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# GLOBAL HEALTH SECURITY: INNOVATIVE THERAPEUTIC AND DIAGNOSTIC APPROACHES AGAINST NIPAH VIRUS - A DISTANT DANGER OR A REAL THREAT?

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**ABSTRACT**

**Background:** Nipah virus (NiV) is an emerging zoonotic paramyxovirus causing severe respiratory distress and devastating neurological complications. Given its high fatality rates and human-to-human transmission, NiV holds significant epidemic potential, prompting the World Health Organization to designate it a priority pathogen.
**Aim:** This review synthesizes current knowledge on the molecular virology, pathogenesis, clinical manifestations, and therapeutic strategies of NiV infection.
**Material and methods:** We analyzed literature from PubMed and Google Scholar, including observational studies, trials, and reviews focusing on the clinical symptoms, diagnostic mechanisms, and molecular virology of NiV.
**Results:** NiV enters cells via highly conserved ephrin-B2/B3 receptors and employs sophisticated immune evasion strategies. We focus on central nervous system (CNS) invasion, detailing how NiV breaches the blood-brain barrier via direct endothelial infection and a leukocyte-mediated "Trojan horse" mechanism. Clinically, NiV induces rapidly progressive acute encephalitis with profound brainstem dysfunction. The virus's unique capacity for persistence often causes delayed-onset or relapsing neurological sequelae, frequently leaving survivors with irreversible cognitive impairments. We address diagnostic complexities, emphasizing the prognostic value of electroencephalography and neuroimaging, alongside rigorous molecular and serological testing. Finally, we review the current frontier of clinical management, including experimental small-molecule antivirals, neutralizing monoclonal antibodies, and next-generation vaccines.
**Conclusions:** Further research into NiV neuroinvasion is essential to develop targeted neuroprotective interventions, improve patient outcomes, and mitigate this severe global health threat.

**KEYWORDS**

Nipah Virus, Encephalitis, Zoonoses, Central Nervous System Infections, Global Health

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## Introduction

Classified within the Paramyxoviridae family, the Nipah virus (NiV) is an extremely virulent RNA pathogen and the second recognized species within the Henipavirus genus. Genetically, it shares approximately 80% of its sequence with the Hendra virus, the inaugural member of this genus responsible for a fatal 1994 outbreak among equines and humans in Australia (Ang et al., 2018). However, unlike NiV, the Hendra virus has never demonstrated the capacity to spread directly between humans (Alam, 2022; Halpin & Rota, 2015). While NiV has primarily endangered public health across South and Southeast Asia for more than twenty years, serological evidence indicates that bat colonies in Oceania, Madagascar, and West Africa also harbor the virus (Alam, 2022; Faus-Cotino et al., 2024).

The inaugural identification of NiV occurred during a 1998 crisis in Malaysia that left 109 individuals dead out of 283 infected (Aditi & Shariff, 2019). Subsequent epidemics have periodically struck the Philippines, India, Bangladesh, and Singapore. In Bangladesh, infections typically surge between December and May, aligning directly with the local date palm sap harvesting period (Ang et al., 2018). This temporal pattern highlights the crucial role of Pteropus fruit bats, which act as the main natural hosts and vectors for the pathogen (Aditi & Shariff, 2019; Faus-Cotino et al., 2024). Furthermore, because NiV utilizes the highly conserved mammalian ephrin-B2 and ephrin-B3 molecules to penetrate cells, it exhibits an unusually extensive host range and species tropism compared to other paramyxoviruses (Aditi & Shariff, 2019; Ang et al., 2018; Xu et al., 2012).

The majority of human cases stem from zoonotic spillover events. These can happen when individuals consume raw fruits or date palm sap tainted by bat excrement, urine, saliva, or by interacting with infected intermediary animals like dogs, cats, horses, or pigs. Even the act of scaling trees soiled with contaminated sap

can precipitate an infection (Alam, 2022; Ang et al., 2018; Faus-Cotino et al., 2024). Intermediate animal vectors were especially critical in driving the outbreaks seen in the Philippines, Singapore, and Malaysia. Environmentally, the pathogen remains viable for a minimum of 7 days in 22°C artificial date palm sap and up to 3 days in fruit juices. However, standard detergents or a 15-minute heat treatment at 100°C can achieve complete viral inactivation. Importantly, the shedding of virions in respiratory droplets and saliva creates a profound risk for human-to-human contagion (Singh et al., 2019).

NiV is associated with devastating lethality, though case fatality rates (CFR) fluctuate dramatically depending on the specific viral variant and geographic location. While the first Singaporean epidemic saw a 21% CFR, mortality in India has soared as high as 82.7%. Between 2014 and 2023, the cumulative fatality rate hovered around 80.1%, with severe viral encephalitis driving roughly 95% of those fatalities (Vasudevan et al., 2024).

Diagnosing the disease early is often challenging due to its presentation as catastrophic neurological and respiratory syndromes. Although the pathogen typically incubates in under two weeks, latency periods exceeding four months have been documented (Madhukalya et al., 2025). Adding to the clinical complexity, the virus can remain dormant and trigger relapsing encephalitic episodes months or years following the initial illness (Alam, 2022; Ang et al., 2018; Clayton, 2017).

The combination of extreme lethality and interpersonal spread emphasizes the desperate necessity for robust disease management frameworks. Clinical identification currently depends on molecular and serological testing. Due to the lack of officially approved targeted antivirals or vaccines, and although various candidates are currently under clinical evaluation, the primary defenses against NiV remain rigorous public awareness campaigns and strict infection control protocols.

India continues to face recurrent viral activity, highlighted by a prominent 2018 incident in Kerala that resulted in over 20 cases, followed by subsequent regional flare-ups (Soman Pillai et al., 2020). A fresh emergence occurred in West Bengal on January 26, 2026, which notably included hospital-acquired infections in a pair of medical professionals. Even though the immediate threat of a major international pandemic is deemed relatively low, the widespread habitat of the reservoir bats coupled with the reality of interpersonal transmission demands intense global surveillance. Consequently, confronting the profound absence of therapeutic options and the clear epidemic threat, the World Health Organization (WHO) elevated NiV to its urgent research and development priority list in 2018 (Klingelhöfer et al., 2025; Madhukalya et al., 2025; Widerspick et al., 2022).

