REVIEW ARTICLE

Mysterious Virus Nipah: A Comprehensive Review

Bidduth Kumar Sarkar[1*], Alam Khan[2], Bithe Saha[3], Susmoy Sarker[4], Farjana Akter[5], Barno Kumar Sarkar[6], Tanvir Ahmed[7], Sukalyan Kumar Kundu[8]

[1,3,4,5,8]Department of Pharmacy, Jahangirnagar University, Savar, Dhaka, Bangladesh
[2,7]Department of Pharmacy, Comilla University, Kotbari, Cumilla, Bangladesh
[6]Faridpur Medical College, Faridpur, Bangladesh

DOI: 10.55489/njcm.160320254827

ABSTRACT

Nipah virus is regarded as one of the most notorious and infectious viruses in the world with high mortality. This narrative literature review aims to offer basic information on the epidemiology, transmission methods, pathophysiology, treatment plan, diagnostic techniques, prevention about Nipah Virus those have been published using the digital repositories such as PubMed and Google Scholar. Results of reviewing relevant articles demonstrated that six hundred fifty (around 700) confirmed human cases of infections due to this virus were reported up until 2023. Between January 4 and February 13, 2023, seven districts in two divisions of Bangladesh (where outbreaks happen almost annually) experienced 73% case fatality rate and in 2024, again Bangladesh faced 100% mortality rate which is alarming issue in concern. The first infection case was recorded in Malaysia in 1998 with a mortality rate of close to 40%. Further outbreaks of the disease have occurred in different countries, particularly in South and Southeast Asia, over two decades later with a mortality rate above 50%. Specially in India, mortality rate reaches to its peak (100%) in two distinct areas in 2007 and 2021. Researchers from around the world are focusing on creating an effective vaccine, advanced diagnostic methods such as CRISPR-based techniques and active therapeutics due to its high pathogenicity in people and the absence of any treatment methods to combat it. Throughout history, viral outbreaks of different frequency and severity have wreaked misery all across the world and the Covid-19 worldwide pandemic provided an example of this type of scenario.

Keywords: Nipah, Epidemics, Nosocomial, Zoonotic, CRISPR-based techniques, Pandemic

ARTICLE INFO

Financial Support: None declared
Conflict of Interest: The authors have declared that no conflict of interests exists.
Received: 01-11-2024, **Accepted**: 04-02-2025, **Published**: 01-03-2025
***Correspondence:** Bidduth Kumar Sarkar (E mail: bidduthks@juniv.edu)

How to cite this article: Sarkar BK, Khan A, Bithe Saha, Sarker S, Akter F, Sarkar BK, Ahmed T, Kundu SK. Mysterious Virus Nipah: A Comprehensive Review. Natl J Community Med 2025;16(3):326-341. DOI: 10.55489/njcm.160320254827

www.njcmindia.com | pISSN: 0976-3325 | eISSN: 2229-6816 | Published by Medsci Publications

INTRODUCTION

In recent years, newly developing viral illnesses have significantly impacted community health. The epidemics were characterized by elevated morbidity and mortality rates, predominantly impacting underdeveloped countries in Asia, Africa, and South America.[1] A total of 1,415 species of infectious organisms have been discovered as dangerous to humans by literature review, comprising 217 viruses and prions, 538 bacteria and rickettsia, 307 fungi, 66 protozoa, and 287 helminths. Seventy-five percent of new infections are zoonotic, spread through interaction between humans and animals. An expansive ecological perspective is essential for comprehending the origins of zoonotic illnesses, given the close interconnection among the environment, humans, domestic animals, wildlife, and their respective diseases.[2]

The Nipah virus (NiV) is a significant wildlife disease that has transitioned to human populations, resulting in a lethal illness, alongside other very lethal pathogens such as avian influenza, HIV, and severe acute respiratory syndrome coronavirus. It is an RNA virus classified within the genus Henipavirus, recognized as one of the most serious bat-borne diseases reported in recent years. Bats, especially Pteropus species, have become reservoir hosts for Henipavirus in many parts of Asia and certain parts of Africa.[3] The initial outbreak of human infections with NiV occurred among pig farmers in Malaysia, presenting with severe febrile encephalitis. Moreover, the virus disseminated in Singapore as a result of the handling and culling of pigs, exhibiting a fatality rate nearing 40%. Since the onset of the epidemic, other outbreaks have occurred in Southeast Asia, particularly in Bangladesh and India, where the mortality rate has escalated to about 70%.[4] The National Institute of Allergy and Infectious Diseases (NIAID) and the Centres for Disease Control and Prevention (CDC) have classified NiV as a category C disease on their list of threats associated with terrorism.[1]

This review comprehensively examines NiV virology, its transmission mechanisms, pathophysiology, and numerous clinical facets. We examine its potential for future pandemic emergence. Ultimately, talks focus on its diagnosis, appropriate treatment management, and research on essential preventive measures and future strategies to address it.

METHODOLOGY

To create a narrative literature review article on NiV, the search phrase incorporated terms such as 'Nipah Virus', "Nipah virus clinical characteristics", "Nipah Virus Disease outbreak", and "Management and Control of Nipah virus", utilising digital repositories like PubMed and Google Scholar. Comprehensive articles concerning the origin, transmission pathways, clinical manifestations, vaccination strategies, diagnostic methods, and management of NiV, along with relevant case reports on these subjects, were thoroughly examined, with a restriction on languages other than English. Additionally, reports from the WHO, the National Centre for Disease Control (NCDC), and various public health organizations were assessed. The search results were limited to published articles from 1999 to 2025. The articles were first assessed independently by each author, followed by a collaborative discussion among them.

Virology of Nipah Virus

NiV is a paramyxovirus classified under the genus Henipavirus, within the Paramyxovirinae subfamily of the Paramyxoviridae family, and part of the order Mononegavirales. It is a significant pathogen that poses a risk to human health, potentially leading to fatal encephalitis and severe respiratory conditions.[5] The Henipavirus genus includes not only NiV but also three species that pose no threat to humans: Cedar virus, Ghanaian bat virus, and Mojiang virus, alongside the highly dangerous Hendra virus (HeV). The Hendra virus antiserum demonstrated a strong response from the virally infected cells. There was no response observed when antiserum from other Paramyxoviruses, including the measles virus, was applied. It was suggested that, while not identical, there may be a close relationship between the Nipah and Hendra viruses.[6] The genomic relationship between NiV and other paramyxoviruses is notably close. When compared to HeV, NiV shows nucleotide homologies ranging from 88% to 70% and anticipated amino acid homologies from 92% to 67%.[7]

Nipah virus is characterised as a non-segmented, single-stranded negative-sense RNA virus, exhibiting helical symmetry in its structural composition. The morphology of the virus transitions from a spherical form to a filamentous structure. The dimensions varied between 40 and 1900 nm, with a single-fringe envelope of surface projections averaging 17 ± 1 nm.The genome of NiV consists of 18,246 to 18,252 base pairs, varying by strain. The genome of NiV Bangladesh consists of 18,252 nucleotides, in contrast to NiV Malaysia, which has a genome length of 18,246 nucleotides.[8] Figure 1 illustrates that along the 3'-5' direction of the NiV RNA genome, there exists a sequence of six consecutive transcriptional elements responsible for the synthesis of the virus's key structural proteins: nucleocapsid (N), phosphoprotein (P), matrix protein (M), fusion glycoprotein (F), attachment glycoprotein (G), and the large protein or RNA polymerase protein (L). The P gene additionally generates the pathogenicity-related NiV proteins V and W (nonstructural protein) and C protein through an alternative open reading frame.[1,9] The formation of the virus ribonucleoprotein (vRNP) involves the binding of the N, P, and L proteins to the viral RNA. The N protein plays a crucial role in the processes of viral replication and transcription. The L and P proteins facilitate the process of transcription, resulting in the production of viral messenger

RNA that is essential for the translation of various functional proteins. The M protein is essential in the final phase of virion assembly, involving the integration of the genome and protein components. In the early stages of the viral life cycle, the attachment of the virion to the cell and its subsequent invasion of the host cell are facilitated by the F and G proteins.[9-10] The F1 subunit, which is generated when the host protease cleaves the F protein into its two components, F1 and F2, features a fusion peptide. This peptide facilitates the fusion of viral and host cellular membranes, enabling the entry of the virus.[11] The attachment of G protein to host cell surface receptors, such as ephrinB2 or ephrinB3, induces conformational changes that activate the F protein, initiating the cellular fusion mechanism, which operates independently of pH 1.5 The virus's ability to persist in its natural environment can vary based on different conditions. The half-life of the virus in fruit bat urine is 18 hours. The duration can extend to three days in specific fruit juices or mango, while it can persist for a minimum of seven days in artificial date palm sap (with 13% sucrose) when stored at 220 C. NiV exhibits a notable level of environmental stability, capable of enduring for one hour at 700 C. Complete deactivation takes place when heated for over 15 minutes at 1000 C. Soaps, detergents, and commercially available disinfectants such as sodium hypochlorite can effectively inactivate NiV.[5,12]

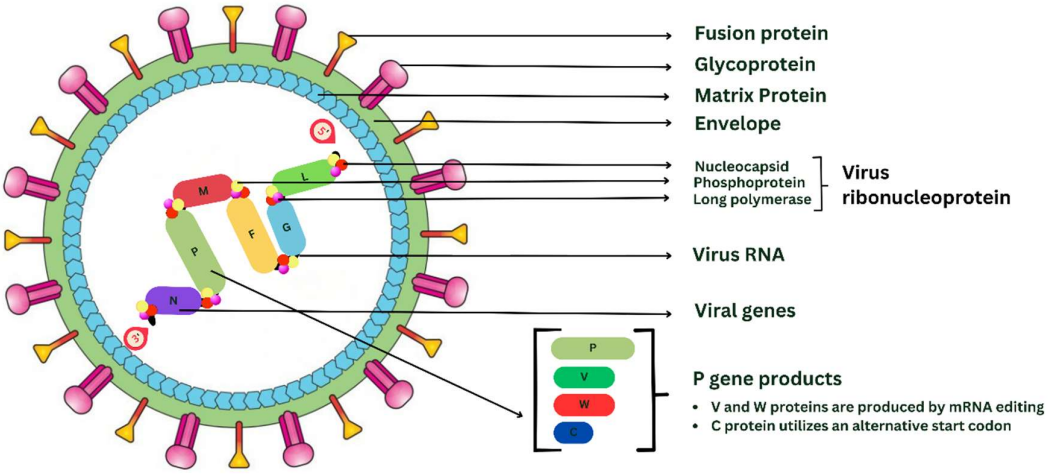

Figure 1: **Structural Representation of Nipah Virus**

Nipah Virus Epidemics: Geographic Distribution

Since the mid-1990s, Henipaviruses have been reported with notable frequency almost every year. This is evidenced by multiple outbreaks occurring in Bangladesh, India, and Pakistan during the years 2001, 2004, 2007, and 2012, alongside the initial outbreaks recorded in Malaysia and Singapore.[13] The virus exhibited a geographical preference for northern Australia, distinct from South and Southeast Asia. There have been 48 documented cases of Hendra viruses in Australia, impacting both the nation's economic stability and its health sector.[5] The consequences of natural catastrophes include the prevention of forest trees from flowering and producing fruit, as well as the potential migration of forest fruit bat populations from their natural habitats to urbanized regions, facilitating the spread of the virus.[1]

a) Malaysia: The geographic centre of South East Asia is situated in Malaysia. For the first time in Malaysia, individuals who interacted with the swine population between September 1998 and June 1999 were identified as having human NiV infection.[14] In late September 1998, a group of patients in Perak state, Peninsular Malaysia, who were associated with pig farming in the Kinta area of Ipoh city, experienced a rare condition called acute febrile encephalitis. They exhibited symptoms such as fever, headaches, and altered levels of awareness, resulting in a high fatality rate among those affected. In December 1998, a similar outbreak was reported in Sikimat, a town in Negeri Sembilan. By February 1999, a comparable illness affecting both pigs and humans was identified in Sungai Nipah village and Bukit Pelandok, the largest pig-farming district in the state. The new virus was first isolated by examining the cerebrospinal fluid (CSF) of a patient from that area and was subsequently named "Nipah."[15] In Malaysia, there were 265 confirmed cases of Nipah encephalitis, predominantly among adult men (Figure 3), with 105 reported fatalities, accounting for 39.6% (Figure 2).

