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Nipah Virus at the Human-Animal Interface: Epidemiology, Zoonotic Transmission, and Public Health Implications

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Abstract

Nipah virus (NiV) is a pathogenic zoonotic virus from the Henipavirus genus, discovered during a 1998-1999 outbreak in Malaysia, particularly in Sungai Nipah. It caused serious illness in pigs and severe encephalitis (brain inflammation) and respiratory issues in humans. The virus primarily transmits from animals, especially fruit bats of the Pteropus genus, to humans, with instances of human-to-human transmission noted. Fruit bats harboring Nipah virus are found throughout South and Southeast Asia, Australia, and East Africa. Two main strains exist: the Malaysia strain (NiV-M), associated with animal-to-human transmission via pigs, and the Bangladesh strain (NiV-B), which has increased human-to-human transmission rates and higher fatality rates. The threat of the Nipah virus is being actively addressed by international health agencies, with the WHO designating it as a priority pathogen for urgent research and development. The UN supports preparation efforts aligned with the Sustainable Development Goals (SDG 3: Good Health and Well-Being). National agencies, including the UK's NHS, engage in monitoring and research collaboration, while NGOs like UNICEF, CDC, and CEPI contribute to outbreak response, vaccine development, and community awareness. Artificial intelligence (AI) has significant potential to reduce Nipah virus outbreaks by improving early detection, predicting spillover risks, enhancing contact tracing, and accelerating the development of vaccines and treatments. AI-based genetic analysis and Modeling can notably shorten the timelines for creating effective medical solutions, offering optimism for future prevention and treatment methods.

Keywords: Nipah virus, Fruit bats (Pteropus), Zoonotic illness, Global health response, Artificial intelligence.

1.0 Nipah Virus: A History of Discovery and Transmission

The Nipah virus surfaced as a notable public health menace in late 1998, when an outbreak of severe encephalitis began impacting pig farmers and those near pigs in peninsular Malaysia. The outbreak, which persisted into early 1999, resulted in 283 cases and 109 fatalities, signifying humanity's initial confrontation with this lethal infection. The virus concurrently emerged in Singapore, impacting eleven abattoir workers who had interacted with pigs imported from the infected Malaysian farms, leading to one death. The original epidemic necessitated extensive control measures, resulting in the killing of over one million pigs in Malaysia, which ultimately terminated the disease by mid-1999 [1,2].

The geographical distribution of the Nipah virus underwent a significant transformation in 2001 with its inaugural emergence in Bangladesh and India. This signified the formation of a unique Bangladesh strain, which would demonstrate fundamentally different traits from the Malaysian strain. The virus shown its capacity to infiltrate new regions, as seen by a significant outbreak in the Siliguri area of West Bengal, India, during this timeframe [3].

From 2003 to 2005, Bangladesh had epidemics in many districts, developing a troublingly consistent pattern. The occurrences demonstrated the Bangladesh strain's increased ability for human-to-human transmission, a trait that significantly differentiated it from the Malaysian strain and heightened concerns among global public health officials. The persistent occurrence of these outbreaks indicated that the Nipah virus has established a viable transmission cycle in the area. Anish [4].

In 2014, the Philippines documented their inaugural and sole Nipah virus outbreak, thereby extending the virus's recognized geographic distribution beyond mainland Asia. This emergence illustrated the potential for the Nipah virus to manifest in previously unexposed areas, although the Philippines has not documented any additional outbreaks. In 2018, Kerala, India, had a significant epidemic, garnering fresh global focus on the Nipah virus. The outbreak resulted in considerable fatalities and necessitated comprehensive public health measures for containment. In 2021, Kerala encountered another outbreak of the Nipah virus, highlighting the region's persistent susceptibility to this illness and the difficulties in preventing its reemergence in ecologically favorable places [5,6].

Since 2001, Bangladesh has witnessed practically annual outbreaks, so identifying the nation as having endemic Nipah virus activity. The ongoing recurrence of Nipah virus has established Bangladesh as a central hub for research and surveillance, yielding essential insights into the virus's behavior and transmission dynamics [5,7].

The two discovered strains demonstrate very distinct transmission mechanisms. The Malaysian strain is largely transferred from infected pigs to humans, with minimal evidence of human-to-human transmission. Conversely, the Bangladesh strain exhibits an increased capacity for direct human-to-human transmission, frequently by the ingestion of contaminated date palm sap or intimate contact with infected persons. The underlying disparity in transmission patterns renders the Bangladesh strain a significantly bigger public health threat, since it exhibits enhanced pandemic potential and poses more intricate obstacles for outbreak control and preventive efforts.

1.1 Chronology of Geographic Distribution

1998-1999: Malaysia and Singapore

2001: Bangladesh and India (first emergence of the Bangladesh strain)

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2003-2005: Various districts in Bangladesh
2014: Philippines
2018: Kerala, India
2021: Kerala, India [2].
Persistent: Almost annual epidemics in Bangladesh since 2001.