Because NiV is classified as a Biosafety Level 4 (BSL-4) agent, scientists must employ the strictest biocontainment measures, severely restricting the number of global facilities equipped to study live samples (Alam, 2022; Madhukalya et al., 2025; Wang et al., 2024). The vast geographical footprint of Pteropus bats, paired with the modern ease of international travel, amplifies fears of unprecedented outbreak events (Aditi & Shariff, 2019; Mathieu et al., 2011; Singh et al., 2019). Taking into account its destructive clinical trajectory and capacity for widespread transmission, decoding the precise pathogenic mechanisms of the virus - especially concerning its neurological impact - stands as a supreme priority for global public health.

## Discussion

### 1. Viral Structure and Mechanisms of Infection

Because of their swift evolutionary capabilities - driven by accelerated generation cycles and elevated mutation frequencies - RNA viruses carry a profound potential for infection (Aditi & Shariff, 2019; Madhukalya et al., 2025). As a result, these pathogens are presently believed to be responsible for as much as 44% of all newly emerging infectious illnesses (Madhukalya et al., 2025). At its core, the Nipah virus (NiV) relies on a negative-sense, single-stranded RNA genome responsible for coding six distinct structural proteins: the nucleocapsid (N), phosphoprotein (P), matrix (M), fusion glycoprotein (F), surface attachment glycoprotein (G), and the large RNA-dependent RNA polymerase (L) (Aditi & Shariff, 2019; Al-Obaidi et al., 2024; Soman Pillai et al., 2020).

The N protein interacts with both the P and L proteins to assemble ribonucleoprotein (RNP) complexes, which play a critical role in regulating the replication and transcription of the viral genome (Devnath et al., 2022; Thakur & Bailey, 2019). Serving as a highly versatile enzyme, the L protein drives the entire process of genome replication and manages every phase of mRNA transcription, from initiation through elongation to termination. Finally, the M protein dictates the structural assembly and subsequent budding of newly formed NiV virions from the infected host cell (Devnath et al., 2022; Faus-Cotino et al., 2024; Ganguly et al., 2025; Madhukalya et al., 2025; Talukdar et al., 2023; Thakur & Bailey, 2019; Wang et al., 2024).

## 2. Mechanisms of Attachment and Host Cell Entry

Cellular invasion and initial host attachment are fundamentally governed by the viral F and G surface glycoproteins. In particular, the virion secures itself to the host through the G protein, which directly binds to the cellular ephrin-B2 and ephrin-B3 receptors. The heavy concentration of ephrin-B2 in arterial tissues explains the virus's strong vascular tropism, while its ability to target neurological pathways corresponds to the abundant distribution of ephrin-B3 across vascular and central nervous system (CNS) (Ang et al., 2018; Tiong et al., 2018; Wang et al., 2024).

The invasion cascade is initiated the moment the viral G protein locks onto the host ephrin-B2 receptor, causing a conformational alteration that stimulates the F glycoprotein. Following a proteolytic cleavage event, this F protein reorganizes into a six-helical bundle that actively punctures the cellular membrane, thereby granting the virus entry to commence replication (Singh et al., 2019; Soman Pillai et al., 2020; Wang et al., 2024). Additionally, as the F and G glycoproteins become expressed on the host's basolateral membranes, they induce the fusion of neighboring epithelial cells, effectively amplifying local viral dissemination. This cellular merging produces multinucleated giant cells, commonly referred to as syncytia, which serve as a classic morphological indicator of paramyxoviral infections (Devnath et al., 2022; Thakur & Bailey, 2019).

### 2.1 Strain Diversity and Pathogenicity

Various lineages of the virus display notable variations in their pathogenic mechanisms, transmission efficiency, and overall lethality. The epidemic spanning Malaysia and Singapore was definitively linked to a singular variant of the NiV-M (Malaysia) lineage, in stark contrast to the Indian and Bangladesh outbreaks, which were fueled by variants of the NiV-B (Bangladesh) lineage. Genetically, these two viral strains share a 91.8% similarity in their nucleotide sequences and a 92% homology across their expressed amino acids (Madhukalya et al., 2025; Thakur & Bailey, 2019).

In vivo studies utilizing ferrets and non-human primates have revealed divergent disease courses; the NiV-B strain generally triggers a more rapid onset of symptoms, accompanied by intensified viral replication within the respiratory tract and elevated oral shedding. On the other hand, infections caused by the NiV-M strain are disproportionately linked to devastating neuroinvasive disease (Madhukalya et al., 2025; Wang et al., 2024).

### 2.2 Immune Evasion Strategies

The P gene is fundamentally important to the virus's pathogenic mechanisms, as it encodes the main P protein alongside three additional non-structural proteins designated W, V, and C. Each of these four proteins acts as a strong antagonist against interferons (IFNs), effectively dampening both the adaptive and innate branches of the host's immune system. By blocking the phosphorylation of STAT1, these viral products successfully dismantle the JAK/STAT signaling cascade, allowing the virus to evade the host's immunological defenses (Al-Obaidi et al., 2024; Singh et al., 2019). Furthermore, the virus disrupts standard antiviral countermeasures by neutralizing the activity of RIG-I and MDA-5 receptors (Al-Obaidi et al., 2024; Devnath et al., 2022). Specifically, IKK-epsilon signaling is obstructed by the W and V proteins, which subsequently cripples the immune cascades normally triggered by Toll-like receptor 3 (TLR3) and circulating viral RNA (Devnath et al., 2022; Madhukalya et al., 2025). Operating within the cellular cytoplasm, the C protein halts the induction of IFN-alpha directly, while also stifling type I IFN pathways indirectly by scaling down the synthesis of viral RNA (Devnath et al., 2022; Madhukalya et al., 2025). Out of all these proteins, the W protein demonstrates the strongest immunosuppressive abilities; it isolates itself inside the host's nucleus to prevent the genetic expression of type I IFNs (alpha/beta). As a direct result, the production and secretion of crucial inflammatory mediators - especially TNF-alpha, CCL4/5, and type I IFNs - are severely curtailed (Al-Obaidi et al., 2024; Faus-Cotino et al., 2024; Sharma et al., 2019; Wang et al., 2024).

### 2.3 Transmission, Systemic Dissemination, and Pathology

The spread of the virus is heavily tied to respiratory pathways, primarily occurring through expelled droplets and aerosolized respiratory secretions generated by sneezing or coughing. Transmission is also facilitated by direct exposure to various contaminated bodily fluids, including breast milk, semen, cerebrospinal fluid, serum, saliva, and urine. Once the virions are deposited in the lower and upper respiratory tracts, they actively invade the local epithelial lining. From there, the virus achieves systemic circulation through viral budding, eventually reaching the mucosa-associated lymphoid tissue (MALT) (Faus-Cotino et al., 2024).