In collaboration with global organisations, the Malaysian government developed a strategy for eradication that involved culling over a million infected pigs and implementing a ban on their movement. The pig farming industry in Malaysia, being one of the largest sectors, suffered economic damages ranging from $350 million to $400 million due to those outbreaks. National monitoring and public education initiatives were also established to mitigate the prevalence.[16-17]

b) Singapore: In 1999, the first recorded case of NiV infection occurred in Singapore, attributed to the transportation of live pigs from regions in Peninsular Malaysia affected by the NiV epidemic. In the cohort of abattoir workers, there were 11 reported human cases (Figure 3), which included one fatality (Figure 2).[14] The Singaporean government acted swiftly and efficiently addressed the NiV epidemic. It is quite remarkable that both Malaysia and Singapore have not documented any new cases since 1999.[18]

c) Bangladesh: In April and May 2001, a community in Bangladesh's Meherpur District reported the first NiV infection. Although the World Health Organization (WHO) and the Bangladesh Ministry of Health conducted preliminary investigations, 2 of the 42 serum samples collected from village residents in May 2001 revealed reactive antibodies to the Nipah virus antigen in tests conducted by the US Centers for Disease Control and Prevention. (CDC).[19] Between 2001 and 2005, Bangladesh saw five epidemics, all of which took place between January and May. Key distinctions between the Malaysian and Singaporean outbreaks and the ones in Bangladesh are suggested by epidemiologic data: a) NiV has spilled over into the human population periodically, b) significant evidence of human-to-human transmission, c) spillover happened without cattle amplifier hosts, d) appears to be seasonal.[20] Different districts including Faridpur, Naogoan, Natore, Nilphamari, Pabna, and Rajbari have been noted as repeated NiV outbreak regions in Bangladesh. Extreme contagious nature of NiV and Bangladesh's inadequate medical infrastructure lead significant mortality and constitute a serious danger to the country's health.[1] It is yet unknown what role domestic animals play in the NiV transmission in Bangladesh because no antibodies were found in any of the 10 birds, 6 pigs, 4 dogs, 2 shrews, and 4 rodents tested in Meherpur and Naogoan but Pteropus bats were discovered to carry antibodies against the NiV especially in Naogoan. 199 (76.2%) fatalities out of 261 NiV infection cases with laboratory confirmation have been documented until 2015 in Bangladesh. More recently from 4 January 2023 to 13 February 2023, in two divisions, 11 cases (10 confirmed and one probable) (Figure 3) including eight deaths (Case Fatality Rate (CFR) of 73%) (Figure 2) have been documented.[18-19,21] Two laboratory-confirmed NiV cases (Figure 3) have been reported from Bangladesh's Dhaka division since January 1, 2024, and both instances have resulted in death, fatality rate, 100% (Figure 2). The first patient, a 38-year-old man from Manikganj district in the Dhaka division, had a fever on January 11, 2024, followed by respiratory trouble, restlessness, and insomnia. The individual in question died on January 28, 2024, after drinking raw date palm sap on December 31, 2023. A 3-year-old girl from the Shariatpur district in the Dhaka division is the second patient; she has been diagnosed with encephalitis, shock altered consciousness, and seizures. Prior to dying on January 31, 2024, this patient had a history of regularly drinking fresh, raw date palm sap.[22]

d) India: There are six outbreaks have been found so far in India. The initial epidemic was noticed in Siliguri, West Bengal, during January and February 2001. With a population of over 500,000 and close to the borders with China, Bangladesh, Nepal, and Sikkim, Siliguri is a significant commercial hub. This outbreak was marked by febrile illnesses and impaired sensorium (bad thinking or concentration skills). Out of 18 patient samples, nine serum/blood samples were found to be positive for NiV by IgM and IgG immunological analysis, and an additional five urine samples showed RNA from NiV in RT-PCR assays through research using the medical records of patients by a group of doctors and epidemiologists from the National Institute of Virology, Pune, India, in conjunction with local public health authorities.[23] According to the patient's observations, none of the cases involved animal's exposure in the transmission of the virus and was mostly disseminated by person-to-person contact, especially through nosocomial transmission. Second smaller outbreak occurred in April, 2007 at village Belechuapara in Nadia district of the West Bengal closely to Bangladesh border area through consuming date-palm alcohol and all infected persons (five patients only) died a week (100% fatality rate) (Figure 2) after contracting the virus.[18] The third outbreak was detected in Kerala's Kozhikode and Malappuram districts (first in South India) in May 2018. A family's loss of three members marked the beginning of the outbreak and an infection claimed the life of a medical professional who assisted in the care of these family members.[24] As of June 1st, 2018, there were 18 confirmed cases (Figure 3) and 17 fatalities (94.4%) documented (Figure 2), where 13 of the 14 confirmed instances resulted in fatalities in the Kozhikode district, while the Malappuram district recorded three fatalities out of four confirmed cases based on the reports of Directorate of Health Services, Kerala.[18] With a mortality rate of 33.33% (Figure 2), Kerala, India, recently experienced the largest known outbreak of the new Nipah virus (NiV). The Ministry of Health and Family Welfare, Government of India, reported six laboratory-confirmed Nipah virus infections (Figure 3), including two fatalities, in the Kozhikode region of Kerala between September 12 and 15, 2023. The deaths of the first and second patients occurred on August 30, 2023, and September 11, 2023, respectively.[25-28] Males between the ages of 9 and 45 accounted for all confirmed cases. The first case, followed by a clustering of patients in family contacts and most likely nosocomial transmission in hospitals, marked the beginning of this sixth outbreak in India. Acute respiratory distress syndrome (ARDS) and pneumonia were the causes of the first fatality case, which occurred a few days after hospitalization. The second fatality case included a person who had pneumonia symptoms and went to the hospital with another patient while the first patient was receiving treatment.[27]

e) Philippines: In the southern Philippines, reports of severe infections in both people and horses

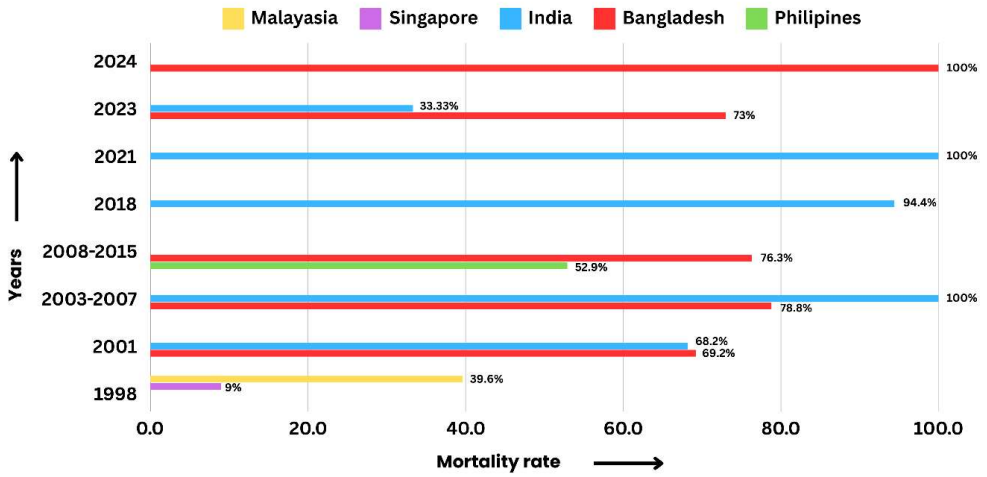

Figure 2: **Rate of Fatality Cases in Population of Distinct NiV Outbreaks**

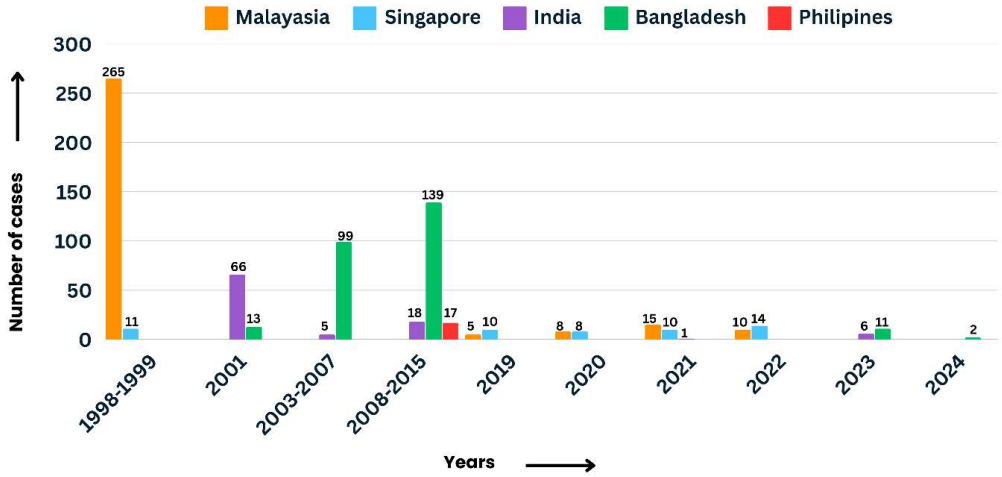

Figure 3: Number of Infectious Cases in Population of Distinct NiV Outbreaks

Table. 1: Comparative study of infection dynamics and disease patterns caused by both strains of Nipah in between three animal disease models

