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Resurgence of Nipah Virus: A Threat to Public Health in India

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Abstract Emerging and re-emerging viral zoonoses pose a serious threat to public health globally. The Nipah virus (NiV), a member of the genus *Henipavirus* within the family *Paramyxoviridae*, is a highly pathogenic zoonotic virus with case fatality rates ranging from 40% to 75%, depending on outbreak conditions and healthcare capacity. Considering case fatality rates ranging from 40% to over 75%, the Nipah virus is a highly pathogenic zoonotic virus that occasionally causes epidemics of severe encephalitis and respiratory sickness in humans. Ever since it first appeared in Malaysia in 1998–1999, in South and Southeast Asia, the Nipah virus has frequently caused epidemics, especially in Bangladesh and India. The principal natural reservoir hosts have been identified as fruit bats of the genus *Pteropus* through extensive epidemiological, ecological, and molecular investigations. Transmission occurs through direct bat-to-human spillover, exposure to infected intermediate animal hosts, consumption of contaminated food products, and human-to-human transmission. This article synthesizes current evidence on the virology, transmission dynamics, epidemiology, clinical manifestations, diagnosis, treatment, and prevention of Nipah virus infection, with emphasis on recent Indian outbreaks. Recent advances in rapid molecular diagnostics, monoclonal antibody–based therapeutics, antiviral candidates, and vaccine development platforms are also critically discussed. Given its epidemic potential, high mortality, and absence of licensed vaccines or specific antiviral therapies, continued surveillance, strengthened outbreak preparedness, and accelerated research into effective medical countermeasures remains public health priority.

Keywords: *Emerging infections, Encephalitis, Nipah virus, One Health, Public health, Zoonotic disease*

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1. Introduction

Despite advances in medical sciences, communicable diseases remain a major challenge to the public health authorities worldwide. Approximately 75% of emerging infectious diseases are of zoonotic origin, and 60% of known human infectious diseases are zoonotic, posing a serious threat to global health security [1]. The creation of novel viruses that can cross species barriers has been hastened by rapid environmental changes, deforestation, agricultural intensification, wildlife commerce, and greater human–animal interactions. Among these emerging zoonotic pathogens, Nipah virus has been recognized by the World Health Organization (WHO) as a priority pathogen because of its high case-fatality rate, epidemic potential, broad host range, and the absence of licensed vaccines or specific antiviral therapies [2].

The World Health Organization documented seasonal outbreaks of Nipah in Bangladesh with 11 cases and eight deaths (~73% case-fatality) between January and February 2023, noting high national risk and low global risk, and urged enhanced surveillance, infection control, and public awareness to reduce transmission. The Nipah virus belongs to a member of the *Paramyxoviridae* family, specifically the genus *Henipavirus.* The virus was initially discovered during a severe encephalitis outbreak that affected pig farmers in Malaysia and Singapore during 1998 and 1999, resulting in over 260 human cases and 105 fatalities [3]. According to epidemiological studies, the outbreak was caused by infected pigs that served as amplifying hosts after contracting the disease from fruit bats [4].

Subsequent outbreaks in Bangladesh and India revealed a distinct epidemiological pattern characterized by recurrent bat-to-human spillover events and sustained human-to-human transmission. These outbreaks were frequently linked with the consumption of raw date palm sap contaminated by bat saliva, urine, or other excreta [5,6]. In contrast to the Malaysian outbreak, outbreaks caused by the Bangladesh lineage of Nipah virus have demonstrated higher case-fatality rates and greater propensity for person-to-person transmission, raising