The specific locations of tissue damage and the pathogen's overall tropism are fundamentally dictated by where the host expresses ephrin-B3 and ephrin-B2 receptors. Notably, NiV exhibits a strong tendency to infect circulating leukocytes, especially CD6-positive T-cells. This CD6 surface protein functions as a binding partner for the activated leukocyte cell adhesion molecule, also known as ALCAM or CD166 (Al-Obaidi et al., 2024; Madhukalya et al., 2025; Wang et al., 2024). Because ALCAM is abundantly present on the endothelial cells lining the microvasculature of both the blood-air and blood-brain barriers, the virus naturally gravitates toward the microscopic vessels within the pulmonary and central nervous systems. Within the lungs, this infection typically triggers massive cytokine release, damage to the microvasculature, pulmonary edema, and bleeding within the alveoli. Clinically, these severe pulmonary lesions align with the rapid development of acute respiratory distress syndrome (ARDS) and interstitial pneumonia (Sharma et al., 2019; Wang et al., 2024).

**3. Neuroinvasion and Neurological Manifestations**

As the infection spreads systemically, it commonly provokes extensive vasculitis (Sejvar et al., 2007). In fact, post-mortem analyses have detected vascular inflammation across the spleen, kidneys, heart, and brain in roughly 62% of infected patients (Wang et al., 2024). The pathogen gains its primary access to the central nervous system (CNS) via the choroid plexus and the complex cerebral blood vessel network (Singh et al., 2019). The movement of infected leukocytes greatly assists this neurological invasion, while the concurrent local secretion of inflammatory cytokines, including IL-1 and TNF-alpha, severely damages the structural integrity of the blood-brain barrier (BBB) (Al-Obaidi et al., 2018; Madhukalya et al., 2025). This collapse of the BBB serves as a major catalyst for the catastrophic neurological symptoms observed in patients, sparking massive ischemia caused by thrombosis and vasculitis, alongside extensive necrosis within the brain parenchyma and diffuse necrotic lesions (Devnath et al., 2022; Faus-Cotino et al., 2024; Thakur & Bailey, 2019; Wang et al., 2024). Moreover, emerging research has identified an additional, direct pathway for neuroinvasion - NiV possesses the ability to circumvent the BBB completely by traveling in a retrograde direction up the olfactory nerve. After initially infecting the epithelial cells of the nasal cavity, the pathogen migrates into the olfactory bulb before finally spreading throughout the ventral cortex in the vicinity of the olfactory tubercle (Al-Obaidi et al., 2024; Devnath et al., 2022; Madhukalya et al., 2025).

Ultimately, the virus inflicts harm upon the nervous system through two closely linked processes - direct infection of the neurons and extensive vascular inflammation (Alam, 2022). Although the mechanisms by which NiV infiltrates the CNS are highly complex, the successful compromise of the BBB remains the most pivotal event. Under normal conditions, the BBB acts as a highly selective boundary that preserves the neurological environment. Constructed from pericytes, astrocytes, and capillary endothelial cells (ECs), this barrier maintains physiological homeostasis by tightly controlling the passage of molecules and blocking peripheral immune cells, toxins, and systemic pathogens from entering the brain (Boardman et al., 2025; Tiong et al., 2018).

The microvascular ECs, firmly anchored to the basement membrane, represent a major target for NiV attack. This vulnerability is due to the dense expression of ephrin-B3 and ephrin-B2 tyrosine kinase receptors on both the brain's endothelial lining and its neurons, which the virus exploits as its main gateways for cellular entry. Furthermore, through structural shifts in its F and G surface glycoproteins, the virus can also utilize micropinocytosis to penetrate certain target cells and deposit its genetic payload directly into the host's cytoplasm (Al-Obaidi et al., 2024; Mathieu et al., 2011).

In a secondary approach, the virus effectively smuggles itself across the BBB using a "Trojan horse" strategy, hitching a ride inside infected circulating leukocytes - most notably immature dendritic cells, monocytes, and lymphocytes (Al-Obaidi et al., 2024; Devnath et al., 2022; Tiong et al., 2018). Even though robust viral replication does not occur within certain immune populations like T-lymphocytes, these cells still enable CNS infiltration through a process of trans-infection. By latching onto the outer membranes of these white blood cells, the pathogen uses them as microscopic transport vehicles to bypass the endothelial defenses. These hijacked leukocytes then undergo diapedesis, migrating out of the blood vessels and directly into the delicate brain parenchyma (Tiong et al., 2018). Once inside, the ensuing localized immune reaction and the heavy secretion of inflammatory cytokines destroy crucial adhesion molecules, basement membranes, and tight junctions, culminating in the total functional collapse of the BBB. Furthermore, studies conducted on non-human primate models have confirmed that NiV is fully capable of establishing direct infections within CD68-positive microglial cells and neurons (Al-Obaidi et al., 2024).

### 3.1 Acute Neurological Manifestations

In the course of the Malaysian epidemic, medical professionals originally confused NiV cases with Japanese encephalitis (JE), given the region's history of pig-related JE outbreaks (Goh et al., 2000; Sharma et al., 2019). Nevertheless, the observed symptoms did not align with classic JE. A striking feature was the high prevalence among adult males, a demographic anomaly eventually traced back to their professional contact with diseased swine in agricultural settings (Farrar, 1999).

The pathogen induces an aggressive, fast-moving encephalitis. The illness usually begins with generalized prodromal signs like muscle pain, fever, emesis, headaches, and breathing difficulties. Within a mere 24 to 48 hours, patients experience a precipitous clinical decline, transitioning from extreme fatigue and disorientation to severe neuropsychiatric complications, acute encephalitic inflammation, and ultimately, a comatose state.

Early indicators of acute brainstem compromise include the disappearance of primal brainstem responses like the doll's eye (oculocephalic) reflex, uncoordinated ocular tracking (gaze palsy), and atypical pupil responses to light stimuli (Aditi & Shariff, 2019; Ang et al., 2018; Hassan et al., 2026; Vasudevan et al., 2024). Alongside these motor dysfunctions, patients frequently suffer from severe autonomic dysregulation, characterized predominantly by high blood pressure and rapid heart rates.

