

Emerging Nipah Virus: From Outbreaks to Public Health Challenges

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ABSTRACT

The Nipah virus is a newly discovered zoonotic paramyxovirus belonging to the genus Henipavirus, which leads to encephalitis and severe respiratory illnesses in people. Fruit bats are the natural reservoir, allowing for frequent spillover to domestic animals and humans because of their widespread distribution throughout South and Southeast Asia, Oceania, and portions of Africa. The epidemiology, clinical characteristics, transmission dynamics, and healthcare response to Nipah virus outbreaks are reviewed in this article. The lack of approved vaccines or particular antivirals in spite of encouraging candidates in animal models and early trials, the scarcity of genetic data from multiple impacted areas, and the requirement for coordinated surveillance at the human–animal–environment interface are further gaps that are highlighted in this article.

Keywords: Nipah Virus, Zoonotic, Outbreak, Transmission, Control

To cite this article: Ismael SS, FB Mikaeel, AJ Sadiq & BH Abdullah. Emerging Nipah Virus: From Outbreaks to Public Health Challenges. Biological Times. 2026. February 5(2): 24-25.

Introduction

The Nipah virus (NiV) is a fatal zoonotic virus; it belongs to the genus Henipavirus that causes severe respiratory infection and encephalitis in humans. In its case, a high fatality ranged between 40 and 75% or more [1, 2, 3]. The natural reservoir host for this virus is fruit bats of the genus *Pteropus* AS SEEN IN Fig. 1, and humans acquired the infection from contact with bats, human-to-human transmission, or through pigs (an intermediate host) [4, 5, 6].



Fig. 1: Fruit bats [6].

Virology and Transmission

NiV is an RNA virus, and its size ranges from 18.2 kb. It has six encoded structural protein genes (F, G, M, N, L, and P) that are necessary for cell entry, immune evasion, and reproduction. [5, 6]. The initially reported Malaysia/Singapore outbreak was primarily pig-to-human, but in Bangladesh and India, human-to-human and bat-to-human (typically through raw date palm sap) transmission are more common. There is ample evidence of nosocomial transmission in hospitals during close, unprotected patient care [7, 8].

Major Outbreaks and Global Epidemiology

Pig farmers in Malaysia had the first known outbreak from 1998 to 1999, which spread to Singapore. Massive pig culling and farm biosecurity were necessary for management, and the death rate was less than 40% [2, 9]. There have been repeated outbreaks in Bangladesh and India since 2001, with a significantly higher case fatality rate (>70%) and effective human-to-human transmission, particularly from patients with respiratory involvement [10, 11]. West Bengal (2001, 2007) and Kerala (2018, 2019, 2023) have both seen epidemics in India. The Kozhikode outbreak in 2018 claimed 23 lives and had a 91% case-fatality rate, and it was mostly caused by hospital transmission from a single community-acquired index case [10, 11]. A more recent outbreak in Kerala in 2023 showed high mortality and significant human-to-human transfer. Several hundred confirmed human

cases have been reported worldwide, and the overall fatality rate sometimes surpasses 50% [12, 13].

Clinical Features and Diagnosis

The following ecological and human behavioral components are closely related to transmission: pig or horse husbandry under bat feeding areas, eating raw date palm sap tainted with bat secretions, roosting bats close to human habitation, and healthcare exposures without proper infection management. The risk of spillover can be increased by habitat loss and changes in temperature or land use, which might increase bat-human contact [14,15]. With regional variations in transmissibility and clinical pattern, phylogenetic analyses reveal at least two major clades: Bangladesh/India (NiV-BD, with a potential unique Indian clade) and Malaysia/Cambodia (NiV-MY) [2,8].

Outbreak Dynamics and One Health Drivers

Spillover is tightly linked to ecological and human behavioral factors: bat roosting near human dwellings, consumption of raw date-palm sap contaminated with bat secretions, pig or horse farming under bat feeding sites, and healthcare exposures without adequate infection control. Habitat loss and climate or land-use change can increase bat–human contact, raising spillover risk [14,15].

Control, Prevention, and Public Health Response

There are currently no approved vaccinations or antiviral medications for human usage; supportive care is provided, and it is crucial to increase people's awareness of the risk factors for infection and the precautions they can take to avoid spreading the disease. WHO advises implementing the actions listed below [13,14]:

- Minimizing the possibility of transmission from bats to humans and the possibility of transmission from animals to humans
- Minimizing the possibility of transmission from person to person
- Managing of the NiV in pigs
- Monitoring infections in hospitals [14,18,19]

Public Health Significance and Future Directions

Because of its high mortality, recurrent outbreaks, and confirmed human-to-human transmission, NiV has been classified by the World Health Organization as an emergency virus with pandemic potential. Among the primary research goals are expanding the genome, clarifying transmission processes, and accelerating vaccine development within a One Health framework [15, 16, 17].

Conclusion

NiV is a zoonotic fatal virus in fruit bats, humans and domestic animals, mainly circulated in in South Asia. The NiV is a novel pathogen that is extremely concerning, not regarding to its high death rate, but also because of the intricate molecular and ecological elements that support its resurgence. As virology, medicine, and vaccine development research pick up speed.

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