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Article Review

Nipah Virus Transmission Dynamics: Zoonotic Origins, Human Spread, and Control Strategies

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ABSTRACT

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A member of the Paramyxoviridae family, Nipah virus is one of the re-emerging viruses as a public health concern since it was first detected at the turn of the century in the late 1990s. Case fatality rates during outbreaks ranged between 40% and 75%, with recurrent cases in Bangladesh, India, and Malaysia. Surveillance data indicate the possibility of virus development in new areas since there is virus circulation among Pteropus bats in larger regions of South and Southeast Asia. It appears to be of zoonotic origin, transmitted mainly from fruit bats to humans. This makes zoonotic transmission a complex interaction between wildlife and human health, implying the significant role of ecology dynamics in the prevention and control of outbreaks. This understanding of routes of transmission has given basis to the devising of evidence-based interventions, including the protection of date palm sap collection sites and enhancement of infection prevention practices in hospitals, which will be very critical for controlling outbreaks and preventing future epidemics. This discussion on Nipah virus transmission dynamics calls for going into detail regarding the zoonotic source and mode of human-to-human transmission that enables human beings to prevent and control this disease.

INTRODUCTION

A zoonotic paramyxovirus commonly known as the Nipah virus (NiV) has been an important public health challenge in South and Southeast Asia. Since it was first isolated in Malaysia in 1998, NiV has mainly caused epidemics in Bangladesh and India, characterized by high case-fatality rates (Pillai, Krishna, and Veettil 2020) (Joshi et al. 2023) (Singhai et al. 2021). Recent epidemics are an example of its continuing presence: Kerala, India, had severe epidemics in 2018 and 2019, killing 17 of the 19 cases in 2018. 33 outbreaks have been reported in Bangladesh from 2001 to 2023; the last epidemic in 2023 killed 14 out of 16 confirmed cases in 7 districts. Outside Malaysia, where the virus was first detected in 1998–1999, it has spread geographically; already identified cases are present in Bangladesh, Singapore, the Philippines, and India. As specific treatments or vaccines are lacking, NiV is now one of the priority pathogens needing immediate attention from scientists according to the WHO. Since its discovery, the transmission dynamics of the Nipah virus have totally changed. The subsequent outbreaks have revealed various modes of transmission, such as bat-to-human direct transmission and human-to-human spread within healthcare settings, but the first Malaysian pandemic was almost entirely pig-to-human. The paper will be an attempt to comprehend the transmission dynamics of the Nipah virus in the light of different geographical scenarios, with spillover events from zoonotic origins and participation by intermediate hosts. Moreover, chains of human-to-human transmissions need to be comprehended for proper formulating of prevention and control measures in sensitive areas.

The purpose of this article is to understand the dynamics of Nipah virus transmission, from its zoonotic source (fruit bats) to human-to-human transmission. This discussion will cover how the virus moves from animals to humans, the role of intermediate animals, and the ways of human-to-human transmission that occur in community and hospital settings. In addition, this article aims to provide an overview of control strategies that can be applied to prevent the further spread of this virus, emphasizing the importance of a "One Health" approach, surveillance, and public awareness of virus transmission.

RESEARCH METHODS

This article uses a literature review approach to explore the available information on the dynamics of Nipah virus transmission in various affected countries. Data sources were obtained from published epidemiological research and reports, including studies on epidemiology, geographical distribution, pathogenesis, and predictive risk models that describe the likelihood of the virus spreading to new areas. This information is used to analyze patterns of viral transmission in nature and society, and to suggest appropriate control measures..

RESULTS AND DISCUSSION

Epidemiology and Geographic Distribution

Outbreaks of NiV have been reported in the Philippines, Malaysia, Singapore, Bangladesh, and India (Bruno et al. 2023). The virus is endemic in Bangladesh where outbreaks occur almost every year in the "Nipah belt" of the country (Faus-Cotino, Reina, and Pueyo 2024). Case fatality rates for the disease have risen steadily overtime. Case fatality during the initial outbreak in Malaysia was about 40% while it has recently risen as high as 93% in subsequent outbreaks (Goh et al. 2020) (Hauser et al. 2021).

