

REVIEW | SJIP 2026

From Bats to Humans: Understanding the Spillover and Spread of Nipah Virus

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Abstract

Nipah virus is a highly pathogenic zoonotic paramyxovirus that causes severe respiratory disease and encephalitis in humans, with case fatality rates ranging from 40% to 75%. Since its first emergence during the 1998-1999 outbreak in Malaysia, the epidemiology of Nipah virus infection has evolved considerably. While the Malaysian outbreak was characterized by transmission through infected pigs, subsequent outbreaks in Bangladesh and India demonstrated recurrent bat-to-human spillover through consumption of contaminated raw date palm sap with evidence of human-to-human transmission. These changing transmission patterns highlight the dynamic ecology of the virus and emphasize the importance of integrated surveillance. This review critically examines the current evidence regarding Nipah virus transmission, distinguishing well-established transmission pathways from those supported by limited evidence. Despite considerable progress in understanding Nipah virus epidemiology, important knowledge gaps remain regarding the determinants of spillover, ecological forecasting, and effective prevention strategies. Strengthening multidisciplinary collaboration between human, animal, and environmental health sectors is essential to minimize the risk of future outbreaks and improve global pandemic preparedness.

Keywords: Fruit bats, infection prevention, Nipah virus, spillover, zoonotic disease

1. Introduction

Nipah virus (NiV) is an emerging zoonotic RNA virus belonging to the genus *Henipavirus* within the family *Paramyxoviridae*. It is classified as a Biosafety Level-4 (BSL-4) pathogen because of its high pathogenicity, absence of licensed specific antiviral therapy, and potential for causing outbreaks with substantial mortality¹. Since its first recognition in Malaysia in 1998², NiV has become one of the World Health Organization's priority pathogens due to lack of effective medical countermeasures³.

Clinically, NiV infection presents with a broad spectrum of manifestations ranging from asymptomatic infection and mild influenza-like illness to severe respiratory disease and rapidly progressive encephalitis⁴. Neurological complications remain the hallmark of severe disease, although respiratory involvement appears to be more prominent in outbreaks reported from Bangladesh⁵ and India⁶ than in the original Malaysian outbreak.

The incubation period generally ranges from 4-14 days but may occasionally extend beyond one-month, complicating surveillance and contact tracing efforts. The reported case fatality rate (CFR) varies

between 40% and 75%, depending on the outbreak setting, availability of intensive care facilities, and surveillance systems⁷. However, mortality may be underestimated in regions where mild or asymptomatic infections remain undetected. The combination of high mortality, absence of licensed vaccines, widespread distribution of reservoir hosts, and evidence of human-to-human transmission has raised global concern regarding the pandemic potential of NiV⁸.

Unlike many zoonotic pathogens that rely on a single transmission mechanism, NiV demonstrates remarkable epidemiological diversity. The transmission dynamics observed during the pig-associated outbreak in Malaysia⁹ differ substantially from the recurrent spillover events documented in Bangladesh¹⁰ and the healthcare-associated outbreaks reported in India¹¹. This evolution of transmission patterns suggests that ecological, behavioral, and socioeconomic factors interact to shape disease emergence in different geographical settings. Consequently, understanding the changing epidemiology of NiV is essential for developing targeted prevention strategies.

Recent advances have expanded knowledge regarding bat ecology, viral persistence, ecological drivers of spillover, vaccine development, monoclonal antibody (mAb) therapies, and integrated One Health

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How to cite this article: Arachchi HRE. From bats to humans: understanding the spillover and spread of Nipah virus. SAAP J Integr Physiol. 2026;1(3):24-29.

surveillance. Nevertheless, predicting when and where spillover will occur remains a major scientific challenge. This review critically examines current evidence regarding NiV transmission, highlights areas of uncertainty, discusses recent developments in prevention and preparedness, and identifies priorities for future research.

2. Changing Epidemiology of Nipah Virus Outbreaks

Since its emergence more than two decades ago, the epidemiology of NiV infection has undergone notable changes. These changes involve not only geographical expansion but also differences in reservoir interactions, transmission pathways, intermediate hosts, and the frequency of human-to-human transmission.