concerns regarding the virus's pandemic potential. There have been several Nipah virus epidemics in India, most notably in Kerala (2018, 2019, 2021) and West Bengal (2001, 2007). With a case fatality rate of almost 85%, the 2018 Kerala outbreak exposed serious weaknesses in infection control, quick diagnosis, and surveillance [7]. Although subsequent outbreaks were rapidly contained through coordinated public health interventions, recurrent spillover events underscore the continued circulation of Nipah virus in bat populations and the persistent risk of emergence in ecologically vulnerable regions**.** Future outbreaks are still quite likely due to Nipah virus's ongoing circulation in bat reservoirs and ideal ecological circumstances for spillover. Among these emerging zoonotic pathogens, Nipah virus (NiV) has been recognized by the World Health Organization as a priority pathogen because of its high case-fatality rate, epidemic potential, broad host range, and the absence of licensed vaccines or specific antiviral therapies [8,9]. In contrast to the Malaysian outbreak, outbreaks caused by the Bangladesh lineage of Nipah virus have demonstrated higher case-fatality rates and greater propensity for person-to-person transmission, raising concerns regarding the virus's pandemic potential [9,10]. The present communication delineates the resurgence of the Nipah virus in India. In addition, pathogenesis, clinical spectrum, epidemiology, diagnostic approaches, and therapeutic advances are also discussed.

2. Review of Literature

2.1. Reservoir and Transmission

a. Natural Reservoirs

The natural reservoir of Nipah virus has been identified as fruit bats belonging to the genus *Pteropus* [11]. Extensive serological, molecular, and ecological investigations conducted across South and Southeast Asia have demonstrated widespread exposure to Nipah virus and related henipaviruses in *Pteropus* bat populations, often in the absence of clinical disease, suggesting long-term virus–host co-evolution and adaptation [9,12]. Evidence of viral RNA, antibodies, and virus shedding has been reported in several *Pteropus* species, supporting their role as the primary reservoir hosts responsible for maintaining Nipah virus in nature [12,13].

b. Transmission Pathways

Nipah virus is transmitted to humans over multiple pathways. During the Malaysian outbreak of 1998–1999, pigs acted as intermediate amplifying hosts, facilitating extensive transmission to humans through close occupational exposure [4]. However, subsequent outbreaks in Bangladesh and India were mainly linked to direct bat-to-human transmission, especially through ingesting raw date palm sap contaminated with bat saliva, urine, or other excreta [5,6,9]. Other transmission routes include consuming fruits partially eaten or contaminated by infected bats, direct contact with infected animals or their bodily fluids [13,14]. Human-to-human transmission has been well documented, particularly among household contacts and healthcare workers. Studies from Bangladesh and India indicate that respiratory secretions, saliva, and close physical contact with infected individuals play a critical role in person-to-person transmission [9,15]. Nosocomial transmission has been reported in several outbreaks, emphasizing the importance of strict infection prevention and control measures in healthcare settings [16].

c. Ecological Drivers

Environmental changes such habitat fragmentation, urbanization, and deforestation have increased human, livestock, and bat contact, increasing the risk of spillover [17]. Alterations in bat foraging behavior caused by habitat loss and food scarcity may increase viral shedding and facilitate spillover events in human-dominated landscapes [12]. Seasonal factors, including bat food scarcity, also have an impact on spillover incidents. Fruit bats of the genus *Pteropus* are naturally infected with the Nipah virus. These bats discharge the virus in their saliva, urine, and faeces while carrying it asymptomatically. Humans can get the disease by swallowing raw date palm sap contaminated by bat secretions, eating infected fruits, or coming into close contact with diseased bats. [18]. Seasonal patterns of spillover have also been observed, particularly during periods when bats aggregate around food sources and when the harvesting of fresh date palm sap is common, contributing to recurrent outbreaks in Bangladesh and neighbouring regions [12,14]. Pigs and other domestic animals have acted as intermediate hosts in previous outbreaks. The virus's nosocomial potential has been highlighted by several outbreaks in India that have demonstrated effective human-to-human transmission, particularly among family carers and medical professionals [7,16]. The recurrent occurrence of spillover events, combined with ecological disruption and increasing human encroachment into wildlife habitats, underscores the importance of adopting a One Health approach for Nipah virus surveillance, prevention, and control [9,13].