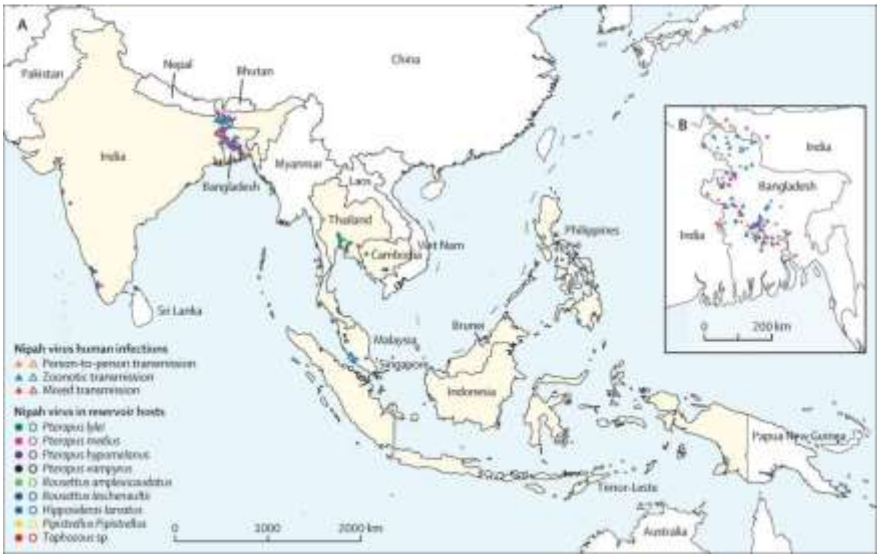

Figure 1. Map representation of Geographical Distribution of Nipah Virus(Sun et al. 2024)

The interrelated environmental, agricultural, human, and healthcare factors are some of the factors that make it possible for the Nipah virus to remain persistent and be transmitted in endemic areas. Environmental disturbances, such as habitat loss and deforestation, increase the risk of viral transmission between Pteropus bats and human populations. In areas where the level of farm biosecurity is not adequate, there are transmission points through traditional farming activities such as high intensity pig farming and unprotected harvesting of date palm sap.

Human behavior increases the risks by eating raw sap and fruits contaminated with bats, while lack of knowledge and personal protective equipment on the part of the workers increase the risks. Health-care settings provide avenues for human-to-human transmission with poor infection control and delays in case recognition, especially within institutions with low resources. Customs such as traditional burials and close-knit communities add to the risk during an outbreak.

Reservoir and Transmission

The natural reservoirs were fruit bats of the genus Pteropus, especially P. medius in Bangladesh (Epstein et al. 2020) (Letko et al. 2020). Human infection can be acquired through several routes of transmission.

Direct bat-to-human transmission:

The direct transmission of the disease happens by contact with infected bats or their excreta. People that work closely near habitats of bats, researchers, cave workers, and inhabitants in areas with bats, are primarily affected. Based on research done in Southeast Asia, transmission levels within groups exposed frequently were 2 to 3%. The virus usually enters into the body through mucous membranes or skin breaks after direct contact with bat secretions or guano. Some of the environmental factors which influence the risk of transmission include habitat disturbance and seasonal bat behavior patterns (Faus-Cotino et al. 2024) (Epstein et al. 2020).

Intermediate host amplification:

The intermediary animals between bats and humans are part of this pathway of transmission, which allows viruses to evolve and become efficient human infectors. Both domestic and wild animals are very important intermediate hosts; the transmission rates have been reported to range from 15% to 30% in some species. There are mechanisms of viral replication and potential genetic changes in these hosts, which enhance the virus's ability to infect human cells. It is through this mode that the geographical distribution of cases near rural communities and wildlife markets has brought into relevance (Bruno et al. 2023) (Hauser et al. 2021).

Human to human transmission:

There are two settings in which human-to-human transmission occurs, namely, healthcare settings and community settings. The secondary attack rates among workers during outbreaks in healthcare settings range between 10 to 20%. The secondary attack rates are mainly due to direct contact and aerosol exposure during medical procedures. Household secondary attack rates in communities range between 15 to 35%, depending on environmental factors and population density. Preventive measures might reduce spreading by as much as 60% in indoor environments, but all of that is lost with confined spaces and improper ventilation (Singhai et al. 2021) (Hauser et al. 2021).

Scientists have documented that the transmission of NiV occurs throughout the year in bat populations across Bangladesh. Density-dependent factors, acquired immunity, and viral recrudescence modulate local-scale transmission dynamics (Epstein et al. 2020).