2.1. Malaysia and Singapore outbreaks

The first recognized outbreak occurred in Malaysia and Singapore between 1998 and 1999. More than 260 human cases were reported, predominantly among pig farmers and abattoir workers. Epidemiological investigations demonstrated that pigs served as the principal amplifying host after becoming infected through exposure to fruits contaminated by saliva or urine from infected *Pteropus* bats, commonly known as fruit bats or flying foxes. Human infection occurred primarily through close occupational contact with infected pigs rather than direct bat exposure. Importantly, sustained human-to-human transmission was not observed during this outbreak. Control measures, including movement restrictions and the culling of more than one million pigs, successfully interrupted transmission but resulted in enormous economic losses for the Malaysian livestock industry¹².

2.2. Bangladesh outbreaks

A distinctly different epidemiological pattern emerged in Bangladesh, beginning in 2001. Unlike Malaysia, pigs played little or no epidemiological role. Instead, repeated spillover events occurred through the consumption of raw date palm sap contaminated by fruit bats. Bangladesh has since experienced outbreaks almost annually, particularly during the winter months when fresh date palm sap is harvested. Epidemiological investigations consistently demonstrated strong associations between raw date palm sap consumption and laboratory-confirmed NiV infection. This unique transmission pathway illustrates how cultural practices can interact with wildlife ecology to facilitate zoonotic spillover¹³.

Equally important, outbreaks in Bangladesh provided convincing evidence that human-to-human transmission can contribute substantially to disease spread¹⁴. Several outbreaks demonstrated transmission across multiple generations, particularly among family caregivers and healthcare workers. Although human-to-human transmission remains less efficient than transmission following zoonotic spillover, these observations fundamentally changed the understanding of NiV epidemiology by demonstrating its capacity for sustained transmission under favorable conditions.

2.3. Indian outbreaks

India has experienced multiple outbreaks with varying epidemiological characteristics. The outbreak in Siliguri, West Bengal, in 2001 represented one of the earliest examples of significant nosocomial transmission¹⁵. More than two-thirds of affected individuals were healthcare workers or hospital visitors, highlighting deficiencies in infection prevention and control practices. Subsequent investigations suggested that transmission occurred primarily through close contact with infected patients, emphasizing the importance of early case detection and isolation.

Another outbreak occurred in Nadia district, West Bengal, in 2007, where person-to-person transmission was again implicated. Although relatively small, this outbreak reinforced concerns regarding healthcare-associated transmission and highlighted the need for

enhanced surveillance in regions bordering Bangladesh¹⁶.

More recently, repeated outbreaks in Kerala since 2018 have attracted considerable international attention. Unlike the eastern Indian outbreaks, these events occurred in southern India, suggesting expansion of the geographical range of NiV. Rapid public health responses, aggressive contact tracing, laboratory confirmation, isolation of cases, and coordinated multisectoral interventions successfully limited onward transmission during these outbreaks. The Kerala experience illustrates the value of preparedness, laboratory capacity, and coordinated outbreak response in containing emerging zoonotic diseases¹⁷.

Collectively, these outbreaks demonstrate a gradual transition from livestock-associated transmission in Malaysia toward direct bat-to-human spillover, and increasing human-to-human transmission in Bangladesh and India. This changing epidemiological landscape highlights the need for region-specific prevention strategies rather than a single universal approach.

3. Ecology of Nipah Virus and Drivers of Spillover

Old World fruit bats belonging to the genus *Pteropus* are widely recognized as the natural reservoir of NiV. Numerous ecological and virological investigations have identified viral RNA, antibodies, or infectious virus in several bat species across South and Southeast Asia, Australia, and parts of Africa. Unlike susceptible mammals, infected bats generally show no evidence of clinical disease, suggesting long-term host-virus adaptation¹⁸.

Although reservoir status is well established, the ecological mechanisms driving spillover remain incompletely understood. Increasing evidence suggests that spillover events result from complex interactions between wildlife ecology, environmental change, and human behavior, rather than simple contact between bats and humans.