2.2. Clinical Manifestation and Pathogenesis

The average incubation period for Nipah virus infection is 4 to 14 days, while longer incubation durations of up to 45 days have been reported [2,19]. The nonspecific initial symptoms include fever, headache, myalgia, sore throat, nausea, and vomiting. As the condition develops, many people develop acute encephalitis, which is characterised by altered awareness, confusion, seizures, and coma [20]. The broad clinical spectrum and nonspecific prodromal manifestations often complicate early diagnosis, particularly in regions where multiple febrile illnesses are endemic [13].

Respiratory involvement, such as cough, dyspnoea, and acute respiratory distress syndrome (ARDS), has been more commonly reported in outbreaks associated with the Bangladesh strain of the Nipah virus and is strongly associated with increased human-to-human transmission [6]. Severe respiratory involvement may occur concurrently with encephalitis and has been identified as an independent predictor of poor clinical outcomes [16]. Particularly in residential and medical settings, respiratory symptoms have been identified as a major risk factor for secondary transmission.

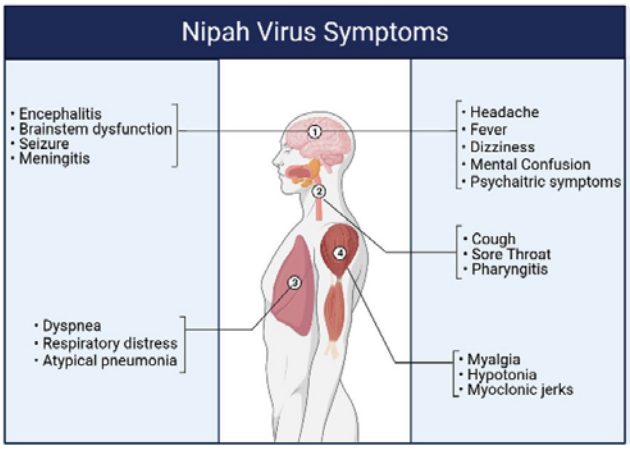

Figure 1. Clinical symptoms exhibited by Nipah virus affected patients [Source: 21]

One characteristic and concerning feature of Nipah virus infection is relapsing or late-onset encephalitis, which can manifest months or even years after the original illness [22]. These instances show viral persistence in the central nervous system and create additional challenges for long-term patient management. The pathogenic characteristics of Nipah virus infection include systemic vasculitis affecting small and medium-sized blood vessels, endothelial cell death, thrombosis, and parenchymal necrosis, particularly the brain and lungs which are the most severely affected organs. [23]. Neurological manifestations may also include segmental myoclonus, brainstem dysfunction, abnormal reflexes, and autonomic instability, reflecting extensive central nervous system involvement [13,24].

Neurones and endothelial cells exhibit viral antigens, which are consistent with the virus's preference for ephrin-B2 and ephrin-B3 receptors [25]. Immune-mediated damage and dysregulated inflammatory responses also have an impact on disease severity and death. After entering the human host, Nipah virus binds to ephrin-B2 and ephrin-B3 receptors, which are widely expressed on endothelial cells and neurons. Viral replication leads to endothelial damage, vasculitis and thrombosis, resulting in multi-organ dysfunction. The virus can cross the blood–brain barrier, leading to severe encephalitis, which is the hallmark of Nipah virus infection [24]. Immune-mediated injury further exacerbates disease severity, contributing to high mortality rates.

The incubation period for Nipah virus infection is between 4 and 14 days, although incubation times of up to 45 days have been reported [2,19]. Among the nonspecific initial symptoms include fever, headache, myalgia, sore throat, nausea, and vomiting. As the condition progresses, many people get acute encephalitis, which is characterized by altered awareness, disorientation, seizures, and coma [20]. In outbreaks linked to the Bangladesh strain of the Nipah virus, respiratory involvement including cough, dyspnoea, and acute respiratory distress syndrome, has been recorded more frequently and is strongly linked to increased human-to-human transmission [6,21]. Respiratory symptoms have been found to be a significant risk factor for secondary transmission, especially in home and healthcare environments**.** Relapsing or late-onset encephalitis, which may appear months or even years after the initial sickness, is a distinctive and worrisome aspect of Nipah virus infection [22]. Clinical manifestations of relapsing encephalitis include recurrent seizures, focal neurological deficits, personality changes, and progressive cognitive impairment, suggesting viral persistence within the central nervous system [9,24]. These examples raise new issues for long-term patient care and indicate viral persistence in the central nervous system.

