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EPIDEMIOLOGICAL PATHWAYS OF NIPAH VIRUS TRANSMISSION

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Abstract

Nipah virus (NiV) is a highly lethal zoonotic pathogen, the reservoir of which is bats of the genus Pteropus. The article analyzes the main ways of its spread: direct (through contaminated food and juice) and indirect (through pigs, horses) zoonotic spillover, as well as interhuman transmission through close contact. Regional differences in epidemiology between the countries of South and Southeast Asia are shown. Preventive measures should be aimed at breaking these chains through improved food hygiene, biosafety of animal husbandry, strict infection control and the "One Health" approach.

Keywords

Nipah virus, Pteropus, zoonotic transmission, interhuman transmission, food route, pigs, date juice, One Health.

Introduction

Nipah virus (NiV) is a recently identified zoonotic paramyxovirus that causes severe outbreaks with a mortality rate of 40-75% or higher in countries of South and Southeast Asia [1,6,11,14,16]. Since it was first described in Malaysia in 1998-1999, the infection has been reported in Malaysia, Singapore, Bangladesh, India, and the Philippines, with outbreaks occurring almost annually in Bangladesh and India

[1,3,6,11,16]. The natural reservoir of NiV is fruit bats of the Pteropodidae family, primarily of the *Pteropus* genus, which are widely distributed in Asia, Oceania, and Africa [1,3,6,8,11,12]. Humans become infected through zoonotic spillover involving bats and intermediate hosts (such as pigs and horses), as well as through human-to-human transmission [1,2,4,6,8]. Understanding the epidemiological transmission pathways is critical for predicting risk, developing preventive measures, and substantiating intersectoral surveillance programs.

The objective of this article is to analyze the main epidemiological transmission pathways of the Nipah virus, their regional specificities, and the factors that determine the risk of outbreaks.

Natural reservoir and prerequisites for spillover

The role of bats of the *Pteropus*

Fruit bats *(Pteropus* spp.) are the primary natural reservoir of NiV; viral RNA and antibodies have been repeatedly detected in them in the absence of pronounced disease [1,6,8,11,16]. The virus is excreted in saliva, urine, and feces, contaminating fruits, juice, and feed for domestic animals [1,8,11,16]. The geographical overlap of *the Pteropus* habitat with NiV hotspots, as well as the ability of bats to migrate and inhabit anthropogenic landscapes (orchards, farms), creates a stable basis for recurring spillovers [1,6,8,11,12,19].

Ecological and anthropogenic factors

Deforestation, changes in land use, urbanization, and the expansion of agricultural land lead to increased contact between bats, domestic animals, and humans [1,5,8,11,12,19]. Intensive livestock farming, high-density pig farms, and the proximity of orchards or palm plantations to bat colonies increase the likelihood of the virus entering production and food chains [1,5,8,12].

Zoonotic transmission routes

Bats → humans via food

In Bangladesh and parts of India, the dominant epidemiological route is foodborne transmission. Bats visit vessels used for collecting raw date palm sap, contaminating them with saliva and urine; humans become infected when consuming the untreated sap and products made from it [2,3,6,7,11,16]. The seasonality of outbreaks coincides with the sap harvesting period in winter, and epidemiological studies consistently identify the consumption of raw date palm sap as a key risk factor [2,3,6,11,16].
An additional route is the consumption of fruit partially eaten or contaminated by bats, which also leads to the infection of humans and domestic animals [1,8,11,16,18].

Bats → pigs → humans

The first major NiV outbreak in Malaysia and Singapore was linked to pig farming [1,6.8,11]. Pigs became infected by eating fruit or feed contaminated with bat excretions, after which intensive pig-to-pig transmission with pronounced respiratory symptoms occurred on farms with high livestock density [1,6,8,11]. Human infection occurred during the care, treatment, slaughter, and processing of pigs through contact with their respiratory secretions, blood, and other bodily fluids [1,6,8,11,18]. In Malaysia, this pathway was the primary source of hundreds of human cases, while human-to-human transmission was minimal [6,8,10,11]. A systematic review of the global epidemiology of NiV confirms that in Malaysia the key route was transmission via infected pigs, whereas in other countries different routes dominate [6].

Bats → other domestic and wild animals → humans

NiV is capable of infecting a number of species, including horses, dogs, cats, goats, and cattle [1,8,11,12,16,18]. In the Philippines, an outbreak was associated with disease in horses and the consumption of their meat, indicating a bat-to-horse-to-human transmission chain [1,6,11,16]. Domestic animals that consume feed contaminated with bat excretions can become intermediate amplifying hosts and sources of the virus for humans [1,8,12].

Human-to-human transmission

Household and community contacts

Accumulated data from Bangladesh show that approximately one-third of NiV cases are due to human-to-human transmission; of 248 cases, 82 were secondary, and the mean reproductive number was 0.33. The risk is especially high with:

- prolonged contact with a patient (more than 48 hours; adjusted odds ratio 13);
- contact with bodily fluids (saliva, sputum, vomit, urine, blood; OR 4.3);
- spousal and other close family contact (infection rate in spouses 14% vs. ~1% in other relatives) [2].

Human-to-human transmission most often occurs when caring for severely ill patients with pronounced shortness of breath and cough, which underscores the importance of respiratory secretions as a source of infection [2,3,4,9]. Furthermore, serological screening of 1,863 asymptomatic contacts revealed no infections, indicating the primary role of clinically apparent cases in sustaining transmission chains [2].