3.1. Destruction of bat habitats

Habitat destruction, rapid urbanization, agricultural expansion, and deforestation have substantially altered bat ecology over recent decades¹⁹. Loss of native forests reduces the availability of natural food sources and roosting habitats, forcing fruit bats to forage increasingly within agricultural landscapes and human settlements. Consequently, opportunities for contamination of cultivated fruits, livestock feed, and date palm sap have increased, facilitating viral spillover.

3.2. Seasonal variations

Seasonal ecological factors also appear to influence spillover risk. Several studies have demonstrated seasonal variation in viral shedding among fruit bats, with increased viral excretion coinciding with periods of nutritional stress and reproductive activity. During pregnancy, lactation, and food shortages, physiological stress may alter immune function, potentially increasing viral replication and shedding²⁰. Although the precise mechanisms remain under investigation, these findings suggest that spillover risk is not constant throughout the year but fluctuates according to ecological conditions.

3.3. Climatic factors

Climate variability may further influence NiV emergence. Changes in rainfall patterns, drought, temperature, and flowering cycles affect fruit availability, bat migration, and population density. Ecological modeling studies increasingly support the hypothesis that environmental disturbances can modify host behavior and increase interfaces between wildlife, livestock, and humans²¹. Nevertheless, accurately predicting future spillover events remains difficult because of the complex interactions among climatic, ecological, and socioeconomic factors.

These observations emphasize that NiV emergence cannot be understood solely through virology or clinical medicine. Instead, spillover represents a multifactorial ecological process requiring

integrated investigation of wildlife ecology, environmental change, livestock management, and human behavior.

4. Transmission Pathways

Spillover of the virus from bats to other species occurs through multiple pathways. NiV has been isolated from bat saliva and urine, providing evidence that transmission primarily happens through these secretions²². Direct transmission from bats to humans can also occur

through hunting bats for consumption or through living in close proximity to bat roosting sites. However, the primary modality of transmission is through contaminated raw date palm sap and pigs, whereas contribution of other animals is inconclusive. Moreover, evidence of direct environmental exposure to bat secretions remains comparatively limited and warrants further investigation. The transmission pathways are presented in Figure 1.