Pathologically, Nipah virus infection is characterized by endothelial cell destruction, thrombosis, parenchymal necrosis, and systemic vasculitis that affects small and medium-sized blood vessels, especially in the brain and lungs [23]. In line with the virus's preference for ephrin-B2 and ephrin-B3 receptors, viral antigens have been found in endothelial cells and neurons [25]. Immune-mediated injury and dysregulated inflammatory responses further contribute to disease severity and mortality. Recent investigations have also highlighted the role of dysregulated innate and adaptive immune responses, excessive cytokine production, and inflammatory-mediated tissue injury in disease progression and mortality. The ability of NiV to penetrate the blood–brain barrier and establish infection within the central nervous system is considered a hallmark of severe disease [24]. Combined direct viral cytopathic effects, vascular injury, and host inflammatory responses contribute to the exceptionally high case-fatality rates observed during Nipah virus outbreaks [9,13].

2.3. Epidemiology

Nipah virus is an emerging zoonotic pathogen with a geographically restricted but highly significant public health impact. Since its first recognized outbreak in Malaysia and Singapore during 1998–1999, recurrent outbreaks have been reported primarily in Bangladesh and India, with case-fatality rates frequently ranging from 40% to 75% and occasionally exceeding 80% [7,8]. Bangladesh has reported almost annual outbreaks since 2001, making it the country with the highest number of documented Nipah virus outbreaks worldwide. These outbreaks are typically associated with the consumption of raw date palm sap contaminated by infected fruit bats and are characterized by substantial human-to-human transmission [6,9].

In contrast, outbreaks in India have been relatively sporadic but have often been associated with high mortality and significant public health concern [7,13]. In India, Nipah virus outbreaks have been reported predominantly from West Bengal (2001 and 2007) and Kerala (2018, 2019, 2021, 2023, and 2024). The 2018 Kerala outbreak was particularly notable because of its high case-fatality rate and documented human-to-human transmission, prompting extensive public health interventions [7]. The harvesting and consumption of fresh date palm sap, cultivation of fruit-bearing trees near human settlements, and close proximity between livestock, bats, and humans further facilitate spillover events [6,14]. Molecular epidemiological studies have identified two major Nipah virus lineages: the Malaysia strain (NiV-MY) and the Bangladesh strain (NiV-BD). The Bangladesh lineage has been associated with higher pathogenicity, greater respiratory involvement, and increased human-to-

human transmissibility, which may partly explain the epidemiological differences observed between outbreaks in South Asia and those in Malaysia [9,13].

Figure 2. Timeline of Nipah virus outbreaks reported in Kerala (2018–2026). Information compiled from published news reports and official health updates [26]

Figure 3. Geographic distribution of bat sampling sites and reported Nipah virus occurrences, along with phylogenetic relationships of Nipah virus isolates from South and Southeast Asia. [Source: 27]

2.4. Diagnosis

Several laboratory techniques, such as virus isolation, serum neutralization, enzyme linked immunosorbent assay (ELISA), reverse transcription polymerase chain reaction (RT-PCR), and immunohistochemistry are employed to confirm the diagnosis of Nipah virus infection [28]. Reverse transcription polymerase chain reaction is a molecular detection of viral RNA, which is the mainly used in laboratories to confirm Nipah virus infection. Blood, cerebrospinal fluid, urine, throat and nasal swabs, and other clinical specimens are frequently employed for diagnosis. RT-PCR demonstrates the highest diagnostic sensitivity during the acute phase of illness when viral loads are elevated and can facilitate rapid confirmation during outbreak investigations [13].