Animal Model	NiV-M strain	NiV-B strain
Hamsters model	1. Rapid disease development with high fatality rate was demonstrated and in vitro, NiV-M exhibited greater cytotoxicity, but in vivo, it displayed greater pathogenicity.[1,33] 2. Post inoculation of 2 days (dpi), hamsters infected oronasally showed a preference for harming pulmonary epithelium rather than nasal tissue, and after 4 dpi, the kind and intensity of lesions in the lung and nasal cavities were indistinguishable for both strains.[31]	1. Slower illness development, immunological response, viral replication and increased survival rates compared to NiV-M strain.[1,33] 2. NiV-B exhibited a preference for olfactory epithelium damage by 2 dpi, as opposed to respiratory damage, suggesting that it enters nasal cavity epithelial cells more quickly than NiV-M.[31]
Ferrets model	1. Blood samples from the ferrets with NiV-M infection had greater virus loads.[32]	1. Although a greater incidence of viral shredding was seen in the oral secretions of NiV-B-infected ferrets, providing a plausible explanation for the high rates of person-to-person transmission in NiV-B epidemics.[32]
African green monkey model	1. A 50% death rate from NiV-M infection was seen in African green monkeys.[1]	1. All experimental subjects who were NiV-B infected yielding a 100% mortality rate with severe respiratory distress.[1]

throughout 2014 revealed significant fatality rates exceeding 50% (Figure 2). The most likely way for a virus to spread from an infected horse to a human were the direct contact with contaminated body fluids of infected horses and eating undercooked meat from them. The offending strain in Philippines was closely linked to the strain from Malaysia.[1,29] Detailed information about the number of infectious patients and fatality rate in population of distinct NiV outbreaks at different times are presented below in (Figure 2) and (Figure 3).[1,18,21]

NIV Strains Associated with the Outbreaks

Two NiV strains which are NiV-M and NiV-B have been found using genomic sequencing from epidemics that occurred in Malaysia and Bangladesh, two different geographic locations respectively and human instances in Bangladesh may be more pathogenic than NiV-M with variations in transmission patterns.[1,31-33] These two strains differ in genomic length despite having nearly identical genetic characteristics (91.8% nucleotide homology).[6,30] According to immunohistochemistry, both NiV isolates were shown to demonstrate endotheliotropism in small- and medium-sized arteries and arterioles in the lung, but not in veins, connected with the presence of ephrin B2, which serves as the primary Nipah virus receptor, in the vasculature.[31] A review study done by Soman Pillai V et al.[30] 2020, found that African green monkeys, ferrets, and hamsters were employed as three animal disease models to explore the dynamics of infection and sickness induced by both strains (Table 1).

Hosts of Nipah Virus

Reservoir Hosts: Nipah virus in Pteropus fruit bats: Due to the serologic cross-reactivity observed with the Hendra virus, which is transmitted by fruit bats, during the outbreak in Malaysia from 1998 to 1999, an investigation was conducted into the fruit bats of the genus Pteropus as possible reservoirs for the Nipah virus.[20] Data from wildlife species surveillance indicates that the Island flying foxes (Pteropus hypomelanus) and the Malayan flying foxes (Pteropus vampyrus) exhibit the highest levels of neutralising antibodies against the Nipah virus.[34] These are basic reservoirs that release the virus through urine, as well as other secretions and excretions including faeces, saliva, and birthing fluids. Fruits become contaminated, which are then consumed by intermediate hosts such as pigs, horses, and non-human primates, leading to human infection through contact with or consumption of products derived from these intermediate animal hosts.[35]

Amplifier Hosts: Nipah Virus in Pig: Pigs can serve as both intermediate hosts and amplifier hosts for NiV, which is extremely contagious among them. The main method of transmission in the Malaysian outbreak of 1999 was direct contact with sick pigs. In contrast, Bangladesh, a Muslim nation, has a smaller scale of pig farming and their breeding is done on a lower basis in India as well.[1,36,37] NiV in pigs affects the respiratory and nervous systems known as porcine respiratory and neurologic syndrome, porcine respiratory and encephalitic syndrome (PRES), and barking pig syndrome (BPS).

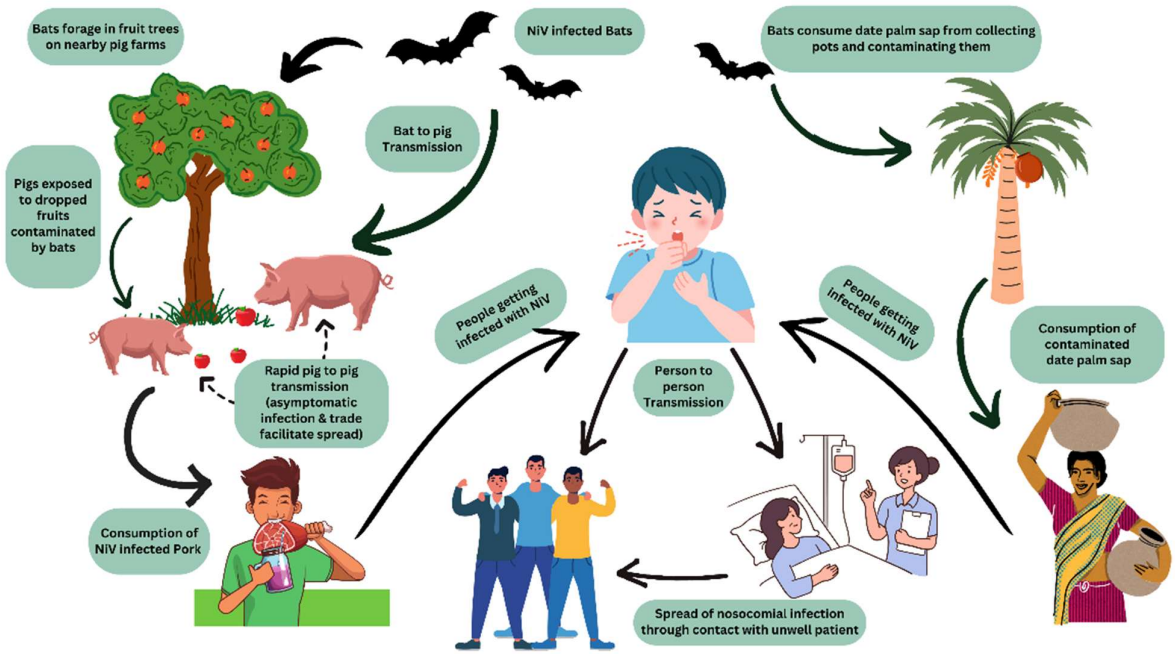

Figure 4: Spreading of Nipah Virus

It exhibits a broad host range in contrast to other Paramyxoviruses, infecting both people and a variety of animal species, including horses, cats, and dogs.[38]

Transmission of Nipah Virus

NiV is spread by consuming foods contaminated with the virus and coming into touch with infected people or animals' bodily fluids (Figure 4). According to research done in Bangladesh between 2001 and 2014, person-to-person transmission of the illness may have caused the NiV infection in 82 (33.06%) of 248 individuals.[1,39,40]

Factors Relating Potentiality of Catastrophic Spread of The Nipah Virus

Epidemiological studies in outbreak locations suggest that various factors significantly contribute to the dissemination of the Nipah virus, including population density, socioeconomic conditions, deforestation, climate change, alterations to reservoir habitats, reservoir transportation, viral shedding and stress in reservoir hosts, nosocomial infections, proximity to NiV-infected animals, and the consumption of contaminated food, such as raw date palm sap, within 30 days preceding disease onset.[30] The potential of NiV to instigate another pandemic is heightened by the risk linked to a specific percentage of subclinical cases, its transmission via respiratory secretions such as saliva from patients exhibiting severe respiratory symptoms, and outbreaks in sparsely populated regions where infection rates may be significantly elevated, particularly in the South East Asia region (SEAR), which comprises 26% of the global population.[1,30,41] The primary variables influencing susceptibility to NiV infection are the age and sex of the individuals infected. The elevated incidence of NiV infections in males, averaging between 37 and 44 years of age, was observed during the Malaysian pandemic, perhaps correlating with their occupations that entail close interaction with infected animals.[42] Forty-two Men aged 41 were predominantly affected by the Nipah virus outbreak in Kozhikode, Kerala, India, in May 2018, while patients in Siliguri province were over 15 years old, with a female to male ratio of 1.4:1.[23,43] An analysis of NiV cases in Bangladesh from 2001 to 2014 revealed a median patient age of 24, with a predominance of males (64%) attributed to their activity of climbing trees inhabited by bats carrying NiV.[39] Both children and adults are vulnerable to NiV infection, as demonstrated by the observation that younger Naogaon patients (12 years old) experienced a shorter duration from disease onset to mortality (4 days compared to 6 days).[1,19] A significant worry regarding the transmission of NiV is via nosocomial infection. In 2001, nosocomial infections constituted the primary source of infection in the Siliguri region of India, affecting 75% of patients who had previously been hospitalised.[23] During the epidemic in Kerala, India (2018), virus transmission occurred in three hospitals, resulting in two healthcare workers contracting the sickness. Likewise, during the epidemics that initially emerged in Bangladesh from 2001 to 2014, three infections among healthcare practitioners were documented.[39,43]

The geographic breadth and seasonal pattern of Nipah outbreaks in Southeast Asia are both distinct. Winter and spring (December to May) were the only seasons in which outbreaks took place. Numerous circumstances, including the date palm sap harvesting season and the bats' enhanced virus shedding during mating season, might be to blame for this and until 2023, there were around 700 recorded instances of NiV infections in humans.[44,45] Additionally, unrelated to people, meteorological conditions influenced the size and severity of specific epidemics. El Nino-caused droughts were followed by the Malaysian NiV outbreak in 1998–1999, and Kerala has experienced similar El Nino-caused droughts in 2016.[30,46]

Clinical Manifestation

In humans, the incubation period of NiV lasted 4 days to 2 months, with more than 90% occurring in 2 weeks or fewer.[36] Clinical symptoms of this varies from asymptomatic infections to some degree of encephalopathy and acute respiratory infection. Initially people experience influenza-like symptoms such as a high temperature, headache, myalgia, sore throat, and weakness followed by changes in awareness, atypical sleepiness, changes in spatial perception, and neurological symptoms of acute encephalitis, which may also be accompanied by nausea and vomiting. Segmental myoclonus (focal, rhythmic jerking of muscles frequently affecting the diaphragm and anterior neck muscles) was also seen in patients.[47,48] Although patients with late-onset or relapse encephalitis had a lower mortality rate (18%) than those with acute NiV encephalitis (40%), they also had more or worse neurological abnormalities (61%) than those with acute encephalitis (22%). Respiratory illness in Bangladesh (69%) had a greater rate than Malaysia (25%).[49,50]