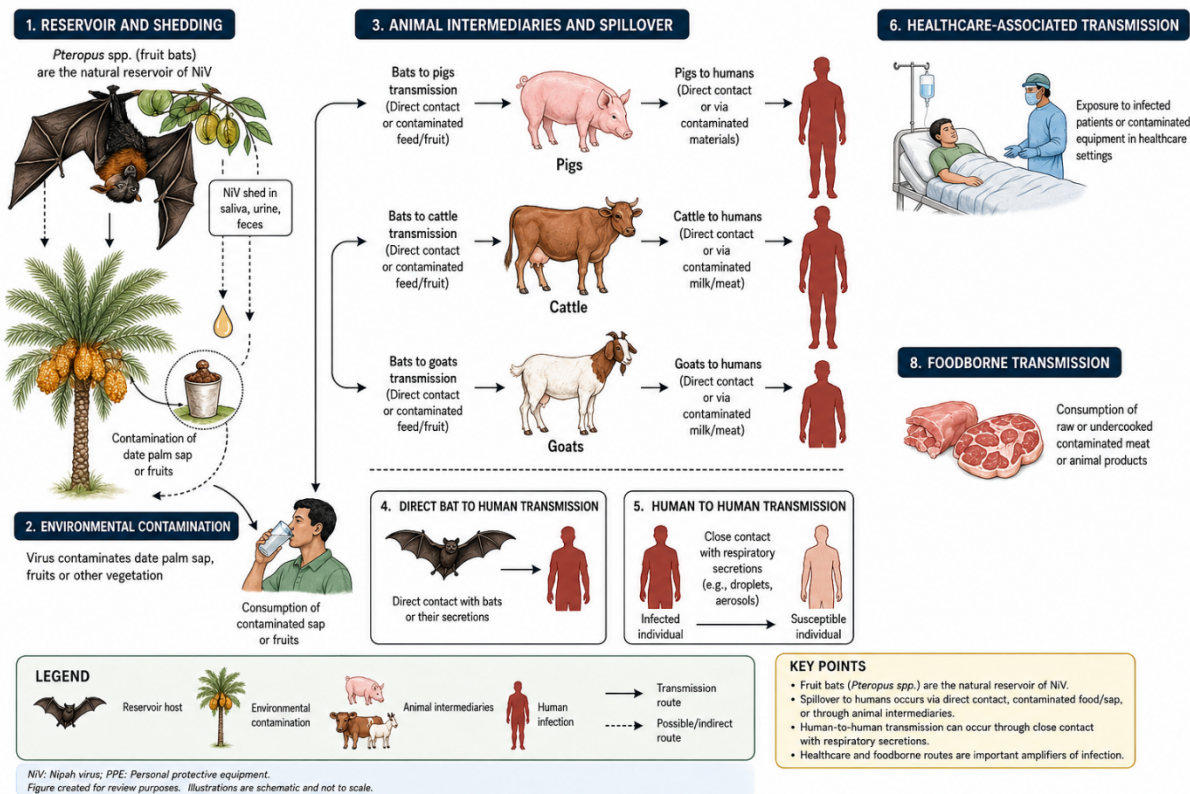


Figure 1: Nipah virus transmission pathways

Fruit bats act as the natural reservoir of Nipah virus and transmit infection directly to humans through contaminated food or indirectly through animal hosts such as pigs, cattle, and goats. Secondary human-to-human transmission occurs through close contact with infected individuals, including in healthcare settings.

4.1. Consumption of raw date palm sap

Direct bat-to-human transmission may occur through exposure to bat saliva, urine, or excreta contaminating food sources. The strongest epidemiological evidence supports transmission through consumption of raw date palm sap contaminated by fruit bats. One of the most common transmission routes in South Asia is the consumption of contaminated raw date palm sap. Date palm sap is a traditional beverage consumed in many regions. Infrared camera studies have repeatedly demonstrated bats visiting palm trees during harvesting season²³. Bats may drink directly from the collection taps or clay pots, contaminating the sap with saliva, urine, feces or even through accidental falls into the containers. Experimental studies have demonstrated that NiV can remain viable in fresh date palm sap for several days under favorable environmental conditions, particularly at lower temperatures, providing biological support for this well-established transmission pathway²⁴. Consumption of contaminated raw sap has been linked to multiple outbreaks, particularly in Bangladesh. Notably, these outbreaks have been associated with areas of high date palm sap consumption and the sap harvesting season.

4.2. Exposure to bat secretions

Direct exposure to bat secretions may represent another, less common, route of zoonotic transmission. During the Goalando

outbreak in Bangladesh in 2004²⁵, individuals who climbed trees were significantly more likely to develop NiV infection than controls, suggesting that direct contact with bat saliva or urine contaminating tree surfaces may occasionally facilitate spillover. Nevertheless, compared with contaminated raw date palm sap, this transmission pathway is thought to contribute relatively little to the overall disease burden.

4.3. Consumption of contaminated fruits

Consumption of fruits partially eaten or contaminated by bat saliva can lead to transmission of the virus to other species, including humans, pigs, cows, goats, and horses. The first known outbreak in Malaysia was believed to have resulted from pigs consuming fruits partially eaten by bats, leading to porcine infection and subsequent transmission to humans. Pigs are the only well-established amplifying host, supported by extensive epidemiological, virological, and experimental evidence from the Malaysian outbreak. After becoming infected through exposure to bat-contaminated fruits, pigs developed respiratory and neurological disease and efficiently transmitted the virus to other pigs and subsequently to humans, particularly pig farmers and abattoir workers²⁶. This amplification within intensive pig farming systems played a pivotal role in the scale of the Malaysian outbreak.