Nipah virus-specific IgM and IgG antibodies can be found by serological tests, such as ELISA [28]. Because of the virus's severe pathogenicity, assays for virus isolation and neutralization are regarded as confirmatory and must be carried out in biosafety level-4 (BSL-4) facilities. In endemic areas, limited access to high-containment labs and diagnostic facilities continues to be a significant problem that frequently causes delays in diagnosis and outbreak response [7]. Therefore, improving regional diagnostic capabilities is essential to readiness. For outbreak containment, early and precise diagnosis is essential. Reverse transcription polymerase chain reaction (RT-PCR) involves molecular detection of viral RNA from blood, cerebrospinal fluid, throat swabs, and urine samples is necessary for laboratory confirmation. IgM and IgG antibodies are found during later stages of infection using serological tests like ELISA. Diagnostic procedures must be carried out in biosafety level-4 laboratories or well-prepared reference facilities due to the severe pathogenicity of Nipah virus [2]. Recent advances in molecular diagnostics have facilitated the development of rapid point-of-care assays, portable nucleic acid amplification platforms, and CRISPR-based diagnostic technologies that may improve early detection in resource-limited settings [8]. Although many of these technologies remain under evaluation, they hold promise for strengthening outbreak preparedness and reducing diagnostic turnaround times.

2.5. Treatment and Therapeutic Advances

Currently, there is no licensed antiviral therapy specifically approved for the treatment of Nipah virus infection. Consequently, clinical management remains largely supportive and focuses on early recognition, intensive monitoring, maintenance of vital organ functions, management of neurological complications, respiratory support, and mechanical ventilation when required [2,13]. Timely diagnosis and prompt supportive care are considered critical determinants of survival and may substantially improve clinical outcomes during outbreaks [16].

Although ribavirin was used empirically during the Malaysian outbreak and was linked to a decrease in mortality in observational studies, there is still conflicting data on its effectiveness [29,30]. As a result, ribavirin is not considered a definitive treatment option. The development of monoclonal antibody treatments has advanced significantly. During outbreaks in Australia and India, exposed people have received the human monoclonal antibody m102.4 on a compassionate-use basis due to its strong neutralizing efficacy against the Nipah virus in animal models [31,32]. Despite the paucity of clinical trial evidence, m102.4 is among the most promising treatment possibilities to date**.**

Recent advances in Immunotherapeutics have expanded beyond m102.4 to include next-generation neutralizing monoclonal antibodies and antibody cocktails designed to target multiple viral epitopes, thereby reducing the risk of viral escape mutations. Furthermore, advances in structural biology and immunogen design are facilitating the development of broadly protective therapeutic strategies against henipaviruses [10]. Preclinical investigations have demonstrated the effectiveness of several antiviral drugs, such as favipiravir and remdesivir, against Nipah virus; however, strong clinical evidence is still absent [33]. Further investigation and clinical assessment of antiviral treatments continue to be priorities. As of right now, there isn't a specific antiviral medication that is authorized to treat Nipah virus infection. The majority of clinical care, including critical care, mechanical ventilation, and

neurological problem management, is still supportive. Experiments using ribavirin have yielded conflicting outcomes. Antiviral drugs and monoclonal antibodies are being studied, providing promise for potential treatments in the future [34].

2.6. Prevention and Control

Prevention of Nipah virus infection requires a comprehensive, multimodal strategy aimed at both reducing zoonotic spillover events and interrupting human-to-human transmission. Because fruit bats of the genus Pteropus serve as the natural reservoir, interventions that minimize human exposure to bat-contaminated food products are of paramount importance. In Bangladesh and India, the use of bamboo skirts or physical coverings on date palm sap collection pots has been shown to significantly reduce bat access and contamination of sap, thereby decreasing the risk of Nipah virus transmission [35].