Pathogenesis of Nipah Virus

Nipah virus is a pathogen with a biosafety level 4 (BSL-4) rating.[18] A number of proteins (the V protein, the C protein, and the W protein) produced by the NiV p gene (encoding the polymerase-associated phosphoprotein) are essential for thwarting human innate defense reactions.[52] Inhibition of IFN α/β production and the ability of it for signaling are the two common defensive activity done by NiV P, V, and W proteins to host and all of these were found to suppress interferon-mediated signaling pathways, particularly the STAT1-stimulated JAK-STAT signaling pathway, which mediates human antiviral responses.[51-53] The cellular receptor Ephrin-B2 (alternative receptor Ephrin-B3), which is expressed on endothelium and smooth muscle cells in high levels in the

brain, then in blood vessels in various other host tissues such as the lungs, placenta, and prostate, causes the first stage of pathogenesis by binding with NiV G glycoprotein. The bronchiole's epithelium cells of lungs are the original target area for early detection. Figure 5 illustrates that other than the lungs, subsequent viremia (entry into the blood stream) result in secondary infections like multiple organ failure.[54-56] It has a significant impact on the CNS (>90%) and respiratory systems (62%), while kidney, heart, and splenic systems are least impacted.[18] Despite being necessary for neuronal growth throughout embryogenesis, ephrin-B2 is overexpressed in the brain and lungs, making these organs vulnerable to viral infection. When lung epithelial cells become infected, inflammatory cytokines are released, which draws immune cells and causes significant inflammation. An illness similar to acute respiratory distress syndrome (ARDS) could arise from this.[5] Viral entrance into the central nervous system (CNS) can happen in one of two ways: hematogenous route or via the olfactory neurons. The choroid plexus or cerebral blood arteries are used in the hematogenous pathway.[5,57] Viral infections enter the central nervous system (CNS) via the blood-brain barrier (BBB) network known as the choroid plexus. In the central nervous system (CNS), where vasculitis causes endothelial cell death, mural necrosis, and immune cell infiltration by polymorphonuclear leukocytes and mononuclear cells, the inflammation is most noticeable. Significant encephalitis, respiratory distress, and brain dysfunction could result from these procedures.[58] The Nipah virus (NiV) can effectively target brain tissues due to its strong neurotropism. Viraemia is caused by a high volume of infectious particles entering the bloodstream after fast replication at the inoculation site or lymphoid organs. The exact mechanism by which viremia alone makes it easier for viruses to get through the blood-brain barrier is still unknown. Although the blood-brain barrier (BBB) presents a formidable challenge due to its strongly sealed endothelial junctions and restricted pinocytosis, certain infections, such as NiV, are able to get through it prior to the development of neutralizing antibodies. Severe viremia can cause acute meningitis by seeding the leptomeninges and cerebrospinal fluid (CSF). Serious encephalitis is the result of the virus's quick transcellular transmission after it has infected the CNS parenchyma.[59] The disruption of the blood brain barrier (BBB) and the expression of IL-1b and tumor necrosis factor (TNF)-are caused by the virus's invasion of the central nervous system (CNS). Plaques and degeneration may be visible in both the gray and white matter.[60,61] IgM antibodies increased first in the serum, then in the CSF, and inclusion bodies may have been present in the instance of an infected central nervous system in a male in particular.[5,8] In several experimental rodent models, the virus can directly reach the CNS through an additional pathway through the olfactory nerve infecting the olfactory epithelium of the nasal turbinates and then spreads through the cribiform plate into the olfactory bulb. In the end, the virus spreads to the olfactory region and the ventral brain.[5,57,62]

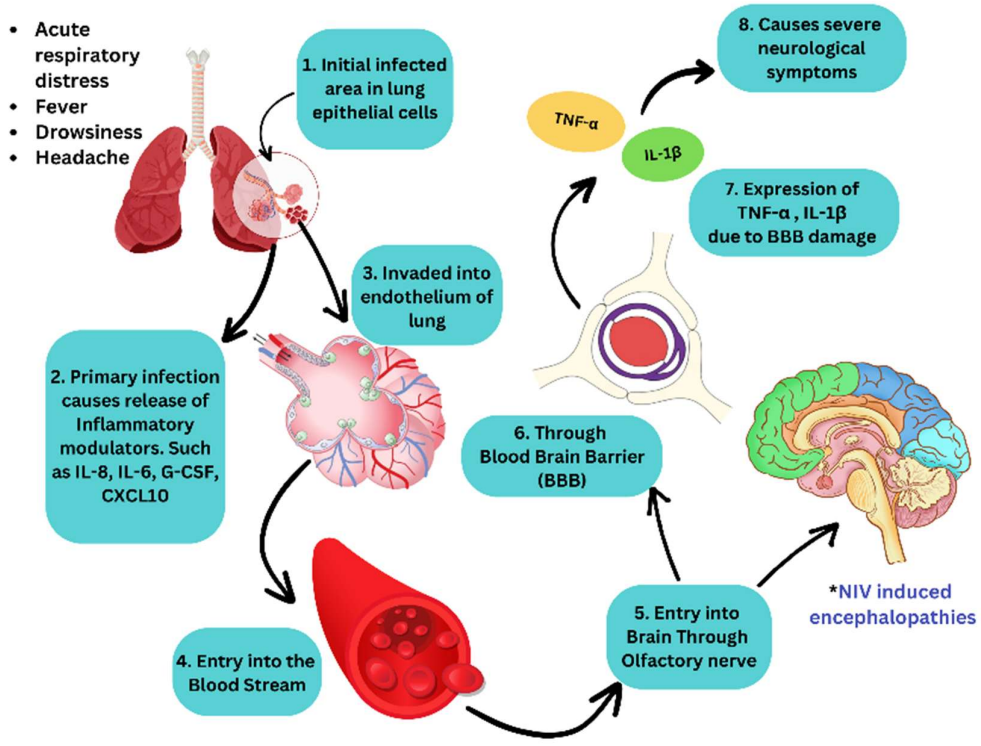

Figure 5: Pathogenesis of Nipah Virus Infection

The Angiopoietin-Tie2 pathway decreases vascular permeability and increases endothelial cell stability via interacting between Angiopoietin-1 (Ang-1) and the Tie2 receptor.[63] During NiV infection, Ang-1 mimetics, such as COMP-Ang1, can strengthen the blood-brain barrier (BBB), lower inflammation, and increase vascular stability which is the most promising treatment strategy.[64] By inhibiting VEGF, and more especially VEGFR-2, inflammation-induced vascular permeability and blood-brain barrier disruption are lessened. Aflibercept and bevacizumab are examples of VEGF inhibitors that maintain the blood-brain barrier.[65,66]

Laboratory Findings

After the initial breakout of NiV in 1998, the virus was identified from cultured mammalian tissues, which later emphasized the concept of a novel infectious etiology. Since then, it has gained recognition on a global scale as a harmful infectious disease.[49,67] The National Institute of Animal Health in Japan has created an immunohistochemical diagnosis method based on monoclonal antibodies for the aim of diagnosing such illnesses.[49,68] For the goal of diagnosis, various samples are taken from sick people and animals such as CSF, urine, blood, and/or throat samples (in virus transport medium) during acute phase of infection.[23,55] In addition to indirect methods like enzyme-linked immunosorbent assays (ELISA) or virus neutralisation tests, NiV infection can be verified by a number of direct identification techniques, including virus isolation, immunohistochemistry or immunofluorescence assays, nucleic acid amplification, or sequencing. Since qRT-PCR has high specificity and sensitivity and may provide a trustworthy diagnosis in a few hours, it is now the method of choice for identifying acute NiV infection.[69]

Molecular Assay of Diagnosing NiV: The Polymerase Chain Reaction is the most popular and accurate molecular diagnostic technique used for NiV identification.[49] Nested RT-PCR, real-time RT-PCR with the use of intercalating dyes (qPCR), real-time RT-PCR with the use of hydrolysis probes (TaqMan), SYBR Green-based assay, multiplex bead-based real-time RT-PCR, or the RT-LAMP assay have all been found to be useful for rapid detection with greater specificity and sensitivity. The highly conserved section of the viral genome's N, M, or P gene was the focus of these RT-PCR tests for NiV.[1,70,71] Not every endemic region has RT-PCR lab infrastructure and takes hours to detect. Three RT-nfoRPA, RT-exoRPA, and RT-RAA rapid isothermal nucleic acid amplification assays with lateral flow detection for Nipah virus (NiV) were developed in a study. These assays are very specific to NiV, deliver findings in 30 minutes, and need very little sample preparation. They allow for early detection in decentralized and rural areas and are designed for low-resource environments.[69,72]

Immunohistochemistry and Electron Microscopy: Immunohistochemistry employs formalin-fixed tissues such as the brain, lung, liver, kidney, lymph nodes, and spleen, facilitating retrospective research on historical data. In the preliminary isolation phase, the visual representation of viruses inside the milieu of infected cells by negative contrast electron microscopy, along with the rapid detection of virus-antibody interactions via immunoelectron microscopy, yields valuable insights into viral architecture and antigenic responsiveness.[55,73] ELISA serves as an alternative diagnostic test option. Diagnostics utilising recombinant proteins may also be employed in laboratories not subject to biocontainment protocols.[17]

Recent advancements in diagnostic tools have led to several creative methods for NiV detection. In as little as 40 minutes, for instance, CRISPR/Cas-based diagnostics like SHERLOCK, DETECTR, and HOLMES provide rapid, accurate, and exact NiV RNA identification.[74]

Therapeutic Management Associated with The Disease

Antiviral Therapeutics: Ribavirin, an antiviral medication, had been used to treat NiV infection during previous epidemics in Malaysia.[18] In an open-label experiment with 140 patients and 54 controls (patients who refused treatment or were not given the medication in any other way), 45 deaths (32%) in the ribavirin group and 29 deaths (54%) in the control arm, representing a 36% decrease in mortality. In this trial, there were no obvious severe adverse effects. but the effectiveness of Ribavirin (mortality rate) was controversial at that time.[42,75] Another drug named Favipiravir (T-705), a purine analogue that inhibits RNA-dependent RNA polymerase and is a licensed medication with Japanese origins used for the treatment of influenza, has demonstrated effectiveness against NiV in animal studies using Syrian hamsters.[55,76] It is able to lower viral loads at 250 M and medication given twice daily, immediately after the infection via the oral route or once daily for two weeks via the subcutaneous method, full prevention has been accomplished in animal models.[5,76] In golden Syrian hamsters, oxidation-resistant synthetic trimeric tandemer (3mG) of GRFT (Griffithsin), a high mannose oligosaccharide-binding lectin has been found antiviral efficacy against NiV and others from four virus families.[1,77]

Favipiravir has demonstrated exceptional effectiveness against the Ebola virus and dramatically lowers the viral load and mortality during West African Ebola outbreaks from 2013 to 2016. Despite promising results from non-human primate research, real-world applications showed inconsistent results, with partial effectiveness relying on the phase of the disease at the beginning of treatment.[78] It received a lot of attention for treating the COVID-19 epidemic. In mild to moderate cases, research from Russia, India, and Japan showed a decreased viral load and symptomatic relief; however, the efficacy in severe cases is

still unclear. Ribavirin, on the other hand, was used less frequently because to its low toxicity and effectiveness against SARS -CoV-2.[79]

A nucleotide analogue prodrug licensed for COVID-19, Remdesivir (GS-5734), was utilized during the Kerala outbreak in 2023. 3 of 6 confirmed NiV cases became afebrile and asymptomatic after initiation of this drug. Bangladesh is responsible for more than half of the world's Nipah cases, yet it has not compassionately used antivirals or monoclonal antibodies.[80]