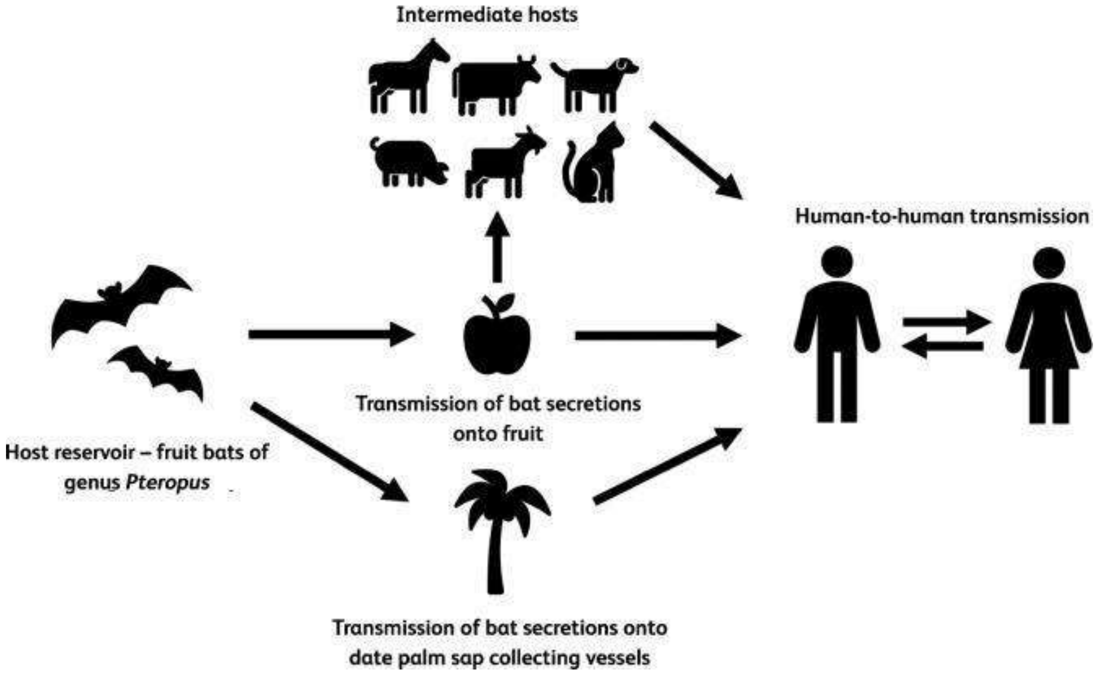

Figure 2. Schematic representation of Nipah Virus Transmission(Alam et al. 2022)

Pathogenesis and Clinical Presentation

In humans, infection with NiV presents usually with severe respiratory disease and/or encephalitis (Faus-Cotino et al. 2024; Pillai et al. 2020). The interferon (IFN) signaling pathway has been the main target for the many complex strategies through which the virus avoids the host defense responses. Direct inhibition with STAT1/STAT2 phosphorylation cascades suppresses type I IFN production, which is an important part of viral pathogenesis. This interference weakens the initial antiviral response of the host severally, and thus allows the virus to replicate speedily in the target tissues (Liew et al. 2022). The virus also has a marvellous ability of pathway alteration that leads towards cellular death particularly by blocking apoptosis and manipulation of the mechanisms of autophagy in infected cells. Sustained alterations in the humoral as well as cellular responses point towards an equivalent influence on the adaptive immune response. There is already research which has indicated derangement of dendritic cell functions along with considerable diminishment of T-cell activation as well as proliferation. Cell counts are usually below 800 cells/μL in a severe case of lymphopenia, which commonly presents as a manifestation of this adaptive immunity disturbance (Liew et al. 2022). Additionally, the virus also disrupts B-cell response through the induction of neutralizing antibodies whose appearance might be delayed or be insufficient and therefore increase the severity of disease.

