission, severe encephalitis and respiratory system make early diagnosis and contain difficulty. This review focuses on transmission route, clinical features, epidemiology and current research on potential treatment and vaccines. Despite ongoing research supportive care remains the only treatment and public awareness is crucial in preventing future outbreaks. The paper highlights the urgent need for continued surveillance, global collaboration and preparation to prevent Nipah virus from becoming a future pandemic.

Keywords: Zoonotic, HENIPAVIRUS, human to human transmission, Fruit bats, Encephalitis.

• Introduction :

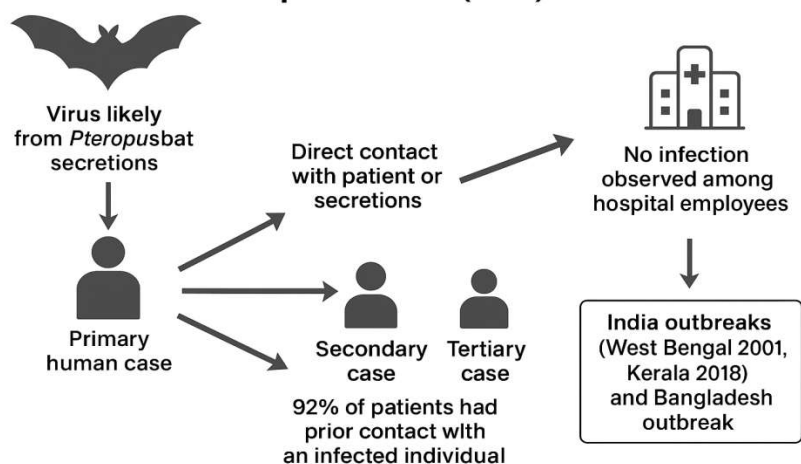
The nipah virus is one of the zoonotic viruses that uses both wild and domesticated animals as its source and vector to spread and multiply. Niv has been found in *Pteropus hypomelanus*, *Pteropus lylei*, and *Pteropus vampyrus* species in Malaysia¹. Early studies in India to find the Niv vector were conducted on insectivorous bats (*Megaderma spasma*); however, fruit bats of the same species, such as *Pteropus giganteus*, were ultimately shown to carry the virus². Bats were the most likely source of human infection during this pandemic, as evidenced by the highest degree of genetic similarity between the Niv genes from infected bats and Indian patients as compared to Malaysia, Cambodia, and Bangladesh. Eating fruit tainted with bat saliva or breathing in an aerosol containing contaminated urine or saliva droplets could have caused it³. The fact that raw date palm juice may possibly be a significant source of the virus supports the idea that the Niv epidemics in Bangladesh occurred during the months of

December through May, when palm fruit is harvested and juice is produced⁴. Nine to twenty-five percent of bat samples from Malaysia, Cambodia, Thailand and Bangladesh that underwent serological testing had NiV⁵. Its identification and monitoring were made possible only by the development of suitable diagnostic technique, such as real-time RT-PCR assays based on the identification of the particular sequence of the N gene⁶.

• Human-to-Human Transmission

Human-to-human transmission of the virus through direct contact with patients and their natural secretions was the main cause of the NiV outbreak in Bangladesh, according to studies on the virus's spread during that time. These were most likely the secretions of bats belonging to the *Pteropus* genus⁷. Although a 2003 study discovered the virus in shared houses, which may suggest human-to-human transmission, it did not completely rule out the potential of infection from the outside⁸. These were most likely the secretions of bats belonging to the *Pteropus* genus. The absence of infection among hospital employees who interacted with patients was the cause of the concerns. Conversely, it was discovered that five instances were probably connected to secondary and tertiary NiV transmission from person to person, and 92% of the patients had come into contact with another afflicted individual prior to being sick. In India, this virus transmission method was also verified during epidemics in West Bengal in 2001 and Kerala in 2018^{9,10}.