Vaccines: A variety of vaccination techniques have been developed, including many live recombinant viral vectors, protein subunit methods, and virus-like particle (VLP) approaches; nevertheless, their efficiency has only been assessed in animal models.[55,81] A multi-epitope vaccine made of many or overlapping peptides is the optimal strategy for the prevention and treatment of viral infections since immune responses play a crucial role in battling these diseases. Currently, computational drug design analysis facilitates the development of innovative NiV vaccines. Soltan, Eldeen et al.[82] 2021 developed a multitope vaccine by analysing the complete proteome of the Nipah virus (nine proteins) and selecting the highest-ranking CTL, HTL, and BCL epitopes from the identified proteins. The vaccine candidate's stability, high immunogenicity, and minimal allergenicity are validated by various advanced immune-informatics techniques.[83] Recently, Srivastava, Verma et al.[84] 2023 developed two Multi-Epitope Vaccines (MEVs) with thirty-three CTL and thirty-eight HTL epitopes. Sixty-one novel epitopes, previously unutilized in vaccine production, targeted nine distinct NiV proteins from a total of 71 epitopes identified by CTL and HTL. Loomis, Stewart-Jones et al.[85] 2020 endeavored to develop an alternative NiV vaccine design by evaluating the principal attachment glycoprotein (G) and the fusion glycoprotein (F) as prospective NiV vaccine antigens. Stable prefusion F (pre-F), multimeric G constructs, and chimeric proteins incorporating both pre-F and G have been produced as potential protein subunit vaccines. Loomis, Stewart-Jones et al.[85] 2020 reported that the post-F trimer immunogen did not induce neutralizing activity in serum, whereas the stabilized pre-F trimer and hexameric G immunogens did. They concluded that the primary candidate for clinical development is the pre-F trimer covalently linked to three G monomers (pre-F/G), which demonstrated strong neutralizing antibody activity and elicited responses to a broad spectrum of antigenic sites, similar to mRNA vaccines. Profectus BioSciences and Emergent BioSolutions were awarded a grant of $25,000,000 from CEPI (Coalition for Epidemic Preparedness Innovations) on May 24, 2018, to collaborate on the development of a vaccine for NiV.[6,49]

A phase 1 clinical trial is in underway for the HeV-sG-V Nipah vaccine contender, a regenerated subunit vaccine containing the G glycoprotein of the Hendra virus. CEPI-backed Auro Vaccines is spearheading the Phase 1 trial, while PATH (Program for Appropriate Technology in Health) oversees operations and provides CEPI money for Phase 2. With support from Moderna and the Vaccine Research Centre at the US National Institute of Allergy and Infectious Disease (NIAID) of the US National Institutes of Health (NIH), a phase 1 clinical study of mRNA-1215, another vaccine candidate, was initiated. PHV02 is a vaccine candidate currently under phase 1 clinical trial that uses a replicating viral vector. Originally invented by the NIAID of the United States, it uses the vesicular stomatitis virus (VSV) as a vector. Public Health Vaccines is currently working on it in partnership with Crozet BioPharma and CEPI.[86] ChAdOx1 Nipah B is currently undergoing a new clinical trial at the University of Oxford. The Oxford Vaccine Group is leading the initiative, which is funded by CEPI and employs the same viral vector vaccine platform as the AstraZeneca COVID-19 vaccine.[87] No safety issues were found in the first-in-human Phase I clinical trial of HeV-sG-V, which elicited a strong immune response marked by a high titer of specific binding and neutralizing antibodies against two NiV strains, NiV B and NiV M.[88] Phase II and III study participant shortages are a major barrier to developing a vaccine against the Nipah virus. It is difficult to recruit enough people for NiV outbreaks since they are seasonal, sporadic, and primarily restricted to Southeast Asia, making Phase III investigations impracticable. The main obstacle to vaccine development in the modern world is the lack of adequate economic incentives and global collaboration.[89]

Nanoparticle-Based Therapies: One new treatment option for delivering targeted medicines and improving antiviral efficacy against the Nipah virus is nanoparticle-based therapy.

Therapeutic Delivery: To improve stability and target the viral proteins or infected cell, nanoparticles can be encapsulated as antiviral agents. For instance:

- **Lipid-based nanoparticles (LNPs):** LNPs have been utilized to deliver small interfering RNA (siRNA) that targets NiV genes, therefore inhibiting viral replication in both in vitro and animal models.[90]

- **Polymeric nanoparticles:** These can carry antiviral medications or RNA molecules, improving delivery to the afflicted tissue and reducing adverse effects.

Direct Antiviral Action: With the help of designed nanoparticles, viral surface proteins such as the G and F glycoproteins can interact and prevent cell entrance. This method can prevent the formation of syncytia, an essential stage in the pathophysiology of NiV.[91]

CRISPR-Based Techniques/Gene Editing for Therapy: The genes that encode the receptors that NiV utilizes to enter host cells, ephrin-B2 and ephrin-B3, can be altered using CRISPR to potentially make cells more resistant to infection.[92]

Real-life Examples of NiV Outbreaks

Ashok Kumar Ghosh, a teacher and Taposhi Ghosh, a former NGO employee in Bangladesh, are mourning the deaths of their two children in February 2011 due to the Nipah virus in the Bandar neighbourhoods of Hatibandha Upazila, Lalmonirhat. The infection was initially discovered in their son, eight-year-old Aronno Kumar, then two days later in four-year-old Ananya. The children may have eaten raw date juice or bat-bitten guavas, according to the couple. Losses also befell other local families. Sixth-grader Sudipta Sarker Dwip, 12 years old school going child, died from the virus after consuming raw date juice with pals. His father, Subal Chandra Sarker, remembers the community's concern and his son's terrible symptoms. After Sudipta passed away, Subal experienced societal rejection. He took his son's remains to the crematory by himself since he was unable to bury him the old-fashioned way. Winter is still a time of worry for these bereaved parents, who spent two years in seclusion.[93]

One case study found by reviewing outbreak patients in Bangladesh, case-patient A, a 45-year-old male, most certainly contracted Nipah virus (NiV) from raw date palm sap in December 2009. He began exhibiting symptoms on January 7 and passed away on January 13. After drinking the sap, three neighbours (cases B, C, and D) were unwell two days later and passed away on January 17. The spouse of Case A (case E) took care of him without maintaining good hygiene, experienced light symptoms on January 15, and then recovered. After being in close proximity to case A or his body, three more people (cases F, G, and H) were ill within 12 days and passed away by January 28.[40]

Preventive Measures for Future Outbreak

Focusing the efforts of researchers and organizations in charge of keeping track on epidemiological dangers on stopping NiV from emerging and supervising them effectively appears acceptable. Adhering to stringent preventative measures is the most effective strategy to combat this infection.[1,49] Preventative measures against foodborne transmission include strongly forbidding the purchase of food products under unhygienic conditions in regions where the NiV virus is prevalent.[30] Avoiding eating unwashed raw fruits that have been bitten by bats or raw date palm juice is advised by the WHO when an epidemic is still active.[55] Date palm sap is often collected in Bangladesh over the course of one night. Through the use of infrared cameras, bats' nighttime behaviors, such as drinking from, urination, or feces in the jars used to collect date palm sap, have been made clear.[94] Using bamboo skirts to cover the date palm trees' sap-producing regions greatly reduces the chance of coming into touch with bats.[1,55] Wearing protective clothes (gloves to cover the hands) while performing work on farm animals, avoid growing fruit trees near the piggery that may attract bats, grazing lands vulnerable to viral infection, cleaning contaminated farms properly with the right detergents and limiting the transportation of animals from infected farms to other places are some significant steps to combat NiV infection from spreading through animal exposure.[1,36,49] A few infection control procedures that must be followed as preventive measures include regular cleaning of the hands, 70% ethanol sanitization, and avoiding near bodily fluids such as suspects' blood, saliva, respiratory droplets, urine, etc. and infected patients in hospital, proper use of personal protective equipment (wearing masks, glasses and gloves etc.), contact tracing to identify contacts, quarantining medical personnel and other high-risk individuals may limit person to person transmission.[5,18] The creation of multidisciplinary teams for the "One Health" approach is urgently needed. Such teams should include medical professionals, such as veterinarians, agriculturists, and doctors; public health officials; vector biologists, as well as ecologists and phylogeneticists, who can work together to prevent any major outbreaks.[5]

In addition to vaccination, effective public health campaigns can make use of a number of other tactics. Educating youngsters about NiV can lead to more information sharing between communities and families. Campaigns in the mass media can effectively raise awareness of NiV by reaching a large audience. Campaigns in the media that highlighted the dangers of consuming raw date palm sap helped to curb risky behavior in Bangladesh.[95,96] Active surveillance, which assists in spotting early indications of oncoming NiV outbreaks, strain analysis, and monitoring of the interaction between environmental variables and the dynamics of epidemic growth should be conducted in NiV-prevalent areas in addition to public awareness.[1,18]

Difficulties in Implementing Preventive Measures: One important way to combat the spread of the Nipah virus is to cover date palm trees to keep bats from contaminating the juice. However, little technical expertise and high labor and material expenses, particularly in rural areas where date palm growing is the primary industry, lessen its efficacy. Environmental influences also affect how long the coverings last and how well they are maintained.[97] It is essential to properly dispose of contaminated materials via deep burial in order to stop environmental contamination and transmission. Due to a shortage of labour and equipment, this approach is difficult to implement in places with low resources. Although burning agricultural waste is a prevalent traditional practice, it releases hazardous substances that can affect human health and the environment. In order to make the shift to deep burial, cultural resistance to change must also be overcome.[98] A variety of human infections in Bangladesh have been linked to corpse-to-person transfer, touching a loved one's body immediately after they pass away, or ritually preparing a corpse for religious burial.[40] To reduce the potential of corpse-to-human virus transmission, incinera-

tion or deep burial to a depth of 10 feet is required, coupled with appropriate PPE and cleaning of the handlers and burial site.[30]

Impact on Public Health

India and Bangladesh demonstrated the highest fatality rate of 70–75% in the first decade following the advent of the Nipah virus. Between 2004 and 2013, Bangladesh saw a 15% decrease in its mortality rate, whilst India continually reported a mortality rate as high as 90%. In contrast, Malaysia experienced a death rate of 35% in the first decade, which later decreased to 8% during the 2004–2013 decade.[99] The Nipah virus exhibits a significant mortality rate that fluctuates with each outbreak and can lead to many clinical manifestations and the majority of survivors experience long-term neurological sequelae or late-onset relapsing encephalitis.[100] During the 1999 outbreak in Malaysia, 30 out of 94 hospitalized patients (32%) with Nipah virus encephalitis died, while 50 (53%) fully recovered and 14 (15%) were released with sequelae or persistent symptoms. Five patients were in a vegetative state, two were released with cognitive impairments requiring lifelong assistance, three displayed mild cognitive impairments, three suffered from cerebellar dysfunction, and two experienced relapses of encephalitis with lasting damage. Among the eight patients infected during the 1999 outbreak in Singapore, only one assessed two years after the beginning of encephalitis had no sequelae; five experienced severe depression, two underwent personality changes, and two reported chronic fatigue syndromes. All seven persons with sequelae displayed impaired memory, mostly visual memory, while some also indicated abnormalities in verbal memory. Two of the seven patients who were employed before to developing encephalitis were unable to resume work: one due to leg weakness and the other due to considerable memory impairment and fatigue. In Bangladesh, 17 patients with a history of Nipah virus encephalitis from 2001 to 2004 were assessed for sequelae in 2005 and 2006. Follow-up assessments of these 17 patients revealed that 7 (32%) exhibited moderate-to-severe sequelae, comprising 4 with cognitive impairment, 2 with ataxia, 2 with focal weakness, 1 with cervical dystonia, and 1 with facial weakness and dysarthria. Four people developed post-discharge symptoms: three demonstrated oculomotor dysfunctions, and one exhibited cervical dystonia. Approximately 70% of participants reported chronic fatigue in self-assessments, 60% indicated mood disturbances, and 40% displayed behavioural abnormalities.[101]