As the disease advances, individuals routinely develop localized muscle weakness, cerebellar deficits, reduced or absent reflexes (hyporeflexia/areflexia), convulsive seizures, and segmental myoclonus. Moreover, distinct focal neurological impairments serve as strong predictors of fatal outcomes, especially in cases driven by the NiV-M strain. Hallmarks of profound pyramidal tract and upper motor neuron destruction - such as the bilateral Babinski sign (extensor plantar response) and the loss of deep tendon reflexes - are particularly ominous.

The highest risk of death, however, correlates with extreme autonomic failure, typically presenting as temperatures exceeding 37.8°C, dangerous hypertension, and tachycardia. This level of autonomic collapse implies widespread viral invasion and resulting tissue death within the brainstem, underscoring the pathogen's destructive affinity for neural tissue and signaling an exceptionally bleak prognosis (Hassan et al., 2026).

### 3.2 Delayed-Onset and Relapsing Neurological Sequelae

Identifying relapsing or delayed-onset presentations represents a major hurdle for clinicians, primarily because bridging an abrupt neurological crisis to a distant viral infection is highly complex. Extended clinical monitoring reveals that up to 26% of afflicted individuals suffer from enduring neurological deficits and long-term sequelae. Within the survivor cohort, roughly 3% were left with devastating physical and cognitive disabilities, such as persistent memory loss, ataxia, optic nerve damage, myopathy, and severe epileptic episodes that demanded hospitalization. An additional 3% endured chronic neuropsychiatric issues, most notably drastic personality shifts and debilitating clinical depression, serving as a grim testament to the permanent, extensive destruction the pathogen unleashes upon the central nervous system (Hassan et al., 2026).

### 3.3 Neuroimaging Findings in Nipah Virus Encephalitis

When evaluating brain alterations linked to the virus, magnetic resonance imaging (MRI) stands out as the most valuable diagnostic modality. To capture acute pathological changes, diffusion-weighted imaging (DWI) proves particularly effective. The emergence of T1-weighted hyperintensities, arriving closely behind distinct punctate DWI lesions, strongly points to ischemic microinfarctions driven by viral microangiopathy. Additionally, fluid-attenuated inversion recovery (FLAIR) protocols provide the clearest visualization of neural lesions. In tandem with MRI, single-photon emission computed tomography (SPECT) scanning can detect focal zones of intense hyperperfusion during the early inflammatory cascade; these same areas ultimately degenerate into states of irreversible hypoperfusion (Alam, 2022; Ang et al., 2018; Rumboldt, 2008; Singh et al., 2019; Tan et al., 2002)**.**

### 3.4 Geographical Variations in Acute Presentation

Interestingly, radiological patterns have varied depending on the geographical origin of the outbreak. In the midst of the Malaysian epidemic, 71% of patients who underwent MRI scans displayed hyperintense cerebral lesions, predominantly localized within the pons, temporal lobe, and cerebral cortex (Hassan et al., 2026). For individuals suffering from delayed or relapsing forms of the disease, imaging primarily highlighted confluent and patchy damage across the cortical regions. Conversely, the Singaporean cohort presented a divergent MRI profile; their scans typically featured numerous sub-centimeter, bilateral lesions distributed widely across the deep white matter and subcortical zones. Following the introduction of contrast agents, a subset of these abnormalities demonstrated enhancement, occasionally extending into the corpus callosum, brainstem, and cortex (Ang et al., 2018).

### 3.5 Long-term Follow-up and Asymptomatic Cases

Longitudinal MRI tracking of the Singaporean patient cohort revealed that initial brain lesions slowly faded away, lacking any radiological signs of disease recurrence. Nevertheless, transient T1-weighted hyperintensities emerged within the cortical regions, generating an appearance that radiologically mimicked laminar cortical necrosis. Surprisingly, when exposed slaughterhouse employees who tested seropositive but never developed symptoms were scanned, delayed MRIs uncovered small, distinct brain abnormalities highly similar to the lesions found in patients suffering from active encephalitis. Even though MRI utilization was less frequent during the later Indian and Bangladesh epidemics, the available scans reliably highlighted both confluent and multifocal damage spanning the cerebral cortex and white matter (Ang et al., 2018; Singh et al., 2019).

### 3.6 Electroencephalography

To functionally assess the gravity of NiV-induced encephalitic disease, electroencephalography (EEG) represents a highly effective diagnostic asset. Even though viral brain infections typically produce non-specific EEG alterations, NiV generates distinctive electrical signatures that are tightly linked to clinical prognosis and the extent of neural damage. The most common electrographic anomalies include widespread, continuous slowing, frequently paired with localized electrical discharges and focal dominance concentrated in the frontal and temporal lobes. Any individual displaying overt cerebral manifestations will consistently yield pathological EEG recordings. In contrast to structural MRI data, the intensity of these EEG disruptions provides a highly precise mirror of the patient's actual neurological deterioration. During extreme acute episodes, recordings regularly expose bilateral temporal periodic complexes a rhythm of slow and sharp waves firing every one to two seconds. This electrographic signature carries heavy prognostic weight, as it typically surfaces in patients who have lapsed into profound comas and nearly always predicts a fatal outcome. Curiously, the clinical manifestation of myoclonus does not correlate meaningfully with the severity recorded on the EEG. Moreover, while the affected brain hemispheres might align, the extreme generalized slowing seen on EEG is not directly reliant on the precise quantity or existence of structural lesions visible on radiological scans. Crucially, the severe bitemporal periodic complexes a defining feature of lethal, acute NiV encephalitis do not appear in individuals suffering from relapsing or late-onset forms of the disease. This absence underscores the fundamentally different pathological mechanisms driving these delayed neurological complications (Misra et al., 2008; Tan et al., 2002).

## 4. Molecular Diagnostic Methods

Because NiV features fluctuating incubation windows and vague initial symptoms, relying entirely on clinical observation for diagnosis is extremely unreliable. Isolating the pathogen relies heavily on cerebrospinal fluid (CSF) as a critical clinical specimen. For diagnostic confirmation, reverse transcription-polymerase chain reaction (RT-PCR) is widely utilized to detect viral RNA, in conjunction with enzyme-linked immunosorbent assays (ELISAs) to identify virus-specific antibodies (Ang et al., 2018; Hassan et al., 2026; Klingelhöfer et al., 2025; Singh et al., 2019; Thakur & Bailey, 2019). Furthermore, successfully culturing the virus straight from a patient's CSF strongly correlates with an increased likelihood of mortality. When managing acute infections, the optimal diagnostic samples involve respiratory swabs, urine, serum, blood, and CSF. If the disease proves fatal, post-mortem evaluations typically involve harvesting tissue from the kidneys, spleen, lungs, and brain. To preserve viability, all collected biological materials require rigorous thermal regulation (maintained between 2–8°C while in transit, and frozen at −20°C if stored for more than 48 hours) (Aditi & Shariff, 2019). To circumvent the logistical challenges of high-biocontainment laboratories, contemporary serological tools utilize recombinant NiV proteins.