Human-to-Human Transmission Pathways of Nipah Virus (NiV)



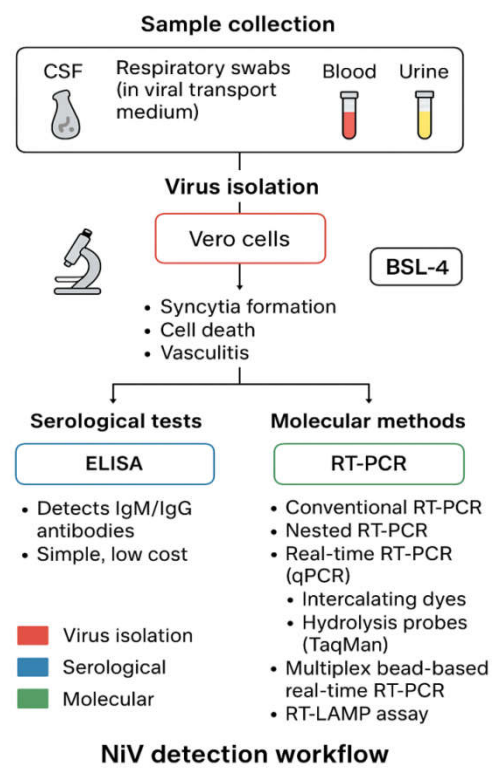
• Risk Factor

One of the primary criteria that can indicate a person's vulnerability to NiV infection is their age and sex. It is believed that the low average age of the affected individual (11.5 years) was associated with the prevalence of actions that increase the risk of infection, such as climbing trees with NiV-carrying bats⁷. In this instance, this factor was deemed more significant than youthful age. In the Naogaon and Meherpur regions, the median age of patients with confirmed or probable NiV infection was 12 and 38 years, respectively. Younger Naogaon patients also showed a shorter duration from the onset of the disease to death (4 days vs. 6 days). These findings imply that NiV infection can affect both adults and children⁸. In

Siliguri province, India, the female to male ratio was 1:4:1 and the patients were above 15 years old ⁹. Men’s activities that require close contact with infected animals or their secretion may be directly responsible for the high percentage of infections in men seen throughout different NiV epidemics. More than 90% of patients lived of worked on a pig far, did work that exposed them to pig farm, did work that exposed them to pigs, or came into contact with pigs or their urine or faeces, according to later research that supported similar findings ¹⁰. Over 40 percent of these individual reported encountering dead animals ¹¹.

• **Nipah Virus Diagnostics**

New NiV foci are confirmed by virus isolation in Vero cells that produce cytopathic effects (syncytia formation and cell death, and an ensuing vasculitis) within 3days. CSF, respiratory swabs (in viral transport medium), blood and urine are samples from which NiV can be isolated; however, all testing procedures must be carried out in BSL-4 laboratories ^{4,5}. ELISA is a straightforward and reasonably priced serological test that relies on the identification of IgM and IgM antibodies ^{4, 5, 12}. It is not entirely specific, though, and could yield inaccurate findings. The sensitivity and specificity of molecular techniques are higher. More sensitive and specific methods, such as conventional reverse transcription PCR (RT-PCR), nested RT-PCR, real time RT-PCR with the use of intercalating dyes (qPCR), real RT-PCR with the use of hydrolysis probes (TaqMan), multiplex bead-based real-time RT-PCR, or the RT-LAMB assay, have already supplanted the polymerase chain reaction (PCR) technique that was used as a standard until recently. A highly conserved area of the N, M or P gene in the viral genome has been the focus of RT-PCR studies of NiV ^{6, 13,14,15,16}.



- **Treatment**

Because there isn't a medication that effectively combats NiV, patients can only be managed with supportive and preventative care ^{17, 5}. When a NiV infection is confirmed, the fundamental clinical procedures include keeping the airway open, preventing venous thrombosis, and maintaining fluid and electrolytes balance ^{4, 12}.