Future Prospectus

Some promises have been shown for passive immunotherapy against NiV infection using the fully humanized monoclonal antibody (mAb) named m102.4 in a nonhuman primate model.[90] Another intriguing candidate, human monoclonal antibody h5B3.1, a humanized variant of mouse monoclonal antibody 5B3 developed against Henipavirus protein, exhibits cross-reactivity against NiV-MY and Ni-BD.[102] Due to the regional heterogeneity of NiV strains, vaccine methods must be particularly customized. Furthermore, getting these vaccines from preclinical stages to clinical trials is essential, as just a few candidates have reached this advancement.[88] Along with intensive care, the surveillance and monitoring of bat populations and their contacts with human societies are essential to anticipate and avert any spillovers that may incite human outbreaks, thereby boosting global health security and safeguarding at-risk populations.[103] Environmental variables, host interactions, and genetic evolution all play a role in NiV adaptability. Chronic outbreaks highlight the necessity of international collaboration in public health and research. To enhance surveillance, outbreak control, and the development of vaccines and treatments, agencies such as WHO must offer financial support and training. In order to better understand NiV transmission and inform successful public health initiatives, research should concentrate on sequencing virus isolates and examining environmental factors. It is essential to tackle the environmental and anthropogenic alterations that jeopardize wildlife habitats to avert future spillovers. This necessitates a multi-disciplinary approach integrating animal conservation and robust public health strategies to address the worldwide issues presented by the Nipah virus.[104,105]

Conclusion

The worldwide population is seriously threatened by the Nipah virus epidemics that have been reported in many regions. The purpose of this study is to make a traditional overview of Nipah Virus in all aspects especially the most recent alarming outbreaks that experienced 100% mortality rate, inexpensive and available advanced diagnostic assays such as CRISPR/Cas-based diagnostics tools and facilities capable of handling viral samples etc. those making the infection challenging to identify nowadays. Scientists have been developing several effective vaccines (HeV-sG-V, mRNA-1215, PHV02 and ChAdOx1) under phase I clinical trials in collaboration with associated organizations. Two promising targeted therapy (mABs) named m102.4 and h5B3.1, have been investigated as innovative therapeutic options for NiV through virus-neutralizing properties and cross-reactivity against two NiV strains respectively. Angiopoietin-1 mimetics like COMP-Ang1 is the most amazing treatment strategy for strengthening the blood-brain barrier during NiV infection. Computationally analyzed various vaccination techniques in today's world are also encouraging for future research. All of their introduction into human clinical trials, changes to risk factors especially managing plans for wildlife such as fruit bats population to counter the danger of NiV infection and public health

campaigns are crucial points to notice in this respect and these developments will surely demonstrate the practical relevance in near future.

Author's Contributions: Conceptualization: BKS; Methodology: AK, BS; Experimentation: BS, SS, TA, FA; Formal analysis and investigation: FA, BKS, AK, BKS; Writing - original draft preparation: AK, BS, SS, TA; Writing - review and editing: BKS, BKS, FA; Funding acquisition: BKS; Resources: BKS, SKK; Supervision: BKS, SKK

REFERENCES

1. Skowron K, Bauza-Kaszewska J, Grudlewska-Buda K, et al. Nipah virus-Another threat from the world of zoonotic viruses. Frontiers in Microbiology. 2022; 12:811157. DOI: https://doi.org/10.3389/fmicb.2021.811157 PMid:35145498 PMCid:PMC8821941
2. Taylor LH, Latham SM, Woolhouse ME. Risk factors for human disease emergence. Philosophical Transactions of the Royal Society of London Series B. Biological Sciences. 2001;356(1411):983-9. DOI: https://doi.org/10.1098/rstb.2001.0888 PMid:11516376 PMCid:PMC1088493
3. Clayton B, Wang L, Marsh G. Henipaviruses: an updated review focusing on the pteropid reservoir and features of transmission. Zoonoses and public health. 2013;60(1):69-83. DOI: https://doi.org/10.1111/j.1863-2378.2012.01501.x
4. Lo MK, Rota PA. The emergence of Nipah virus, a highly pathogenic paramyxovirus. Journal of Clinical Virology. 2008; 43(4):396-400. DOI: https://doi.org/10.1016/j.jcv.2008.08.007 PMid:18835214
5. Singh RK, Dhama K, Chakraborty S, et al. Nipah virus: epidemiology, pathology, immunobiology and advances in diagnosis, vaccine designing and control strategies-a comprehensive review. Veterinary Quarterly. 2019;39(1):26-55. DOI: https://doi.org/10.1080/01652176.2019.1580827 PMid:31006350 PMCid:PMC6830995
6. Ramphul K, Mejias SG, Agumadu VC, et al. The killer virus called Nipah: a review. Cureus. 2018;10(8):e3168. DOI: https://doi.org/10.7759/cureus.3168
7. Harcourt BH, Tamin A, Ksiazek TG, et al. Molecular characterization of Nipah virus, a newly emergent paramyxovirus. Virology. 2000;271(2):334-49. DOI: https://doi.org/10.1006/viro.2000.0340 PMid:10860887
8. Wong K, Shieh W, Zaki S, et al. Nipah virus infection, an emerging paramyxoviral zoonosis. Springer seminars in immunopathology. 2002;24(2):215-28. DOI: https://doi.org/10.1007/s00281-002-0106-y PMid:12503066
9. Sun B, Jia L, Liang B, et al. Phylogeography, transmission, and viral proteins of Nipah virus. Virologica Sinica. 2018; 33:385-93. DOI: https://doi.org/10.1007/s12250-018-0050-1
10. Hauser N, Gushiken AC, Narayanan S, et al. Evolution of Nipah virus infection: past, present, and future considerations. Tropical medicine and infectious disease. 2021;6(1): 24. DOI: https://doi.org/10.3390/tropicalmed6010024
11. Eaton BT, Broder CC, Middleton D, et al. Hendra and Nipah viruses: different and dangerous. Nature Reviews Microbiology. 2006;4(1):23-35. DOI: https://doi.org/10.1038/ nrmicro1323 PMid:16357858 PMCid:PMC7097447
12. de Wit E, Prescott J, Falzarano D, et al. Foodborne transmission of nipah virus in Syrian hamsters. PLoS pathogens. 2014;10(3): e1004001. DOI: https://doi.org/10.1371/ journal.ppat.1004001 PMid:24626480 PMCid:PMC3953481
13. Rana S, Singh S. Nipah Virus: Effects of Urbanization and Climate Change. In: Proceedings of the 3rd International Conference on Biological, Chemical & Environmental Sciences (BCES-2015); 2015 Sep 21-22; Kuala Lumpur, Malaysia.
14. Chua KB. Nipah virus outbreak in Malaysia. Journal of Clinical Virology. 2003;26(3):265-75. DOI: https://doi.org/10.1016/S1386-6532(02)00268-8 PMid:12637075
15. Chua KB, Goh KJ, Wong KT, et al. Fatal encephalitis due to Nipah virus among pig-farmers in Malaysia. The Lancet. 1999;354(9186):1257-9. DOI: https://doi.org/10.1016/S0140-6736(99)04299-3 PMid:10520635
16. Uppal P. Emergence of Nipah virus in Malaysia. Annals of the New York Academy of Sciences. 2000;916(1):354-7. DOI: https://doi.org/10.1111/j.1749-6632.2000.tb05312.x PMid:11193645
17. Kulkarni D, Tosh C, Venkatesh G, et al. Nipah virus infection: current scenario. Indian Journal of Virology. 2013;24(3):398-408. DOI: https://doi.org/10.1007/s13337-013-0171-y PMid:24426305 PMCid:PMC3832692
18. Sharma V, Kaushik S, Kumar R, et al. Emerging trends of Nipah virus: A review. Reviews in medical virology. 2019;29(1): e2010. DOI: https://doi.org/10.1002/rmv.2010 PMid:30251294 PMCid:PMC7169151
19. Hsu VP, Hossain MJ, Parashar UD, et al. Nipah virus encephalitis reemergence, Bangladesh. Emerging infectious diseases. 2004;10(12):2082. DOI: https://doi.org/10.3201/eid1012.040701 PMid:15663842 PMCid:PMC3323384
20. Epstein JH, Field HE, Luby S, et al. Nipah virus: impact, origins, and causes of emergence. Current infectious disease reports. 2006;8(1):59-65. DOI: https://doi.org/10.1007/s11908-006-0036-2 PMid:16448602 PMCid:PMC7088631
21. WHO's Health Emergencies Programme: acute emergencies monthly summary-February 2023-Programme. Weekly Epidemiological Record. 2023;98(13):139-44.
22. World Health Organization. Disease Outbreak News; Nipah virus infection - Bangladesh. Available at: https://www.who.int/emergencies/disease-outbreak-news/item/2024-DON508 Accessed 27th February, 2024.
23. Chadha MS, Comer JA, Lowe L, et al. Nipah virus-associated encephalitis outbreak, Siliguri, India. Emerging infectious diseases. 2006;12(2):235-240. DOI: https://doi.org/10.3201/eid1202.051247 PMid:16494748 PMCid:PMC3373078
24. Chatterjee P. Nipah virus outbreak in India. The Lancet. 2018;391(10136):2200. DOI: https://doi.org/10.1016/S0140-6736(18)31252-2 PMid:31876482
25. Verma A, Jain H, Sulaiman SA, et al. An impending public health threat: analysis of the recent Nipah virus outbreak and future recommendations-an editorial. Annals of Medicine and Surgery. 2024 Feb 1;86(2):638-42. DOI: https://doi.org/10.1097/MS9.0000000000001627 PMid:38333322
26. Cui Z, Li J, Meng L, et al. Nipah virus: A re-emerging public health concern. The Lancet Microbe. 2024 Mar 1;5(3): e212. DOI: https://doi.org/10.1016/S2666-5247(23)00361-0
27. World Health Organization. Disease Outbreak News; Nipah Virus Infection in India. Available at: https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON490 Accessed 3th October, 2024.
28. As AK, Sahay RR, Radhakrishnan C, et al. Clinico-epidemiological presentations and management of Nipah virus infection during the outbreak in Kozhikode district, Kerala state, India 2023. Journal of Medical Virology. 2024 Mar;96(3): e29559. DOI: https://doi.org/10.1002/jmv.29559 PMid:38529536
29. Ching PKG, de Los Reyes VC, Sucaldito MN, et al. Outbreak of henipavirus infection, Philippines, 2014. Emerging infectious diseases. 2015;21(2):328-331. DOI: https://doi.org/10.3201/eid2102.141433 PMid:25626011 PMCid:PMC4313660