Nevertheless, molecular testing continues to serve as the absolute diagnostic standard. For detecting active NiV cases, standard RT-PCR and quantitative real-time PCR (qRT-PCR) offer unparalleled sensitivity (Madhukalya et al., 2025). These molecular assays generally home in on highly stable genomic sequences, primarily focusing on the phosphoprotein (P), matrix (M), and nucleocapsid (N) genes, along with the specific intergenic space located between the G and F genes. Although Next-Generation Sequencing (NGS) demands extensive processing time and high financial costs - making it impractical for routine clinical diagnosis - it serves as an indispensable tool for tracing mutational shifts and conducting phylogenetic mapping (Madhukalya et al., 2025).

Whenever an unfamiliar outbreak emerges, actual viral isolation remains the ultimate reference method. Moreover, during post-mortem evaluations, formalin-fixed tissues can be analyzed using

immunohistochemistry (IHC), which reliably exposes NiV antigens embedded in the respiratory lining, neurons, and vascular endothelial cells. To manage epidemics and conduct broad epidemiological surveillance, ELISAs offer an accelerated method for evaluating IgG and IgM antibody levels. Because the N protein is produced in massive quantities, it acts as the primary biomarker for early diagnosis, utilized extensively in IgM capture ELISAs to spot acute infections (frequently detectable within just 5 days of symptom onset) (Madhukalya et al., 2025). On the other hand, indirect IgG ELISAs are vital for prolonged serological monitoring. This assay is widely applied to verify immunological recovery in human survivors, as well as to screen intermediate animal vectors and natural bat reservoirs (Madhukalya et al., 2025; Singh et al., 2019).

**5. Acute Supportive Care**

Any individual presenting with suspected NiV infection must be subjected to strict and immediate isolation. The foundation of clinical intervention relies entirely on robust supportive therapies, with a primary emphasis on stabilizing electrolyte balances and systemic fluid levels. When patients develop acute respiratory failure or severe pneumonic complications, supplemental oxygen becomes mandatory, frequently requiring the implementation of mechanical ventilation. Because viral-induced vascular inflammation routinely precipitates venous thrombosis, typically hemorrheologic medications and anticoagulants - notably pentoxifylline and aspirin are administered to mitigate clotting risks.

Additional palliative measures involve deploying anticonvulsants (such as phenytoin) to suppress seizures, antipyretics to reduce high body temperatures, and highly targeted therapies to counteract hemodynamic shock, severe hypoglycemia, and dangerous spikes in intracranial pressure. Finally, to combat potential opportunistic infections, standard medical protocol dictates the empirical administration of broad-spectrum antibiotics, typically azithromycin and ceftriaxone (Goh et al., 2000; Hassan et al., 2026).

**6. Experimental Small-Molecule Antivirals**

Although the medical community lacks officially sanctioned antiviral therapeutics for NiV, multiple compounds designed to disrupt various stages of the viral replication cycle are either currently undergoing or awaiting clinical scrutiny. During the inaugural Malaysian epidemic, patients frequently received ribavirin through both intravenous and oral routes. Initial observations linked this treatment to a decrease in lingering neurological impairments and a 36% drop in the mortality rate. Nevertheless, its therapeutic value during the 2018 Kerala crisis was heavily disputed; additionally, in vivo animal research has yielded inconsistent outcomes and raised alarms regarding potential teratogenic effects (Devnath et al., 2022; Madhukalya et al., 2025).

Operating as an inhibitor of RNA synthesis, remdesivir - a broad-spectrum nucleotide prodrug widely recognized for its application in COVID-19 management - has shown remarkable promise. Specifically, in vivo lethal challenge models demonstrated that it secured a 100% survival rate, exhibiting exceptionally potent activity against the NiV-B lineage (Amirian & Levy, 2020; Faus-Cotino et al., 2024; Lo et al., 2019; Madhukalya et al., 2025). Another compound, the RNA-dependent RNA polymerase (RdRp) inhibitor favipiravir, successfully shielded animal models completely from the NiV-M variant when dosed continuously for 14 days right after viral exposure (Amirian & Levy, 2020; Faus-Cotino et al., 2024; Soman Pillai et al., 2020). Experts currently view favipiravir as one of the most promising antiviral candidates, particularly when deployed in combination with monoclonal antibody therapies.

Similarly, the RdRp inhibitor 4'-azidocytidine aggressively suppresses viral multiplication at low micromolar concentrations (Hotard et al., 2017; Madhukalya et al., 2025). Balapiravir, another polymerase inhibitor, has displayed strong in vitro activity and is currently awaiting in vivo testing (Hotard et al., 2017; Madhukalya et al., 2025). In a unique mechanistic approach, griffithsin - a specialized protein derived from red algae - disrupts both the formation of syncytia and initial cellular penetration at merely nanomolar levels (Lusvarghi & Bewley, 2016; Wang et al., 2024). On the other hand, while chloroquine initially demonstrated in vitro potential by obstructing the F glycoprotein, subsequent in vivo assessments concluded that it fails to halt the systemic spread of the virus (Aditi & Shariff, 2019; Faus-Cotino et al., 2024; Ganguly et al., 2025; Mishra et al., 2024; Pallister et al., 2009; Wang et al., 2024).

### 6.1 Monoclonal Antibodies (mAbs)

In the realm of acute disease management and post-exposure prophylaxis, neutralizing monoclonal antibodies (mAbs) stand at the forefront of modern therapeutic innovation.