Clinical Manifestations and Disease Progressions

Presentation of the disease occurs after incubation time of 3–14 days; however, a wide variability is reported due to varying initial viral loads and different modes of transmission. In clinical manifestations, it also includes serious neurological complications, some mild respiratory manifestations, and multi-organ failure at times. The first common symptoms are fever in over 90% of the cases followed by neurological symptoms including headache and altered consciousness or respiratory symptoms including cough and dyspnea. Such wide variation in clinical presentations does not allow an easy early diagnosis of the patient with the right treatment. The disease course is described as a generally predictable progression divided into three distinct phases. The mild, frequently non-specific symptoms are present throughout the early phase (days 1-3) and it is difficult to diagnose. A marked increase in inflammatory markers and organ-specific symptoms develop during the peak phase (days 4-7). The hallmarks of the crucial phase are an onset of healing processes or a sharp decline with complications that occur after day 8. Case fatality rates may vary substantially (25–75%) depending on the prevalent form of disease and at what point in the course of disease treatment intervention is begun.

Risk Factors and Predictive Modeling

By overlaying ecological niche models for P. lylei onto regional data on cattle density, fruit production, and human population, the researchers constructed risk maps for NiV spillover in Thailand, Cambodia, and Vietnam (Chaiyes et al. 2022). Their models forecast expansion of suitable bat habitat under climate change may yield new areas of risk for human infection.

For instance, through case studies in Thailand and Cambodia, predictive modeling studies conducted in Southeast Asia have greatly improved our understanding of the risks associated with bat-borne disease transmission. Bat breeding cycles are correlated with seasonal fluctuations in 23 high-risk areas in central and eastern Thailand, according to Species Distribution Models monitoring Pteropus lylei colonies. Since climate change is going to increase the acceptable bat habitat by 15% by 2050, early warning systems will be established in 12 provinces. Environmental niche modeling for Cambodia's study on Cardamom Mountains and Mekong River floodplains revealed eight new possible spillover hotspots. Research works demonstrated that human-bat interaction areas will increase near areas of agriculture, and area expansion in the northeastern directions is expected to be by 20%. In general, by 2030–2050, with the influence of climate warming, the area of optimal habitat is expected to enlarge by 25–30%, and species are assumed to spread northward along with the formation of the interface zones between urban areas and wildlife. The main places where emerging risk areas emerge are industrial parks next to bat roosting areas and urban growth areas that overlap residential buildings into the forest. There has been unprecedented movement of bats across human regions along climate-driven migration corridors, and it is something that calls for increased observation.

Community readiness programs, surveillance for diseases, and population monitoring in real time are some of the mitigation techniques for the risk. These are establishment of integrated regional surveillance networks, the impact of climate change on the evolution of diseases, and filling data gaps in long-term bat population dynamics.

Public health interventions will require further advances in predictive modeling techniques while bat habitats remain under changes from human development and climatic change. It is only through workable integration of these modeling techniques into public health initiatives and the tactics of engaging the communities that disease outbreaks will be stopped.

Control Strategies

Prevention and control of NiV outbreaks are very multi-scale issues :

Monitoring: Research has provided a framework with six epidemiologic indicators to monitor changes in spillover risk, interhuman transmission, and morbidity/mortality (Nikolay et al. 2020). One Health Approach: Study suggested multi-sectorial coordination between the human health, animal health, and environmental sectors to respond to NiV outbreaks (Singhai et al. 2021). Biosecurity Practices: Maintenance of high level biosecurity agriculture, livestock practices, and health care at all junctures are most critical in preventing transmission (Orosco 2023).

Vaccination: There are several possibilities, including live-attenuated vaccine virus-like particle vaccines and mRNA-based vaccinations. Amaya and Broder summarize the current state of NiV vaccine development focusing on approaches tested within animal challenge models 2020 (Amaya and Broder 2020).

Antiviral Agent Discovery: Several antiviral agents, including remdesivir, ribavirin, and favipiravir, are found to have potential in inhibiting NiV replication (Orosco 2023). Public Awareness: Study revealed that in communities, the knowledge about bat ecology and NiV transmission is very poor and targeted educational interventions are required (Hassan et al. 2020).

CONCLUSION

NiV will remain a public health threat for South and Southeast Asia and has the potential for greater geographic spread. Its high pathogenicity, human-to-human transmissibility, and lack of approved therapeutics position it as a priority pathogen for pandemic preparation. Future research into viral ecology, pathogenesis, and host-pathogen interaction will play an important role in preparing to decrease the chances of future NiV disease outbreaks, since research into effective vaccines and treatments is required..

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