4.4. Transmission through livestock, domestic, and peridomestic animals

Another pathway of spillover has been reported to occur through livestock and domestic animals acting as bridging hosts. Fruit bats commonly drop partially eaten fruits contaminated with saliva, which are subsequently consumed by domestic animals²⁷. Furthermore, date palm sap contaminated with bat saliva, urine, or feces and considered unsuitable for human consumption is occasionally fed to livestock, providing another plausible route of exposure. Although these observations support the possibility of bat-to-domestic animal transmission, the epidemiological significance of this pathway remains incompletely understood.

Evidence supporting transmission from cows, goats, and horses are considerably less certain. Sporadic reports have documented infections in these species during outbreaks in Bangladesh and the Philippines, but current evidence suggests that they function primarily as incidental hosts rather than major amplifying reservoirs. During the 2001 outbreak in Meherpur, Bangladesh, close contact with a sick cow was strongly associated with NiV infection, suggesting that cattle may occasionally transmit the virus to humans²⁸. Serological studies have also demonstrated evidence of NiV exposure in a small proportion of goats, indicating that these animals can become infected following spillover from bats, raising the possibility that they may occasionally act as bridging hosts.

Evidence for horses is similarly limited. During the 2014 outbreak in the Philippines, transmission was associated with exposure during the slaughtering and butchering of infected horses intended for human consumption²⁹. Although this confirms that horses are susceptible to NiV infection, current evidence suggests they function as incidental rather than major amplifying hosts.

Furthermore, antibodies against NiV have been detected in horses, suggesting that these animals may occasionally become infected through contact with infected bats or contaminated materials³⁰.

4.5. Other modalities of transmission

Although transmission through handling or consumption of infected animal tissues has occasionally been suggested, direct evidence supporting foodborne transmission from raw or undercooked meat remains limited. The Philippines outbreak involved extensive exposure during slaughtering and butchering, making it difficult to distinguish whether infection resulted from direct contact with infected tissues or subsequent meat consumption²⁹. Consequently, close contact with infected live animals or their bodily fluids is considered a substantially greater risk than meat consumption itself.

5. Human-to-Human Transmission: Evolving Evidence and Implications for Outbreak Control

Initially, NiV was considered a zoonotic pathogen with limited capacity for human-to-human transmission because the Malaysian outbreak was almost entirely associated with infected pigs. However, epidemiological investigations conducted during subsequent outbreaks in Bangladesh and India substantially changed this understanding. It is now well recognized that although zoonotic spillover remains the primary mechanism initiating outbreaks, secondary human-to-human transmission is capable of sustaining local outbreaks³¹.

Transmission between humans occur predominantly through close contact with infected patients, particularly exposure to respiratory secretions, saliva, urine, or other bodily fluids during the acute phase of illness. Household caregivers are consistently identified as one of the highest-risk groups because they frequently provide prolonged, close, unprotected care³². Healthcare workers are similarly vulnerable, particularly before a diagnosis of NiV infection is suspected and appropriate infection prevention measures are implemented.

The extent of human-to-human transmission varies considerably between outbreaks. While some outbreaks terminate after the index case, others have demonstrated sustained transmission chains involving several generations of infection. The Faridpur outbreak in Bangladesh provided compelling evidence that prolonged close contact with severely ill patients can facilitate onward transmission³³. Heterogeneity in transmission suggests that viral, host, environmental, and behavioral factors all contribute to outbreak dynamics.

Hospital-associated transmission has emerged as a particularly important concern. The Siliguri outbreak in India highlighted how inadequate infection prevention and control measures, overcrowded wards, delayed recognition of cases, and insufficient personal protective equipment (PPE) can facilitate nosocomial spread³⁴. Similar risks have been recognized during subsequent outbreaks, emphasizing that healthcare settings can become amplification points if early diagnosis and isolation are delayed.

Current evidence indicates that prolonged close contact is generally required for transmission, and widespread community spread has not been observed. Nevertheless, the repeated occurrence of healthcare-associated outbreaks and sustained household transmission underscores the importance of maintaining vigilance, particularly because viral evolution could potentially alter transmissibility in the future. Continued genomic surveillance is therefore essential to monitor viral diversity and detect changes that may influence transmission dynamics.