The two strains exhibit considerable differences in transmission patterns, with the Bangladesh strain demonstrating an increased capacity for human-to-human transmission, hence posing a bigger public health risk [7].

Fruit bats inhabit tropical and subtropical climates globally.

Fruit bats (flying foxes) are not found in the Americas and Europe, while other bat species inhabit those areas. The highest diversity of fruit bat species is seen in Southeast Asia, Australia, and the Pacific islands [8].

2.0 The Nipah Virus: Transmission from Bats to Humans

The Nipah virus is classified within the family Paramyxoviridae and the genus Henipavirus. The transition from the animal kingdom to humans exemplifies zoonotic spillover, wherein a pathogen transfers from animals to humans [9].

2.1 The Connection Between Animals and Humans

Species of fruit bats in the Pteropus genus act as the natural reservoir for the Nipah virus. These volant mammals harbor the virus asymptomatically, rendering them ideal reservoirs for prolonged viral persistence in the environment. The virus resides in bats and is excreted through their saliva, urine, and partially consumed fruit.

The primary transmission to humans transpired via an intermediary host: swine. The virus disseminated to domestic pigs when infected bats discarded half consumed fruit on pig farms or when their bodily fluids tainted pig feed. Pigs contracted respiratory disease and acted as amplifying hosts, indicating that the virus proliferated extensively within them. Farmers and others in proximity to infected pigs subsequently acquired the virus by direct contact with ill animals or their contaminated excretions.

Direct transmission from bats to humans happens, especially when individuals ingest date palm sap contaminated by diseased bats. Bats frequent palm trees nocturnally to consume the sweet nectar, subsequently depositing saliva and urine that harbor the virus. The consumption of this polluted sap in its unprocessed form might lead to infection in individuals. Moreover, ingesting fruit that has been partially consumed by infected bats may result in infection. Transmission Between Humans.

After the virus establishes itself in a human host, it can disseminate across individuals via multiple pathways. The virus exists in respiratory secretions, saliva, and various body fluids of infected persons. Proximity to an infected individual-especially caregivers, family members, and healthcare professionals exposes individuals to danger.

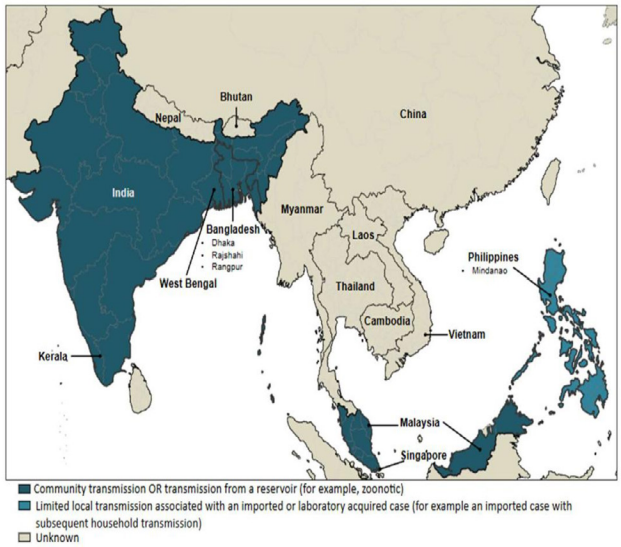
The virus transmits via respiratory droplets expelled by infected persons during coughing or sneezing. Direct exposure to contaminated bodily fluids, such as urine and blood, further facilitates the transmission of the virus. Hospital environments are especially susceptible to epidemics, as healthcare professionals caring for critically ill patients may be exposed via aerosol-generating procedures or insufficient infection control protocols.

The Dual Viral Variants

The Nipah virus comprises two unique genetic lineages or strains, each designated by its first identification location. The Bangladesh strain (NiV-B) and the Malaysia strain (NiV-M) exhibit significant differences that influence illness outcomes [8]. The Malaysia strain generally induces heightened respiratory symptoms in both pigs and humans, with a considerable percentage of patients experiencing acute respiratory distress. Nonetheless, it exhibits reduced efficacy in human-to-human transmission [10].

The Bangladesh strain manifests differently, resulting in more neurological problems and demonstrating a greater capacity for human-to-human transmission. This strain has been linked to several clusters of human illnesses among family members and healthcare personnel. The Bangladesh variation exhibits heightened neurotropism, indicating a greater propensity to infiltrate and harm the nervous system, resulting in encephalitis-brain inflammation. Both strains induce severe illness with elevated fatality rates; but, the Bangladesh variant's enhanced capacity for human transmission renders it especially alarming from a public health standpoint. Comprehending these distinctions enables authorities to customize their outbreak response techniques, prioritizing isolation and infection control measures suited to the transmission patterns of each strain [11].