When respiratory symptoms are severe, mechanical ventilation is performed. Broad-spectrum antibiotics are also administered to NiV-infection individuals ¹². Both the efficacy of acyclovir used in Singapore and the efficacy of ribavirin given during the pandemic in Malaysia are up for debate ^{5, 12, 18, 19}. In cell cultures, the antimalarial medication chloroquine effectively inhibited NiV; however, this was not substantiated in animal studies ^{4, 12, 16}. Human studies for the monoclonal antibody m102.4 are now in Phase I ²⁰. Adverse events associated to eighty-six treatments were reported; the rates in the treated and placebo groups were comparable. No fatalities have been reported ^{20, 21}. Assessed the synthesized trimeric tandem (3mG) and GRFT (Griffithsin's) in vitro antiviral efficacy against NiV and other viruses belonging to four different virus families. High mannose oligosaccharide-binding lectin GRFT has demonstrated a wide range of antiviral activities in vivo ²¹.

- **Vaccines**

Because there aren't many new virus outbreaks, there aren't many clinical trials for vaccines that protect against NiV. Animal models are used to examine possible preparations' efficacy. More than ten vaccines based on viral vectors, mRNA, recombinant protein subunits, or virus-like particles have been studied to date ^{22, 23}. The subunit vaccine based on soluble recombinant Hendra G-glycoprotein (HeV-sG), which also triggers a cross-immune response against NiV, has been the subject of the most research to date. While it did not demonstrate efficacy in pigs, it has been shown to be totally successful in protecting horses, cats, ferrets, and non-human primates against NiV, MY, NiV BD, and HeV²⁴⁻²⁹. Equivac, manufactured by Zoetis, Inc., is the only vaccine that has received formal approval and registration from the Australian Pesticides and Veterinary Medicines Authority (APVMA). Horses are treated with it as a preventative measure ^{4, 12, 16, 30}. The effectiveness of recombinant vesicular stomatitis viruses has also been demonstrated in animal trials ³¹⁻³³. An essential component of the fight against the epidemic is vaccination. It is imperative that new vaccines against NiV be developed further, particularly in light of clinical trials.

- **Prevention**

Avoiding direct contact with the virus's hosts and their secretions, as well as avoiding contaminated food, are the main preventive measures to minimize the emergence of new epidemic outbreaks and the spread of those that have already begun. On the one hand, it is advised to thoroughly inspect and clean the fruit of bat-inhabited trees. However, measures are put in place to restrict their access to locations and equipment used to gather date palm juice ^{5, 12}. Avoiding direct human-to-human contact is a crucial prevention measure that can successfully lower the scope of the NiV virus's propagation. When caring for someone who has an illness or is suspected of having one, conventional practices include hand washing, cleaning with 70% ethanol, using gloves and other protection gear, and avoiding direct contact with bodily fluids ⁵.

• Nipah Virus – Pandemic Potential

The quick and efficient spread of the virus from person to person, particularly when exposed individuals lack immunity, is one of the characteristics that suggested the possibility of a viral pandemic. During the outbreaks in Bangladesh and India, it was established that this pathway of NiV transmission was crucial. Direct contact with an infected person or their secretions can result in infection, and patients who have severe respiratory symptoms and a cough are at further risk of contracting the virus through saliva particles³⁴. Since the SARS-CoV-2 virus is primarily spread by air, general directives to implement suitable preventative measures have been implemented in the pandemic society³⁵. Contact with animals can also result in NiV infection, in addition to human-to-human contact. Bats are the main source of NiV and are probably also the cause of human COVID-19 infection. According to recent studies, pigs that were not considered a source of the virus during an epidemic in Bangladesh can nevertheless contract NiV-B without exhibiting any symptoms of illness. The probability that asymptomatic infected pigs could infect vulnerable animals and propagate the virus could be indicated by the presence of an infectious virus in the nasal wash³⁷.

Conclusion:

Drawing inferences from the COVID-19 pandemic, we must be prepared for the fact that any zoonotic virus, especially one with the ability to human-to-human transmission, can be exceedingly hazardous and contribute to a worldwide pandemic. A major rationale justifying the concerns about the introduction of NiV in the human population is the lack of vaccinations and treatments with proven effectiveness. They don't produce the desired results, and when combined with the issues with healthcare efficiency that the ongoing COVID-19 pandemic has exposed in both the most developed and the poorest nations, they can have major global repercussions^{38, 39}.