6. One Health Perspective

The emergence of NiV highlights the close interconnection between human, animal, and environmental health, requiring a multidisciplinary One Health approach. Environmental changes such as deforestation, agricultural expansion, urbanization, and climate change increase contact between *Pteropus* bats, livestock, and humans, facilitating viral spillover³⁵.

Integrated surveillance is central to prevention. Monitoring bat populations, viral shedding, and habitat changes can help identify periods of increased spillover risk, while veterinary surveillance of livestock enables early detection of amplification events. Environmental monitoring of land-use changes and climate variability may further improve outbreak prediction. Effective implementation requires collaboration among clinicians, veterinarians, ecologists, wildlife biologists, epidemiologists, and public health authorities through integrated surveillance and rapid information sharing³⁶.

7. Future Directions

As no licensed antiviral therapy or vaccine is currently available, prevention remains the cornerstone of NiV control. Community interventions should focus on reducing zoonotic exposure through avoidance of raw date palm sap, use of protective barriers at sap collection sites, proper washing of fruits, and culturally appropriate public education. In healthcare settings, early case detection, patient isolation, appropriate PPE, hand hygiene, and strict infection prevention and control measures are essential to prevent nosocomial transmission.

Rapid laboratory diagnosis using RT-PCR is critical for case confirmation and outbreak control, while expansion of molecular diagnostic capacity in endemic regions remains a priority. Veterinary measures including farm biosecurity, surveillance, movement restrictions, and, where necessary, culling of infected pigs can limit amplification. However, culling of fruit bats will be ineffective and ecologically harmful.

Preparedness for major outbreaks will require rapid response teams, laboratory surge capacity, standardized clinical protocols, effective contact tracing, risk communication, and cross-border surveillance to enable coordinated responses.

8. Conclusion

Nipah virus has evolved from a livestock-associated zoonosis into a complex emerging disease with multiple transmission pathways. Bat-to-human transmission through contaminated date palm sap, pig-mediated amplification, and human-to-human spread are well established, whereas the role of other animal hosts requires further investigation. As environmental change continues to increase the chances of spillover, strengthening One Health surveillance, laboratory capacity, infection prevention, community engagement, and international collaboration remains the most effective strategy for reducing the impact of future outbreaks.

Disclosure of AI Use

During the preparation of the manuscript, ChatGPT (OpenAI, free version) was exclusively used for language editing and grammatical refinement. No AI-generated content was accepted without critical review and revision by the author, who takes full responsibility for the final manuscript. The schematic illustration in Figure 1 was generated using ChatGPT (OpenAI, free version) and subsequently reviewed and edited by the author for scientific accuracy.