Nosocomial outbreaks

Nosocomial clusters affecting medical personnel and other patients have been repeatedly described in outbreaks in India and Bangladesh [3,6,8,9,11,13]. Infection occurred due to the absence or insufficient use of personal protective equipment, especially during procedures involving close contact with respiratory secretions and blood (intubation, aspiration, resuscitation). Reviews emphasize that implementing basic infection control measures (masks, gloves, eye protection, hand hygiene, patient isolation) significantly reduces the risk of human-to-human transmission and can prevent hospital-acquired outbreaks [4,7,8,9,13].

Characteristics of Strains and Clinical Forms

Epidemiological and molecular data distinguish at least two main NiV clades: the Malaysian (NiV-MY) and the Bangladeshi (NiV-BD), as well as a distinct Indian variant [6,10,13,14]. NiV-MY is characterized by a predominance of zoonotic transmission via pigs and a low frequency of human-to-human transmission, whereas NiV-BD is associated with pronounced respiratory forms and more intensive person-to-person transmission [3,4,13,14]. Analysis of outbreaks shows that the presence of severe respiratory symptoms (shortness of breath) in a patient is a predictor of higher contagiousness and an increase in the reproductive number to values approaching 1, especially in older patients [2,4].

Regional Differences in Epidemiological Pathways

A systematic review of the global molecular epidemiology of NiV demonstrates that the primary transmission routes vary by country [6]:

- **Malaysia and Singapore (NiV-MY)** - Main route: "bats → pigs → humans"; human-to-human transmission is minimal [1,6,8,11].
- **Bangladesh** - Key routes: consumption of raw date palm sap (bats → humans) and human-to-human transmission within families and healthcare facilities [2,3,6,7,11,16].
- **India** - A combination of foodborne spillover, direct contact with bats/animals, and significant human-to-human transmission during outbreaks (e.g., in Kerala) [3,6,8,11,13].
- **Philippines** - Route via horses and consumption of their meat, with subsequent transmission to humans [1,6,8,11].

This geographical variability is explained by differences in livestock farming structures, dietary habits, bat ecology, and strain-specific characteristics of the virus [1,6,8,11,12,13,14].

Prevention and Breaking Epidemiological Chains

Foodborne and Zoonotic Routes

To reduce the risk of spillover through food and animals, the following measures are recommended [1,6,7,8,11,16]:

- using physical barriers (nets, lids) on containers for collecting date palm sap;
- avoiding the consumption of raw sap and ensuring it is heat-treated;
- restricting bat access to livestock feed and water troughs;
- improving biosecurity on pig farms and other agricultural holdings;
- veterinary surveillance of pigs, horses, and other potential intermediate hosts.

Human-to-Human Transmission and Infection Control

To break the chain of human-to-human transmission during NiV outbreaks, the key measures are [3,4,6,8,9,11,13]:

- early identification of cases and isolation of patients with suspected NiV;
- use of personal protective equipment (PPE) (masks, gloves, eye protection, gowns) when caring for patients;
- strict hand hygiene and limiting the number of caregivers;
- safe handling of the bodies of the deceased and avoidance of practices involving close, unprotected contact.

Main Transmission Routes of the Nipah Virus

Summary of Main Zoonotic and Human-to-Human NiV Transmission Pathways

Transmission Pathway	**Mechanism and Context**	**Typical Regions**	**Citations**
Bats → Human (food)	Raw date palm sap, fruit	Bangladesh, India	[1,2,3,6,7,11,16]
Bats → Pigs → Human	Contaminated feed, contact with pigs	Malaysia, Singapore	[1,6,8,10,11,18]
Bats → Other animals → Human	Horses, goats, dogs, cats, cattle	Philippines, other outbreaks	[1,8,11,12,16,18]
Human → Human	Close contact, biofluids, healthcare facilities, family	Bangladesh, India	[2,3,4,6,7,8,9,11,13]

The One Health Approach

Current reviews emphasize the need for an integrated "One Health" approach, which combines medical, veterinary, and environmental surveillance for the early detection of spillover events and the management of risk factors (e.g., land use, animal husbandry, interaction with wildlife) [1,6,8,12,14,19]. Expanding the genomic monitoring of NiV strains across different countries is seen as key to better understanding the virus's pathways of spread and adaptation [6]. The epidemiological pathways of Nipah virus transmission form a complex, multicomponent system that includes a natural reservoir *(Pteropus spp.)*, intermediate hosts (primarily pigs and horses), foodborne routes, and sustained human-to-human transmission through close contact with infected secretions. Regional differences between Malaysia, Bangladesh, India, and the Philippines demonstrate how the combination of environmental conditions, livestock practices, dietary habits, and the genetic characteristics of viral strains determines the dominant epidemiological pathways. In the absence of approved vaccines and specific antiviral therapy, the priority remains to break key transmission chains by changing dietary behaviors, improving biosecurity in animal husbandry, and enforcing strict infection control in healthcare facilities, as well as implementing the intersectoral "One Health" approach. Given the widespread distribution of reservoir bats, a high case fatality rate, and the proven capacity for human-to-human transmission, the Nipah virus remains a significant potential threat to global health, requiring ongoing epidemiological and scientific attention.

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