A leading candidate, the humanized mAb m102.4, effectively prevents the viral G glycoprotein from binding to the host's ephrin-B2 and ephrin-B3 receptors. Having passed Phase I human clinical trials, this antibody has proven highly safe while maintaining robust neutralizing power against both Hendra and Nipah viruses, even if given five days after initial exposure (Faus-Cotino et al., 2024; Madhukalya et al., 2025; Devnath et al., 2022; Mishra et al., 2024; Mathieu et al., 2018; Hassan et al., 2024; Gonepudi et al., 2025). Furthermore, the h5B3.1 antibody zeros in on the F (fusion) glycoprotein by blocking the structural shifts required for membrane fusion; remarkably, it has guaranteed total survival in animal subjects, even when deployed in the later stages of infection (Devnath et al., 2022; Faus-Cotino et al., 2024; Ganguly et al., 2025; Madhukalya et al., 2025; Mishra et al., 2024). To counter the threat of viral escape mutations, scientists are actively investigating mAb cocktails. These therapeutic blends, such as the pairing of HENV32 and HENV26, are engineered to latch onto distinct, non-overlapping antigenic regions across the viral envelope (Mishra et al., 2024).

## 7. Vaccine Development

Because live NiV mandates the strictest BSL-4 biocontainment protocols, creating conventional live-attenuated vaccines is practically impossible. As a result, current scientific efforts are overwhelmingly directed toward subunit formulations and recombinant platforms. Although human-approved vaccines do not yet exist, an adenovirus-vectored candidate is presently undergoing its inaugural human trials (Madhukalya et al., 2025). Relying on specific glycoprotein fragments, subunit vaccines have already achieved clinical success in the Australian equine industry, demonstrating substantial capacity to interrupt zoonotic transmission pathways (Devnath et al., 2022; Ganguly et al., 2025; Madhukalya et al., 2025; Thakur & Bailey, 2019). For human applications, a formulation built around the pre-F/G protein structure remains a primary focal point (Mishra et al., 2024). Virus-Like Particles (VLPs) have also exhibited remarkable efficacy in vivo; by perfectly imitating the physical structure of the NiV virion - minus the infectious genetic material - they safely stimulate comprehensive adaptive B-cell and innate immune responses (Faus-Cotino et al., 2024; Pallister et al., 2009; Talukdar et al., 2023; Thakur & Bailey, 2019).

Contemporary strategies frequently employ viral vector vaccines, wherein weakened substitute viruses are repurposed to express NiV F or G antigens (Pallister et al., 2009). The Recombinant Vesicular Stomatitis Virus (rVSV) stands out as a highly potent vector, quickly mobilizing both adaptive and innate defenses to provide absolute immunity in non-human primates, even when inoculated just prior to a lethal viral exposure (Pallister et al., 2009; Wang et al., 2024). Other vectors, such as the Modified Vaccinia Ankara (MVA) strain and the recombinant measles virus (MV), boast superior BSL-1 safety ratings. Crucially, these vectors avoid host genome integration while still conferring total protection in mammalian test subjects (Pallister et al., 2009; Singh et al., 2019). Additionally, enduring immunological memory spanning up to 16 weeks has been achieved using the Adeno-Associated Virus (AAV) vector, whereas the simian adenovirus platform, ChAdOx1, is actively advancing through preliminary human studies (Ganguly et al., 2025; Pallister et al., 2009; Van Doremalen et al., 2022). On the veterinary front, vectors such as the Newcastle Disease Virus (NDV) and Canarypox (ALVAC) have proven highly effective at curbing viral shedding among swine populations, representing an essential intervention for severing the epidemiological chain of transmission (Ganguly et al., 2025; Pallister et al., 2009; Singh et al., 2019).

Lastly, harnessing the mRNA breakthroughs popularized during the COVID-19 outbreak, vaccines utilizing lipid nanoparticles to deliver mRNA coding for pre-F/G antigens have generated powerful humoral defenses, aggressive CD8+ T-cell activity, and enhanced T-follicular helper (Tfh) cell responses, securing robust protection across animal models (Faus-Cotino et al., 2024; Madhukalya et al., 2025; Pallister et al., 2009)

### 8. Theoretical Risks and Future Immune Targets

Within the sphere of vaccine and immunotherapeutic design, Antibody-Dependent Enhancement (ADE) persists as a theoretical hazard. Familiar to researchers studying the Dengue virus, ADE occurs when non-neutralizing or sub-optimal antibodies accidentally assist the pathogen in invading host cells. Because the envelope proteins of NiV exhibit lower conservation and high structural variation, the actual probability of ADE is deemed quite low; nonetheless, stringent surveillance for this phenomenon remains an indispensable requirement for clinical safety. Finally, analyzing the genomic disparities between highly vulnerable animals (e.g., African green monkeys) and species that harbor the virus without manifesting clinical symptoms (e.g., cynomolgus macaques) provides an exciting pathway for discovering entirely new therapeutic targets for human medicine (Singh et al., 2019; Talukdar et al., 2023).

### Conclusion and Future Directions

Despite substantial strides in decoding the overarching pathogenesis of NiV, the precise molecular mechanisms facilitating central nervous system (CNS) invasion remain incompletely understood. Clinically, the disease presents a formidable diagnostic hurdle. Physicians must maintain a high index of suspicion when evaluating complex neurological cases, particularly in patients with travel history to high-risk regions. Given the pathogen's unusual capacity to trigger delayed and relapsing encephalitic episodes, comprehensive patient exposure assessments must extend well beyond standard clinical timeframes. The variations observed in this study further highlight the critical need for upgraded surveillance infrastructure, which is essential for capturing early radiological markers and ultimately improving patient outcomes. Moving forward, research must prioritize mapping the routes of CNS infiltration and elucidating how the virus physically degrades the blood-brain barrier to facilitate the development of specialized neuroprotective drugs. Only by fully unraveling NiV neuropathogenesis can targeted therapeutics and effective vaccines be designed to mitigate this severe global health threat (Burki, 2023).