References

- Sun B, Jia L, Liang B, Chen Q, Liu D. Phylogeography, transmission, and viral proteins of Nipah virus. *Virus*. 2018;33(5):385-93. DOI: 10.1007/s12250-018-0050-1.
- Chua KB. Nipah virus outbreak in Malaysia. *J Clin Virol*. 2003;26(3):265-75. DOI: 10.1016/s1386-6532(02)00268-8.
- World Health Organization. Nipah virus. WHO, Geneva, 2026. Available from: <https://www.who.int/news-room/fact-sheets/detail/nipah-virus>; Accessed on 5.07.2026.
- Chua KB, Goh KJ, Wong KT, Kamarulzaman A, Tan PS, Ksiazek TG, et al. Fatal encephalitis due to Nipah virus among pig-farmers in Malaysia. *Lancet*. 1999;354(9186):1257-9. DOI: 10.1016/S0140-6736(99)04299-3.
- Nikolay B, Salje H, Hossain MJ, Khan AKMD, Sazzad HMS, Rahman M, et al. Transmission of Nipah virus - 14 years of investigations in Bangladesh. *N Engl J Med*. 2019;380(19):1804-14. DOI: 10.1056/NEJMoa1805376.
- Chadha MS, Comer JA, Lowe L, Rota PA, Rollin PE, Bellini WJ, et al. Nipah virus-associated encephalitis outbreak, Siliguri, India. *Emerg Infect Dis*. 2006;12(2):235-40. DOI: 10.3201/eid1202.051247.
- Madhukalya R, Yadav U, Parray HA, Raj N, Lupitha SS, Kumar V, et al. Nipah virus: pathogenesis, genome, diagnosis, and treatment. *Appl Microbiol Biotechnol*. 2025;109(1):158. DOI: 10.1007/s00253-025-13474-6.
- Luby SP. The pandemic potential of Nipah virus. *Antiviral Res*. 2013;100(1):38-43. DOI: 10.1016/j.antiviral.2013.07.011.
- Chua KB, Bellini WJ, Rota PA, Harcourt BH, Tamin A, Lam SK, et al. Nipah virus: a recently emergent deadly paramyxovirus. *Science*. 2000;288(5470):1432-5. DOI: 10.1126/science.288.5470.1432.
- Hossain MJ, Gurley ES, Montgomery JM, Bell M, Carroll DS, Hsu VP, et al. Clinical presentation of Nipah virus infection in Bangladesh. *Clin Infect Dis*. 2008;46(7):777-84. DOI: 10.1086/529147.
- Ang BSP, Lim TCC, Wang L. Nipah virus infection. *J Clin Microbiol*. 2018;56(6):e01875-17. DOI: 10.1128/JCM.01875-17.
- Uppal PK. Emergence of Nipah virus in Malaysia. *Ann N Y Acad Sci*. 2000;916:354-7. DOI: 10.1111/j.1749-6632.2000.tb05312.x.
- Luby SP, Rahman M, Hossain MJ, Blum LS, Husain MM, Gurley E, et al. Foodborne transmission of Nipah virus, Bangladesh. *Emerg Infect Dis*. 2006;12(12):1888-94. DOI: 10.3201/eid1212.060732.
- Luby SP, Gurley ES, Hossain MJ. Transmission of human infection with Nipah virus. *Clin Infect Dis*. 2009;49(11):1743-8. DOI: 10.1086/647951.
- Veggalam S, Ca J, Balaji O, Madhu MT, Hussain MH, H S, et al. Nipah virus outbreaks in India: A comprehensive update. *Cureus*. 2025;17(9):e92420. DOI: 10.7759/cureus.92420.
- Plowright RK, Becker DJ, Crowley DE, Washburne AD, Huang T, Nameer PO, et al. Prioritizing surveillance of Nipah virus in India. *PLoS Negl Trop Dis*. 2019;13(6):e0007393. DOI: 10.1371/journal.pntd.0007393.
- Balasubramanian R, Mohandas S, Thankappan UP, Shete A, Patil D, Sabarinath K, et al. Surveillance of Nipah virus in *Pteropus medius* of Kerala state, India, 2023. *Front Microbiol*. 2024;15:1342170. DOI: 10.3389/fmicb.2024.1342170.
- Schountz T. Immunology of bats and their viruses: challenges and opportunities. *Viruses*. 2014;6(12):4880-901. DOI: 10.3390/v6124880.
- Bhowmik A, Hasan M, Redoy MMH, Saha G. Nipah virus outbreak trends in Bangladesh during the period 2001 to 2024: a brief review. *Sci One Health*. 2024;4:100103. DOI: 10.1016/j.soh.2024.100103.
- Mortlock M, Geldenhuys M, Dietrich M, Epstein JH, Weyer J, Pawęska JT, et al. Seasonal shedding patterns of diverse henipavirus-related paramyxoviruses in Egyptian rousette bats. *Sci Rep*. 2021;11:24262. DOI: 10.1038/s41598-021-03641-w.
- Ahmed AS, Bekele A, Kasso M, Atickem A. Impact of climate change on the distribution and predicted habitat suitability of two fruit bats (*Rousettus aegyptiacus* and *Epomophorus labiatus*) in Ethiopia: implications for conservation. *Ecol Evol*. 2023;13:e10481. DOI: 10.1002/ece3.10481.
- Singh RK, Dhama K, Chakraborty S, Tiwari R, Natesan S, Khandia R, 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. DOI: 10.1080/01652176.2019.1580827.
- Khan MSU, Hossain J, Gurley ES, Nahar N, Sultana R, Luby SP. Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. *Ecohealth*. 2010;7(4):517-25. DOI: 10.1007/s10393-010-0366-2.
- Fogarty R, Halpin K, Hyatt AD, Daszak P, Mungall BA. Henipavirus susceptibility to environmental variables. *Virus Res*. 2008;132(1-2):140-4. DOI: 10.1016/j.virusres.2007.11.010.
- Montgomery JM, Hossain MJ, Gurley E, Carroll DS, Croisier A, Bertherat E, et al. Risk factors for Nipah virus encephalitis in Bangladesh. *Emerg Infect Dis*. 2008;14(10):1526-32. DOI: 10.3201/eid1410.060507.
- Nor MNM, Gan CH, Ong BL. Nipah virus infection of pigs in peninsular Malaysia. *Rev Sci Tech*. 2000;19(1):160-5. DOI: 10.20506/rst.19.1.1202.
- Islam A, Cannon DL, Rahman MZ, Khan SU, Epstein JH, Daszak P, et al. Nipah virus exposure in domestic and peridomestic animals living in human outbreak sites, Bangladesh, 2013-2015. *Emerg*