30. Soman Pillai V, Krishna G, Valiya Veettil M. Nipah virus: past outbreaks and future containment. Viruses. 2020;12(4):465. DOI: https://doi.org/10.3390/v12040465 PMid:32325930 PMCid:PMC7232522

31. Baseler L, de Wit E, Scott DP, et al. Syrian hamsters (Mesocricetus auratus) oronasally inoculated with a Nipah virus isolate from Bangladesh or Malaysia develop similar respiratory tract lesions. Veterinary pathology. 2015;52(1):38-45. DOI: https://doi.org/10.1177/0300985814556189 PMid:25352203 PMCid:PMC6309986

32. Mire CE, Satterfield BA, Geisbert JB, et al. Pathogenic differences between Nipah virus Bangladesh and Malaysia strains in primates: implications for antibody therapy. Scientific reports. 2016;6(1):1-16. DOI: https://doi.org/10.1038/srep30916 PMid:27484128 PMCid:PMC4971471

33. DeBuysscher BL, de Wit E, Munster VJ, et al. Comparison of the pathogenicity of Nipah virus isolates from Bangladesh and Malaysia in the Syrian hamster. PLoS neglected tropical diseases. 2013;7(1): e2024. DOI: https://doi.org/10.1371/journal.pntd.0002024 PMid:23342177 PMCid:PMC3547834

34. Lam SK, Chua KB. Nipah virus encephalitis outbreak in Malaysia. Clinical Infectious Diseases. 2002;34(Supplement_2): S48-S51. DOI: https://doi.org/10.1086/338818

35. Han H-J, Wen H-l, Zhou C-M, et al. Bats as reservoirs of severe emerging infectious diseases. Virus research. 2015; 205:1-6. DOI: https://doi.org/10.1016/j.virusres.2015.05.006

36. Ang BS, Lim TC, Wang L. Nipah virus infection. Journal of clinical microbiology. 2018;56(6): e01875-17. DOI: https://doi.org/10.1128/JCM.01875-17 PMid:29643201

37. Jose BP. Nipah: The deadly menace. J Acad Clin Microbiol 2018;20:66-73. DOI: https://doi.org/10.4103/jacm.jacm_34_18

38. McLean RK, Graham SP. Vaccine development for Nipah virus infection in pigs. frontiers in Veterinary Science. 2019; 6:16. DOI: https://doi.org/10.3389/fvets.2019.00016

39. Nikolay B, Salje H, Khan AD, et al. A framework to monitor changes in transmission and epidemiology of emerging pathogens: lessons from Nipah virus. The Journal of Infectious Diseases. 2020;221(Supplement_4): S363-S9. DOI: https://doi.org/10.1093/infdis/jiaa074 PMid:32392322

40. Sazzad HM, Hossain MJ, Gurley ES, et al. Nipah virus infection outbreak with nosocomial and corpse-to-human transmission, Bangladesh. Emerging infectious diseases. 2013;19(2): 210-217. DOI: https://doi.org/10.3201/eid1902.120971 PMid:23347678 PMCid:PMC3559054

41. Mondal MSH. The implications of population growth and climate change on sustainable development in Bangladesh. Jàmbá: Journal of Disaster Risk Studies. 2019;11(1):1-10. DOI: https://doi.org/10.4102/jamba.v11i1.535

42. Goh KJ, Tan CT, Chew NK, et al. Clinical features of Nipah virus encephalitis among pig farmers in Malaysia. New England Journal of Medicine. 2000;342(17):1229-35. DOI: https://doi.org/10.1056/NEJM200004273421701

43. Thomas B, Chandran P, Lilabi M, et al. Nipah virus infection in Kozhikode, Kerala, South India, in 2018: epidemiology of an outbreak of an emerging disease. Indian journal of community medicine: official publication of Indian Association of Preventive & Social Medicine. 2019;44(4):383-387. DOI: https://doi.org/10.4103/ijcm.IJCM_198_19 PMid:31802805 PMCid:PMC6881878

44. Uwishema O, Wellington J, Berjaoui C, et al. A short communication of Nipah virus outbreak in India: An urgent rising concern. Annals of Medicine and Surgery. 2022; 82:104599. DOI: https://doi.org/10.1016/j.amsu.2022.104599

45. Chattu VK, Kumar R, Kumary S, et al. Nipah virus epidemic in southern India and emphasizing "One Health" approach to ensure global health security. Journal of family medicine and primary care. 2018;7(2):275-283. DOI: https://doi.org/10.4103/jfmpc.jfmpc_137_18 PMid:30090764

46. Chua KB. Risk factors, prevention and communication strategy during Nipah virus outbreak in Malaysia. The Malaysian journal of pathology. 2010;32(2):75-80.

47. Giangaspero M. Nipah virus. Trop Med Surg. 2013;1:129. DOI: https://doi.org/10.4172/2329-9088.1000129

48. Tan C-T, Chua K-B. Nipah virus encephalitis. Current infectious disease reports. 2008;10(4):315-20. DOI: https://doi.org/10.1007/s11908-008-0051-6 PMid:18765105

49. Ochani RK, Batra S, Shaikh A, et al. Nipah virus-the rising epidemic: a review. Infez Med. 2019;27(2):117-27.

50. Halpin K, Rota P. A review of Hendra virus and Nipah virus infections in man and other animals. Zoonoses-Infections Affecting Humans and Animals: Focus on Public Health Aspects. 2015:997-1012. DOI: https://doi.org/10.1007/978-94-017-9457-2_40 PMCid:PMC7120151

51. Shaw ML. Henipaviruses employ a multifaceted approach to evade the antiviral interferon response. Viruses. 2009; 1(3):1190-203. DOI: https://doi.org/10.3390/v1031190 PMid:21994589 PMCid:PMC3185527

52. Basler CF. Nipah and Hendra virus interactions with the innate immune system. Henipavirus: Ecology, Molecular Virology, and Pathogenesis. 2012:123-52. DOI: https://doi.org/10.1007/82_2012_209 PMid:22491899

53. Prescott J, de Wit E, Feldmann H, et al. The immune response to Nipah virus infection. Archives of virology. 2012; 157:1635-41. DOI: https://doi.org/10.1007/s00705-012-1352-5 PMid:22669317 PMCid:PMC3432143

54. Chua K, Lam S, Goh K, et al. The presence of Nipah virus in respiratory secretions and urine of patients during an outbreak of Nipah virus encephalitis in Malaysia. Journal of Infection. 2001;42(1):40-3. DOI: https://doi.org/10.1053/jinf.2000.0782 PMid:11243752

55. Shariff M. Nipah virus infection: A review. Epidemiology & Infection. 2019;147:e95. DOI: https://doi.org/10.1017/S0950268819000086 PMid:30869046 PMCid:PMC6518547

56. Liebl DJ, Morris CJ, Henkemeyer M, et al. mRNA expression of ephrins and Eph receptor tyrosine kinases in the neonatal and adult mouse central nervous system. Journal of neuroscience research. 2003;71(1):7-22. DOI: https://doi.org/10.1002/jnr.10457 PMid:12478610

57. Weingartl H, Czub S, Copps J, et al. Invasion of the central nervous system in a porcine host by Nipah virus. Journal of virology. 2005;79(12):7528-34. DOI: https://doi.org/10.1128/JVI.79.12.7528-7534.2005 PMid:15919907

58. Mehnaz S, Anjum R, Mithila FR, et al. The Current Pathogenicity and Potential Risk Assessment of Nipah Virus as Potential Cause of "Disease X": A Narrative Review. Health Science Reports. 2024;7(12): e70241. DOI: https://doi.org/10.1002/hsr2.70241 PMid:39633830 PMCid:PMC11615694

59. Wiley CA. Emergent viral infections of the CNS. Journal of Neuropathology & Experimental Neurology. 2020 Aug 1;79(8):823-42. DOI: https://doi.org/10.1093/jnen/nlaa054 PMid:32647884

60. Escaffre O, Borisevich V, Rockx B. Pathogenesis of Hendra and Nipah virus infection in humans. Journal of infection in developing countries. 2013;7(4):308-11. DOI: https://doi.org/10.3855/jidc.3648 PMid:23592639

61. Rockx B, Brining D, Kramer J, et al. Clinical outcome of henipavirus infection in hamsters is determined by the route and dose of infection. Journal of virology. 2011;85(15):7658-71. DOI: https://doi.org/10.1128/JVI.00473-11

62. Munster VJ, Prescott JB, Bushmaker T, et al. Rapid Nipah virus entry into the central nervous system of hamsters via the olfactory route. Scientific reports. 2012;2(1):1-8. DOI: https://doi.org/10.1038/srep00736 PMid:23071900

63. Hakanpaa L, Sipila T, Leppanen VM, et al. Endothelial destabilization by angiopoietin-2 via integrin β1 activation. Nature communications. 2015 Jan 30;6(1):5962. DOI: https://doi.org/10.1038/ncomms6962 PMid:25635707

64. Kawamura K, Takahashi T, Kanazawa M, et al. Effects of angiopoietin-1 on hemorrhagic transformation and cerebral edema after tissue plasminogen activator treatment for ischemic stroke in rats. PLoS One. 2014 Jun 4;9(6): e98639. DOI: https://doi.org/10.1371/journal.pone.0098639

65. Kim ID, Cave JW, Cho S. Aflibercept, a VEGF (vascular endothelial growth factor)-trap, reduces vascular permeability and stroke-induced brain swelling in obese mice. Stroke. 2021 Aug;52(8):2637-48. DOI: https://doi.org/10.1161/STROKEAHA.121.034362 PMid:34192895

66. Genovese T, Impellizzeri D, D'Amico R, et al. Role of bevacizumab on vascular endothelial growth factor in apolipoprotein E deficient mice after traumatic brain injury. International Journal of Molecular Sciences. 2022 Apr 9;23(8):4162. DOI: https://doi.org/10.3390/ijms23084162

67. Wang L-F, Daniels P. Diagnosis of henipavirus infection: current capabilities and future directions. Henipavirus: Ecology, Molecular Virology, and Pathogenesis. 2012:179-96. DOI: https://doi.org/10.1007/82_2012_215 PMid:22481141

68. Tanimura N, Imada T, Kashiwazaki Y, et al. Monoclonal antibody-based immunohistochemical diagnosis of Malaysian Nipah virus infection in pigs. Journal of comparative pathology. 2004;131(2-3):199-206. DOI: https://doi.org/10.1016/j.jcpa.2004.03.006 PMid:15276859