References :

1. Alam AM. Nipah virus: an emerging zoonotic disease causing fatal encephalitis. *Clin Med*. 2024. PMID: 35760448.
2. Aditi, Shariff M. Nipah virus: a review. *Clin Med*. 2019; 147:e95. PMID: 30869046.
3. Lu D, Yang M, Chai S, Jia H. Nipah virus: epidemiology, pathogenesis, treatment and prevention. *Front Med (Lausanne)*. 2024. PMID: 39417975.
4. Wang L, Lu D, Yang M, Chai S, Du H, Jiang H. Nipah virus: epidemiology, pathogenesis, treatment, and prevention. *Front Med (Lausanne)*. 2024;18(6):969–987. PMID: 39417975.
5. Singh RK, Dhama K, Chakraborty S, et al. Nipah virus: epidemiology, pathology, immunobiology and advances in diagnosis, vaccine designing and control strategies—a comprehensive review. *Vet Q*. 2019; 39(1):26–55. PMID: 31006350.
6. Goh KJ, Tan CT, Chew NK, et al. Clinical features of Nipah virus encephalitis among pig farmers in Malaysia. *N Engl J Med*. 2000; 342(17):1229–1235. PMID: 10781618.
7. Wang L, Lu D, Yang M, Chai S, Du H, Jiang H. Zoonotic and human-to-human transmission dynamics of Nipah virus. *Front Med (Lausanne)*. 2024. PMID: 39417975.
8. Chong HT, Kamarulzaman A, Tan CT, et al. Nipah encephalitis outbreak in Malaysia: clinical features, typical presentation, high mortality, and diagnostic challenges. *Clin Infect Dis*. 2002; 34(9):1185–1191. PMID: 11858542.

9. Priyadarsinee L, Sarma H, Sastry GN. Glycoprotein attachment with host cell surface receptor ephrin B2 and B3 in mediating entry of Nipah and Hendra virus: a computational investigation. *J Chem Sci (Bangalore)*. 2022; 134(4):114. PMID: 36465097.
10. The rising threat of Nipah virus: a highly contagious and deadly zoonotic pathogen. *Virol J*. 2025; 22:139. PMID: 39858892.
11. Hafeez MH. Navigating Nipah virus: insights, challenges, and emerging timelines. *Front Public Health Rep*. 2025. PMCID: PM119030718.
12. Improving clinical care of patients in Nipah outbreaks: moving beyond “compassionate use.” *Clin Infect Dis*. 2025. PMID: 39866590.
13. Sharma V, Kaushik S, Kumar R, Yadav JP. Emerging trends of Nipah virus: a review. *Rev Med Virol*. 2019; 29:e2010. doi:10.1002/rmv.2010.
14. Thakur N, Bailey D. Advances in diagnostics, vaccines and therapeutics for Nipah virus. *Microbes Infect*. 2019; 21(7):278–286. doi:10.1016/j.micinf.2019.02.002.
15. Aditi SM, Shariff M. Nipah virus infection: a review. *Epidemiol Infect*. 2019; 147:e95. doi: 10.1017/S0950268819000759.
16. Montgomery S, Chatamra K, Pauer L, Whalen E, Baldinetti F. Efficacy and safety of pregabalin in elderly people with generalised anxiety disorder. *Br J Psychiatry*. 2008; 193(5):389–394. doi:10.1192/bjp.bp.107.037788.
17. Hsu VP, Hossain MJ, Parashar UD, Ali MM, Ksiazek TG, Kuzmin IV, Breiman RF. Nipah virus encephalitis reemergence, Bangladesh. *Emerg Infect Dis*. 2004; 10(12):2082–2087. doi:10.3201/eid1012.040701.
18. Chadha MS, Comer JA, Lowe L, Rota PA, Rollin PE, Bellini WJ, Ksiazek TG, Mishra AC. Nipah virus–associated encephalitis outbreak, Siliguri, India. *Emerg Infect Dis*. 2006;12(2):235–240. doi:10.3201/eid1202.051247.
19. Parashar UD, Sunn LM, Ong F, Mounts AW, Arif MT, Ksiazek TG, Kamaluddin MA, Mustafa AN, Kaur H, Ding LM, Othman G, Radzi HM, Kitsutani PT, Stockton PC, Arokiasamy J, Gary HE Jr, Anderson LJ. Case-control study of risk factors for human infection with a new zoonotic paramyxovirus, Nipah virus, during a 1998–1999 outbreak of severe encephalitis in Malaysia. *J Infect Dis*. 2000;181(5):1755–1759. doi: 10.1086/315457.
20. Goh KJ, Tan CT, Chew NK, Tan PS, Kamarulzaman A, Sarji SA, Wong KT, Abdullah BJ, Chua KB, Lam SK. Clinical features of Nipah virus encephalitis among pig farmers in Malaysia. *N Engl J Med*. 2000;342(17):1229–1235. doi:10.1056/NEJM200004273421701.
21. Aditi, Shariff M. Nipah virus infection: a review. *Epidemiol Infect*. 2019;147:e95. doi:10.1017/S0950268819000086.
22. Sharma V, Kaushik S, Kumar R, Yadav JP, Kaushik S. Emerging trends of Nipah virus: a review. *Rev Med Virol*. 2019;29:e2010. doi:10.1002/rmv.2010.
23. Ambat AS, Zubair SM, Prasad N, Pundir P, Rajwar E, Patil DS, et al. Nipah virus: a review on epidemiological characteristics and outbreaks to inform public health decision making. *J Infect Public Health*. 2019;12:634–639. doi:10.1016/j.jiph.2019.02.013.
24. Guillaume V, Contamin H, Loth P, Georges-Courbot MC, Lefevre A, Marianneau P, Chua KB, Lam SK, Buckland R, Deubel V, et al. Nipah virus: vaccination and passive protection studies in a hamster model. *J Virol*. 2004;78:834–840.
25. Mazzola LT, Kelly-Cirino C. Diagnostics for Nipah virus: a zoonotic pathogen endemic to Southeast Asia. *BMJ Glob Health*. 2019;4(Suppl 2):e001118. doi:10.1136/bmjgh-2018-001118.
26. Ochani RK, Batra S, Shaikh A, Asad A. Nipah virus – the rising epidemic: a review. *Infez Med*. 2019;27:117–127.