- Infect Dis. 2023; 29(2):393-6. DOI: 10.3201/eid2902.221379.
28. Hsu VP, Hossain MJ, Parashar UD, Ali MM, Ksiazek TG, Kuzmin I, et al. Nipah virus encephalitis reemergence, Bangladesh. *Emerg Infect Dis.* 2004;10(12):2082-7. DOI: 10.3201/eid1012.040701.
29. Ching PKG, de los Reyes VC, Sucaldito MN, Tayag E, Columna-Vingno AB, Malbas Jr FF, et al. Outbreak of henipavirus infection, Philippines, 2014. *Emerg Infect Dis.* 2015;21(2):328-31. DOI: 10.3201/eid2102.141433.
30. Daniels P, Ksiazek T, Eaton BT. Laboratory diagnosis of Nipah and Hendra virus infections. *Microbes Infect.* 2001;3(4):289-95. DOI: 10.1016/s1286-4579(01)01382-x.
31. Pritchard S, Hornsey E. The role of infection prevention and control in the mitigation of human-to-human transmission of Nipah virus: a systematic review. *Antimicrob Resist Infect Control.* 2025;15(1):1. DOI: 10.1186/s13756-025-01677-5.
32. Arunkumar G, Chandni R, Mourya DT, Singh SK, Sadanandan R, Sudan P, et al. Outbreak investigation of Nipah virus disease in Kerala, India, 2018. *J Infect Dis.* 2019;219(12):1867-78. DOI: 10.1093/infdis/jiy612.
33. Gurley ES, Montgomery JM, Hossain MJ, Bell M, Azad AK, Islam MR, et al. Person-to-person transmission of Nipah virus in a Bangladeshi community. *Emerg Infect Dis.* 2007;13(7):1031-7. DOI: 10.3201/eid1307.061128.
34. Harit AK, Ichhpujani RL, Gupta S, Gill KS, Lal S, Ganguly NK, et al. Nipah/Hendra virus outbreak in Siliguri, West Bengal, India in 2001. *Indian J Med Res.* 2006;123(4):553-60. PMID: 16783047.
35. Yadav PD, Baid K, Patil DY, Shirin T, Rahman MZ, Peel AJ, et al. A One Health approach to understanding and managing Nipah virus outbreaks. *Nat Microbiol.* 2025;10(6):1272-81. DOI: 10.1038/s41564-025-02020-9.
36. Singhai M, Jain R, Jain S, Bala M, Singh S, Goyal R. Nipah virus disease: recent perspective and One Health approach. *Ann Glob Health.* 2021;87(1):102. DOI: 10.5334/aogh.3431.