69. Garbuglia AR, Lapa D, Pauciullo S, et al. Nipah virus: an overview of the current status of diagnostics and their role in preparedness in endemic countries. Viruses. 2023 Oct 7;15(10):2062. DOI: https://doi.org/10.3390/v15102062 PMid:37896839 PMCid:PMC10612039

70. Mazzola LT, Kelly-Cirino C. Diagnostics for Nipah virus: a zoonotic pathogen endemic to Southeast Asia. BMJ global health. 2019;4(Suppl 2): e001118. DOI: https://doi.org/10.1136/bmjgh-2018-001118 PMid:30815286

71. Guillaume V, Lefeuvre A, Faure C, et al. Specific detection of Nipah virus using real-time RT-PCR (TaqMan). Journal of virological methods. 2004;120(2):229-37. DOI: https://doi.org/10.1016/j.jviromet.2004.05.018 PMid:15288966

72. Pollak NM, Olsson M, Marsh GA, et al. Evaluation of three rapid low-resource molecular tests for Nipah virus. Frontiers in microbiology. 2023 Feb 9; 13:1101914. DOI: https://doi.org/10.3389/fmicb.2022.1101914 PMid:36845977

73. Daniels P, Ksiazek T, Eaton BT. Laboratory diagnosis of Nipah and Hendra virus infections. Microbes and infection. 2001;3(4):289-95. DOI: https://doi.org/10.1016/S1286-4579(01)01382-X PMid:11334746

74. Jin K, Huang P, Li B, et al. A Single-Copy Sensitive and Field-Deployable One-Pot RT-RPA CRISPR/Cas12a Assay for the Specific Visual Detection of the Nipah Virus. Transboundary and Emerging Diseases. 2024;2024(1):4118007. DOI: https://doi.org/10.1155/2024/4118007

75. Chong HT, Kamarulzaman A, Tan CT, et al. Treatment of acute Nipah encephalitis with ribavirin. Annals of Neurology: Official Journal of the American Neurological Association and the Child Neurology Society. 2001;49(6):810-3. DOI: https://doi.org/10.1002/ana.1062 PMid:11409437

76. Dawes BE, Kalveram B, Ikegami T, et al. Favipiravir (T-705) protects against Nipah virus infection in the hamster model. Scientific reports. 2018;8(1):1-11. DOI: https://doi.org/10.1038/s41598-018-25780-3 PMid:29765101

77. Lo MK, Spengler JR, Krumpe LR, et al. Griffithsin inhibits Nipah virus entry and fusion and can protect Syrian golden hamsters from lethal Nipah virus challenge. The Journal of infectious diseases. 2020;221(Supplement_4): S480-S92. DOI: https://doi.org/10.1093/infdis/jiz630 PMid:32037447 PMCid:PMC7199786

78. Sissoko D, Laouenan C, Folkesson E, et al. Experimental treatment with favipiravir for Ebola virus disease (the JIKI Trial): a historically controlled, single-arm proof-of-concept trial in Guinea. PLoS medicine. 2016 Mar 1;13(3): e1001967. DOI: https://doi.org/10.1371/journal.pmed.1002066

79. Shinkai M, Tsushima K, Tanaka S, et al. Efficacy and safety of favipiravir in moderate COVID-19 pneumonia patients without oxygen therapy: a randomized, phase III clinical trial. Infectious diseases and therapy. 2021 Dec;10(4):2489-509. DOI: https://doi.org/10.1007/s40121-021-00517-4

80. Hassan MZ, Rojek A, Olliaro P, et al. Improving clinical care of patients in Nipah outbreaks: moving beyond 'compassionate use'. The Lancet Regional Health-Southeast Asia. 2025 Jan 3; 33:100527. DOI: https://doi.org/10.1016/j.lansea.2024.100527 PMid:39866590 PMCid:PMC11755010

81. Amaya M, Broder CC. Vaccines to emerging viruses: Nipah and Hendra. Annual review of virology. 2020; 7:447-73. DOI: https://doi.org/10.1146/annurev-virology-021920-113833 PMid:32991264 PMCid:PMC8782152

82. Soltan MA, Eldeen MA, Elbassiouny N, et al. Proteome based approach defines candidates for designing a multitope vaccine against the Nipah virus. International Journal of Molecular Sciences. 2021;22(17):9330. DOI: https://doi.org/10.3390/ijms22179330 PMid:34502239

83. Majee P, Jain N, Kumar A. Designing of a multi-epitope vaccine candidate against Nipah virus by in silico approach: a putative prophylactic solution for the deadly virus. Journal of Biomolecular Structure and Dynamics. 2021;39(4):1461-80. DOI: https://doi.org/10.1080/07391102.2020.1734088

84. Srivastava S, Verma S, Kamthania M, et al. Exploring the structural basis to develop efficient multi-epitope vaccines displaying interaction with HLA and TAP and TLR3 molecules to prevent NIPAH infection, a global threat to human health. Plos one. 2023;18(3): e0282580. DOI: https://doi.org/10.1371/journal.pone.0282580

85. Loomis RJ, Stewart-Jones GB, Tsybovsky Y, et al. Structure-based design of Nipah virus vaccines: a generalizable approach to paramyxovirus immunogen development. Frontiers in Immunology. 2020; 11:842. DOI: https://doi.org/10.3389/fimmu.2020.00842

86. Rodrigue V, Gravagna K, Yao J, et al. Current progress towards prevention of Nipah and Hendra disease in humans: A scoping review of vaccine and monoclonal antibody candidates being evaluated in clinical trials. Tropical Medicine & International Health. 2024 May;29(5):354-64. DOI: https://doi.org/10.1111/tmi.13979 PMid:38415314

87. Jeon J, Kim E. Exploring Future Pandemic Preparedness Through the Development of Preventive Vaccine Platforms and the Key Roles of International Organizations in a Global Health Crisis. Vaccines. 2025 Jan 10;13(1):56. DOI: https://doi.org/10.3390/vaccines13010056 PMid:39852835 PMCid:PMC11768803

88. Leyva-Grado VH, Promeneur D, Agans KN, et al. Establishing an immune correlate of protection for Nipah virus in nonhuman primates. npj Vaccines. 2024 Dec 19;9(1):244. DOI: https://doi.org/10.1038/s41541-024-01036-2

89. Mishra G, Prajapat V, Nayak D. Advancements in Nipah virus treatment: Analysis of current progress in vaccines, antivirals, and therapeutics. Immunology. 2024 Feb;171(2):155-69. DOI: https://doi.org/10.1111/imm.13695

90. Geisbert TW, Mire CE, Geisbert JB, et al. Therapeutic treatment of Nipah virus infection in nonhuman primates with a neutralizing human monoclonal antibody. Science translational medicine. 2014;6(242):242ra82-ra82. DOI: https://doi.org/10.1126/scitranslmed.3008929

91. García-Murria MJ, Expósito-Domínguez N, Duart G, et al. A bimolecular multicellular complementation system for the detection of syncytium formation: A new methodology for the identification of Nipah virus entry inhibitors. Viruses.

2019 Mar 7;11(3):229. DOI: https://doi.org/10.3390/v11030229 PMid:30866435 PMCid:PMC6466393

92. Negrete OA, Wolf MC, Aguilar HC, et al. Two key residues in ephrinB3 are critical for its use as an alternative receptor for Nipah virus. PLoS pathogens. 2006 Feb;2(2): e7. DOI: https://doi.org/10.1371/journal.ppat.0020007

93. As Winter Nears, many in Bangladesh Fear a Nipah Virus Re-emergence. Available at: https://earthjournalism.net/ stories/as-winter-nears-many-in-bangladesh-fear-a-nipah-virus-re-emergence Accessed 4th February, 2025.

94. Salah Uddin Khan M, Hossain J, Gurley ES, et al. Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. Ecohealth. 2010; 7:517-25. DOI: https://doi.org/10.1007/s10393-010-0366-2 PMid:21207105

95. Ghosh S, Malik YS. Drawing comparisons between SARS-CoV-2 and the animal coronaviruses. Microorganisms. 2020 Nov 23;8(11):1840. DOI: https://doi.org/10.3390/microorganisms8111840 PMid:33238451 PMCid:PMC7700164

96. Hughes JM, Wilson ME, Luby SP, et al. Transmission of human infection with Nipah virus. Clinical infectious diseases. 2009 Dec 1;49(11):1743-8. DOI: https://doi.org/10.1086/647951 PMid:19886791 PMCid:PMC2784122

97. Alotaibi KD, Alharbi HA, Yaish MW, et al. Date palm cultivation: A review of soil and environmental conditions and future challenges. Land Degradation & Development. 2023 May 30;34(9):2431-44. DOI: https://doi.org/10.1002/ldr.4619

98. Kavvadias V, Le Guyader E, El Mazlouzi M, et al. Using date palm residues to improve soil properties: the case of compost and biochar. Soil Systems. 2024 Jun 24;8(3):69. DOI: https://doi.org/10.3390/soilsystems8030069

99. Vasudevan SS, Subash A, Mehta F, et al. Global and regional mortality statistics of nipah virus from 1994 to 2023: a comprehensive systematic review and meta-analysis. Pathogens and Global Health. 2024 Aug 17;118(6):471-80. DOI: https://doi.org/10.1080/20477724.2024.2380131

100. Singh M, Goldin K, Flagg M, Williamson BN, et al. Intracranial inoculation rapidly induces Nipah virus encephalitis in Syrian hamsters. PLOS Neglected Tropical Diseases. 2024 Oct 28;18(10): e0012635. DOI: https://doi.org/10.1371/journal.pntd.0012635 PMid:39466844 PMCid:PMC11542853

101. Kvam KA, Stahl JP, Chow FC, et al. Outcome and Sequelae of Infectious Encephalitis. Journal of Clinical Neurology (Seoul, Korea). 2024 Jan;20(1):23. DOI: https://doi.org/10.3988/jcn.2023.0240 PMid:38179629 PMCid:PMC10782093

102. Mire CE, Chan YP, Borisevich V, et al. A cross-reactive humanized monoclonal antibody targeting fusion glycoprotein function protects ferrets against lethal Nipah virus and Hendra virus infection. The Journal of infectious diseases. 2020 May 1;221(Supplement_4): S471-9. DOI: https://doi.org/10.1093/infdis/jiz515 PMid:31686101 PMCid:PMC7199785

103. Khan S, Akbar SM, Al Mahtab M, et al. Twenty-five years of Nipah outbreaks in Southeast Asia: A persistent threat to global health. IJID regions. 2024 Dec 1; 13:100434. DOI: https://doi.org/10.1016/j.ijregi.2024.100434

104. Mohapatra P, Khatib MN, Shabil M, et al. Addressing the Nipah virus threat: A call for global vigilance and coordinated action. Clinical Infection in Practice. 2024 Oct 12:100390. DOI: https://doi.org/10.1016/j.clinpr.2024.100390

105. Branda F, Ceccarelli G, Giovanetti M, et al. Nipah Virus: A Zoonotic Threat Re-Emerging in the Wake of Global Public Health Challenges. Microorganisms. 2025 Jan 9;13(1):124. DOI: https://doi.org/10.3390/microorganisms13010124 PMid:39858892 PMCid:PMC11767623