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## REFERENCES

1. Aditi, & Shariff, M. (2019). Nipah virus infection: A review. *Epidemiology and Infection, 147*, e95. https://doi.org/10.1017/S0950268819000086
2. Alam, A. M. (2022). Nipah virus, an emerging zoonotic disease causing fatal encephalitis. *Clinical Medicine, 22*(4), 348–352. https://doi.org/10.7861/clinmed.2022-0166
3. Al-Obaidi, M. M. J., Bahadoran, A., Wang, S. M., Manikam, R., Raju, C. S., & Sekaran, S. D. (2018). Disruption of the blood brain barrier is vital property of neurotropic viral infection of the central nervous system. *Acta Virologica, 62*(1), 16–27. https://doi.org/10.4149/av_2018_102
4. Al-Obaidi, M. M. J., Muthanna, A., & Desa, M. N. M. (2024). Nipah virus neurotropism: Insights into blood-brain barrier disruption. *Journal of Integrative Neuroscience, 23*(5), 90. https://doi.org/10.31083/j.jin2305090
5. Amirian, E. S., & Levy, J. K. (2020). Current knowledge about the antivirals remdesivir (GS-5734) and GS-441524 as therapeutic options for coronaviruses. *One Health, 9*, 100128. https://doi.org/10.1016/j.onehlt.2020.100128
6. Ang, B. S. P., Lim, T. C. C., & Wang, L. (2018). Nipah virus infection. *Journal of Clinical Microbiology, 56*(6), e01875-17. https://doi.org/10.1128/JCM.01875-17
7. Boardman, S. A., Hetherington, C., Hughes, T., Cook, C., Galea, I., Hilton, O., Solomon, T., Luster, A. D., Allan, S., Kurt-Jones, E., Forth, J., Patabendige, A., Egbe, F. N., Dunai, C., & Michael, B. D. (2025). Viral infection and the blood-brain barrier: Molecular research insights and therapies. *The Journal of Infectious Diseases, 232*(6), 1273–1282. https://doi.org/10.1093/infdis/jiaf455
8. Burki, T. (2023). Nipah virus: An ever-present threat. *The Lancet Infectious Diseases, 23*(11), e473–e474. https://doi.org/10.1016/S1473-3099(23)00643-6
9. Clayton, B. A. (2017). Nipah virus: Transmission of a zoonotic paramyxovirus. *Current Opinion in Virology, 22*, 97–104. https://doi.org/10.1016/j.coviro.2016.12.003
10. Devnath, P., Wajed, S., Chandra Das, R., Kar, S., Islam, I., & Masud, H. M. A. A. (2022). The pathogenesis of Nipah virus: A review. *Microbial Pathogenesis, 170*, 105693. https://doi.org/10.1016/j.micpath.2022.105693
11. Farrar, J. J. (1999). Nipah-virus encephalitis—Investigation of a new infection. *The Lancet, 354*(9186), 1222–1223. https://doi.org/10.1016/S0140-6736(99)90124-1
12. Faus-Cotino, J., Reina, G., & Pueyo, J. (2024). Nipah virus: A multidimensional update. *Viruses, 16*(2), 179. https://doi.org/10.3390/v16020179

13. Ganguly, A., Mahapatra, S., Ray, S., Chattopadhyay, S., Islam, M. J., Garai, S., Dutta, T. K., Chattaraj, M., & Chattaraj, S. (2025). The rising threat of Nipah virus: A highly contagious and deadly zoonotic pathogen. *Virology Journal, 22*(1), 139. https://doi.org/10.1186/s12985-025-02728-4
14. Goh, K. J., Tan, C. T., Chew, N. K., Tan, P. S. K., Kamarulzaman, A., Sarji, S. A., Wong, K. T., Abdullah, B. J. J., Chua, K. B., & Lam, S. K. (2000). Clinical features of Nipah virus encephalitis among pig farmers in Malaysia. *New England Journal of Medicine, 342*(17), 1229–1235. https://doi.org/10.1056/NEJM200004273421701
15. Gonepudi, N. K., Baffour Awuah, H., Xu, W., Katte, R. H., & Lu, M. (2025). Structure-guided design of peptide inhibitors targeting class I viral fusion proteins. *Pathogens, 15*(1), 32. https://doi.org/10.3390/pathogens15010032
16. Halpin, K., & Rota, P. (2015). A review of Hendra virus and Nipah virus infections in man and other animals. In A. Sing (Ed.), *Zoonoses—Infections affecting humans and animals* (pp. 997–1012). Springer Netherlands. https://doi.org/10.1007/978-94-017-9457-2_40
17. Hassan, M. Z., Ibrahim, S. K., Harriss, E., Horby, P., Olliaro, P., & Rojek, A. (2026). Interpreting the natural history and pathogenesis of Nipah virus disease through clinical data, to inform clinical trial design: A systematic review. *The Lancet Microbe*, 101295. https://doi.org/10.1016/j.lanmic.2025.101295
18. Hassan, M. Z., Shirin, T., Satter, S. M., Rahman, M. Z., Bourner, J., Cheyne, A., Torreele, E., Horby, P., & Olliaro, P. (2024). Nipah virus disease: What can we do to improve patient care? *The Lancet Infectious Diseases, 24*(7), e463–e471. https://doi.org/10.1016/S1473-3099(23)00707-7
19. Hotard, A. L., He, B., Nichol, S. T., Spiropoulou, C. F., & Lo, M. K. (2017). 4′-Azidocytidine (R1479) inhibits henipaviruses and other paramyxoviruses with high potency. *Antiviral Research, 144*, 147–152. https://doi.org/10.1016/j.antiviral.2017.06.011
20. Klingelhöfer, D., Braun, M., Naser, C. A., Brüggmann, D., & Groneberg, D. A. (2025). Emerging Nipah virus with pandemic potential and high mortality rates: Is the scientific community learning from former pandemics? *Reviews in Medical Virology, 35*(2), e70028. https://doi.org/10.1002/rmv.70028
21. Lo, M. K., Feldmann, F., Gary, J. M., Jordan, R., Bannister, R., Cronin, J., Patel, N. R., Klena, J. D., Nichol, S. T., Cihlar, T., Zaki, S. R., Feldmann, H., Spiropoulou, C. F., & De Wit, E. (2019). Remdesivir (GS-5734) protects African green monkeys from Nipah virus challenge. *Science Translational Medicine, 11*(494), eaau9242. https://doi.org/10.1126/scitranslmed.aau9242
22. Lusvarghi, S., & Bewley, C. (2016). Griffithsin: An antiviral lectin with outstanding therapeutic potential. *Viruses, 8*(10), 296. https://doi.org/10.3390/v8100296
23. Madhukalya, R., Yadav, U., Parray, H. A., Raj, N., Lupitha, S. S., Kumar, V., Saroj, A., Agarwal, V., Kumar, D., Das, S., & Kumar, R. (2025). Nipah virus: Pathogenesis, genome, diagnosis, and treatment. *Applied Microbiology and Biotechnology, 109*(1), 158. https://doi.org/10.1007/s00253-025-13474-6
24. Mathieu, C., Pohl, C., Szecsi, J., Trajkovic-Bodennec, S., Devergnas, S., Raoul, H., Cosset, F.-L., Gerlier, D., Wild, T. F., & Horvat, B. (2011). Nipah virus uses leukocytes for efficient dissemination within a host. *Journal of Virology, 85*(15), 7863–7871. https://doi.org/10.1128/JVI.00549-11
25. Mathieu, C., Porotto, M., Figueira, T. N., Horvat, B., & Moscona, A. (2018). Fusion inhibitory lipopeptides engineered for prophylaxis of Nipah virus in primates. *The Journal of Infectious Diseases, 218*(2), 218–227. https://doi.org/10.1093/infdis/jiy152
26. Mishra, G., Prajapat, V., & Nayak, D. (2024). Advancements in NIPAH virus treatment: Analysis of current progress in vaccines, antivirals, and therapeutics. *Immunology, 171*(2), 155–169. https://doi.org/10.1111/imm.13695
27. Misra, U. K., Tan, C. T., & Kalita, J. (2008). Viral encephalitis and epilepsy. *Epilepsia, 49*(S6), 13–18. https://doi.org/10.1111/j.1528-1167.2008.01751.x
28. Pallister, J., Middleton, D., Crameri, G., Yamada, M., Klein, R., Hancock, T. J., Foord, A., Shiell, B., Michalski, W., Broder, C. C., & Wang, L.-F. (2009). Chloroquine administration does not prevent Nipah virus infection and disease in ferrets. *Journal of Virology, 83*(22), 11979–11982. https://doi.org/10.1128/JVI.01847-09
29. Rumboldt, Z. (2008). Imaging of topographic viral CNS infections. *Neuroimaging Clinics of North America, 18*(1), 85–92. https://doi.org/10.1016/j.nic.2007.12.006
30. Sejvar, J. J., Hossain, J., Saha, S. K., Gurley, E. S., Banu, S., Hamadani, J. D., Faiz, M. A., Siddiqui, F. M., Mohammad, Q. D., Mollah, A. H., Uddin, R., Alam, R., Rahman, R., Tan, C. T., Bellini, W., Rota, P., Breiman, R. F., & Luby, S. P. (2007). Long-term neurological and functional outcome in Nipah virus infection. *Annals of Neurology, 62*(3), 235–242. https://doi.org/10.1002/ana.21178
31. Sharma, V., Kaushik, S., Kumar, R., Yadav, J. P., & Kaushik, S. (2019). Emerging trends of Nipah virus: A review. *Reviews in Medical Virology, 29*(1), e2010. https://doi.org/10.1002/rmv.2010
32. Singh, R. K., Dhama, K., Chakraborty, S., Tiwari, R., Natesan, S., Khandia, R., Munjal, A., Vora, K. S., Latheef, S. K., Karthik, K., Singh Malik, Y., Singh, R., Chaicumpa, W., & Mourya, D. T. (2019). Nipah virus: Epidemiology, pathology, immunobiology and advances in diagnosis, vaccine designing and control strategies—A comprehensive review. *Veterinary Quarterly, 39*(1), 26–55. https://doi.org/10.1080/01652176.2019.1580827
33. Soman Pillai, V., Krishna, G., & Valiya Veettil, M. (2020). Nipah virus: Past outbreaks and future containment. *Viruses, 12*(4), 465. https://doi.org/10.3390/v12040465