Public health interventions should focus on avoiding the consumption of raw date palm sap, preventing contact with sick animals, and discouraging the consumption of fruits contaminated by bat secretions [6,14]. Community-based awareness programs, culturally appropriate risk communication, and behavioural change interventions have proven effective in reducing high-risk practices associated with Nipah virus transmission [9,21]. Strict infection prevention and control (IPC) measures are essential to prevent nosocomial transmission—the spread of infections within healthcare settings. [15]. These measures include the use of personal protective equipment (PPE) to safeguard healthcare workers and patients from infection, hand hygiene, early case identification, patient isolation, environmental decontamination, and the safe handling of clinical specimens and bodily fluids. Healthcare workers should receive regular training in outbreak preparedness and infection control protocols, particularly in regions at risk for recurrent Nipah virus outbreaks [16].

Contact tracing, quarantine of exposed individuals, active surveillance, and timely laboratory confirmation are critical components of outbreak containment [1]. Rapid response teams, integrated disease surveillance systems, and coordinated public health communication strategies are essential for limiting secondary transmission and ensuring effective outbreak management [8,13]. The One Health approach, which integrates human, animal, and environmental health, has become a cornerstone of Nipah virus prevention and control. Coordinated surveillance in wildlife reservoirs, livestock populations, and human communities facilitates early detection of spillover events and supports evidence-based intervention strategies [36,37]. Strengthening ecological surveillance, monitoring bat populations, reducing environmental risk factors, and enhancing community participation are fundamental to sustainable Nipah virus control programs [12,13].

2.7. Vaccine Development

Nipah virus is designated as a priority pathogen that needs immediate investigation and development [2]. In animal models, a number of vaccination platforms, such as recombinant subunit vaccines, viral vector-based vaccines, and virus-like particle vaccines, have shown protective effectiveness [38,39]. Many vaccine candidates target the highly conserved Nipah virus glycoprotein (G protein), which plays a critical role in viral attachment and host-cell entry [10]. Among the leading candidates, the HeV-sG subunit vaccine, originally developed against Hendra virus, has demonstrated cross-protective immunity against Nipah virus in multiple animal studies [38]. More recently, several CEPI-supported vaccine candidates have progressed into early-phase clinical development, representing an important milestone in global Nipah virus preparedness efforts [13,40]. No vaccine has been approved for use in humans despite encouraging preclinical findings. The intermittent nature of outbreaks, the lack of commercial incentives, and the logistical and ethical challenges of carrying out extensive efficacy trials are some of the challenges. The Coalition for Epidemic Preparedness Innovations (CEPI) is spearheading international efforts to expedite clinical testing and vaccine development.

3. Conclusion

With several outbreaks documented over the previous ten years and the most recent cluster recorded in Kerala in 2025, Nipah virus is a significant and recurrent public health concern in India as of 2026. These incidents demonstrate the persistent risk of zoonotic spillover caused by ecological disturbance, seasonal variables, and human behavioural patterns, as well as the ongoing circulation of Nipah virus in fruit bat reservoirs. The fact that outbreaks continue to occur in spite of increased knowledge highlights the necessity of ongoing attention to detail and long-term planning.

Recent outbreaks in India have shown quantifiable advancements in coordinated epidemic response, contact tracking, and quick case detection. However, there are still issues with risk communication, early clinical identification, peripheral laboratory confirmation, and nosocomial transmission avoidance. Together with the lack of approved vaccines and targeted antiviral treatments as of 2026, the persistently high case fatality rate restricts treatment options and emphasizes the significance of prevention-focused approaches. For risk reduction and early warning, it is still essential to fortify integrated surveillance systems at the human-animal-environment interface. The best foundation for controlling Nipah virus is offered by the One Health approach, which places a strong emphasis on community involvement, health system readiness, and coordinated surveillance in bats and domestic animals. To lessen the effects of future outbreaks and safeguard India's most vulnerable communities, ongoing investments in vaccine research, monoclonal antibody development, and public health infrastructure are crucial. Continued investment in vaccine development, monoclonal antibody therapies, antiviral research, ecological surveillance, and public health infrastructure will be essential for improving preparedness and mitigating the impact of future Nipah virus outbreaks.

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Author Contributions

All the authors contributed equally to the conception, drafting, and critical revision of this manuscript.

Conflict of Interest

The authors declare no conflicts of interest.

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