27. Thakur N, Bailey D. Advances in diagnostics, vaccines and therapeutics for Nipah virus. *Microbes Infect.* 2019;21:278–286. doi:10.1016/j.micinf.2019.02.002.
28. Chakraborty S, et al. Evolving epidemiology of Nipah virus infection in Bangladesh: evidence from outbreaks during 2010–2011. *Emerg Infect Dis.* 2019. (Context: Nipah virus transmission dynamics).
29. Devnath P, Al Masud H. Nipah virus: a potential pandemic agent in the context of the current severe acute respiratory syndrome coronavirus 2 pandemic. *New Microbes New Infect.* 2021;41:100873. doi:10.1016/j.nmni.2021.100873.
30. Playford EG, et al. Phase I human trial of monoclonal antibody m102.4 targeting Nipah virus. *Lancet Infect Dis.* 2020. (Title partially recovered).
31. Lo MK, et al. In vitro antiviral activity of Griffithsin and its trimeric tandem (3mG) against Nipah virus and protective efficacy of Q-GRFT in a lethal hamster model. *Antiviral Res.* 2020;178:104786.
32. Broder CC. Hendra virus (HeV) and Nipah virus (NiV) animal vaccines. In: *Hendra and Nipah Viruses: Pathogenesis, Animal Models, and Recent Breakthroughs in Vaccination*. Amsterdam: Elsevier; 2016.
33. Weingartl H. Hendra and Nipah viruses: pathogenesis, animal models and recent breakthroughs in vaccination. *Vet Res.* 2015;46:59–74.
34. Mire CE, Satterfield BA, Geisbert JB, Agans KN, Borisevich V, Yan L, Geisbert TW. Pathogenic differences between Nipah virus Bangladesh and Malaysia strains in primates: implications for antibody therapy. *Sci Rep.* 2016;6:30916.
35. Singh RK. Nipah virus: epidemiology, pathology, immunobiology and advances in diagnosis, vaccine design and control strategies. *Front Microbiol.* 2019;10:573.