34. Talukdar, P., Dutta, D., Ghosh, E., Bose, I., & Bhattacharjee, S. (2023). Molecular pathogenesis of Nipah virus. *Applied Biochemistry and Biotechnology, 195*(4), 2451–2462. https://doi.org/10.1007/s12010-022-04300-0
35. Tan, C. T., Goh, K. J., Wong, K. T., Sarji, S. A., Chua, K. B., Chew, N. K., Murugasu, P., Loh, Y. L., Chong, H. T., Tan, K. S., Thayaparan, T., Kumar, S., & Jusoh, M. R. (2002). Relapsed and late-onset Nipah encephalitis. *Annals of Neurology, 51*(6), 703–708. https://doi.org/10.1002/ana.10212
36. Thakur, N., & Bailey, D. (2019). Advances in diagnostics, vaccines and therapeutics for Nipah virus. *Microbes and Infection, 21*(7), 278–286. https://doi.org/10.1016/j.micinf.2019.02.002
37. Tiong, V., Shu, M.-H., Wong, W. F., AbuBakar, S., & Chang, L.-Y. (2018). Nipah virus infection of immature dendritic cells increases its transendothelial migration across human brain microvascular endothelial cells. *Frontiers in Microbiology, 9*, 2747. https://doi.org/10.3389/fmicb.2018.02747
38. Van Doremalen, N., Avanzato, V. A., Goldin, K., Feldmann, F., Schulz, J. E., Haddock, E., Okumura, A., Lovaglio, J., Hanley, P. W., Cordova, K., Saturday, G., De Wit, E., Lambe, T., Gilbert, S. C., & Munster, V. J. (2022). ChAdOx1 NiV vaccination protects against lethal Nipah Bangladesh virus infection in African green monkeys. *NPJ Vaccines, 7*(1), 171. https://doi.org/10.1038/s41541-022-00592-9
39. Vasudevan, S. S., Subash, A., Mehta, F., Kandrikar, T. Y., Desai, R., Khan, K., Khanduja, S., Pitliya, A., Raavi, L., Kanagala, S. G., & Gondaliya, P. (2024). Global and regional mortality statistics of Nipah virus from 1994 to 2023: A comprehensive systematic review and meta-analysis. *Pathogens and Global Health, 118*(6), 471–480. https://doi.org/10.1080/20477724.2024.2380131
40. Wang, L., Lu, D., Yang, M., Chai, S., Du, H., & Jiang, H. (2024). Nipah virus: Epidemiology, pathogenesis, treatment, and prevention. *Frontiers of Medicine, 18*(6), 969–987. https://doi.org/10.1007/s11684-024-1078-2
41. Widerspick, L., Vázquez, C. A., Niemetz, L., Heung, M., Olal, C., Bencsik, A., Henkel, C., Pfister, A., Brunetti, J. E., Kucinskaite-Kodze, I., Lawrence, P., Muñoz Fontela, C., Diederich, S., & Escudero-Pérez, B. (2022). Inactivation methods for experimental Nipah virus infection. *Viruses, 14*(5), 1052. https://doi.org/10.3390/v14051052
42. Xu, K., Broder, C. C., & Nikolov, D. B. (2012). Ephrin-B2 and ephrin-B3 as functional henipavirus receptors. *Seminars in Cell & Developmental Biology, 23*(1), 116–123. https://doi.org/10.1016/j.semcdb.2011.12.005