2.3 Nipah virus distribution map in Southeast Asia and South Asia from 1999 onwards



(Nipah Virus: Epidemiology, Outbreaks and Guidance, 2026)

3.0 Digital Transformation in Medical Science: The Function of Innovation and Monitoring in Nipah Virus Management

The Nipah virus (NiV) is a highly consequential zoonotic infection associated with considerable mortality in humans. Efficient medical responses increasingly rely on digital technology that improve detection, measurement, therapy design, and the analysis of intricate biological data. Conventional laboratory techniques are inadequate to satisfy the swift timeframes and accuracy demanded by new viruses like NiV; therefore, sophisticated digital approaches are being incorporated into medical research and clinical processes.

A significant improvement in NiV diagnostics is the adoption of digital polymerase chain reaction (dPCR) technologies, particularly droplet digital PCR (ddPCR). In contrast to traditional quantitative PCR (qPCR), ddPCR divides samples into numerous nanoliter droplets and employs statistical models to enumerate positive amplifications, facilitating absolute quantification of target nucleic acid molecules with elevated sensitivity and reliable performance, even in low viral load matrices. This method improves the reliability of early NiV identification, especially in intricate clinical or environmental samples where virus RNA may be limited [12,13].

In addition to PCR improvements, metagenomic next-generation sequencing (mNGS) combined with sophisticated bioinformatics represents a crucial digital method for impartial pathogen identification and monitoring. mNGS procedures, facilitated by high-throughput sequencing technologies, concurrently sequence all nucleic acids inside a sample and depend on computational reference libraries for the classification of various organisms. When integrated with AI-driven analytical workflows, these solutions can significantly decrease the interval between sample collection and etiological identification, converting raw sequence data into useful clinical insights while minimizing analytical bottlenecks [14].

Artificial intelligence (AI) and machine learning (ML) are crucial in diagnostic interpretation and therapeutic research. In diagnostics, AI models can automate the interpretation of intricate sequence or laboratory data, improving turnaround time and standardization among laboratories. In therapeutic discovery, machine learning-assisted in silico drug screening has been utilized for Nipah virus targets, including the viral glycoprotein. Computational frameworks can analyze extensive chemical libraries, implement predictive binding affinity models, and enhance lead compounds using molecular dynamics simulations and optimization methods. These computerized methodologies considerably expedite the initial phases of antiviral medication discovery, diminishing dependence on laborious wet-lab testing [15,16].

The amalgamation of computational genomics and predictive modeling facilitates proactive strategies for viral evolution. Although not exclusive to NiV, AI systems trained on viral genomic datasets can predict probable mutation pathways, guide vaccine development, and prioritize genomic areas for focused surveillance. These predictive models utilize patterns in high-dimensional sequence data, providing a proactive approach to epidemic preparedness and the systematic design of medicinal countermeasures [17,18].

Moreover, digital infrastructure for data integration and real-time analytics enables the application of test results in clinical practice. Automated sequencing analysis, cloud-based data exchange, and standardized digital reporting formats minimize the delay between detection and treatment decisions. These technologies are especially important in outbreak situations where swift clinical evaluations are essential to direct therapeutic measures, allocate hospital resources, and commence antiviral treatments [19].

The digital progression of medicine in addressing the Nipah virus involves an integrated ecosystem of digital diagnostics, AI-enhanced analytics, computational drug discovery, and genomic technologies. These advances enhance both the sensitivity and specificity of NiV detection while also expediting the process from pathogen identification to treatment hypothesis formulation-an essential requirement during high-threat viral outbreaks [20,21].

4.0 UN strategic initiatives in Promoting SDG Health Objectives: Tackling Nipah virus via Global Health Programs

The United Nations has exhibited its dedication to Sustainable Development Goal 3 (Good Health and Well-Being) by implementing proactive measures against new infectious disease risks such as the Nipah virus. This zoonotic disease, initially discovered in Malaysia in 1998, illustrates the "One Health" difficulties that the UN tackles through its health-oriented sustainable development framework.

The UN's strategy on the Nipah virus directly corresponds with the aims of SDG 3, which focus on enhancing ability to manage health risks and attaining universal health coverage. The World Health Organization, a specialized body of the UN, has created coordinated monitoring systems in endemic regions, especially in South and Southeast Asia. These efforts advance SDG 3.3's objective to address communicable illnesses by improving early detection and outbreak response systems [22].

UN health initiatives have emphasized enhancing laboratory capabilities in at-risk countries for the swift diagnosis of the Nipah virus. This infrastructural development directly supports SDG 3.b, which highlights the necessity of ensuring access to medicines and vaccines for diseases impacting developing nations. Educating healthcare professionals in impacted areas fosters enduring local proficiency, diminishing reliance on external emergency interventions.

(Goal 3: Good Health and Well-being - the Global Goals, 2024).

(Goal 3: Good Health and Well-being - the Global Goals, 2024)

The United Nations' focus on prevention aligns with Sustainable Development Goal 3.d's emphasis on enhancing early warning systems for health hazards. In Bangladesh and India, where Nipah outbreaks frequently occur, educational initiatives have focused on promoting behavioral modifications, including the avoidance of raw date palm sap drinking and the reduction of human-animal interactions in areas susceptible to epidemics. These community-based programs illustrate that SDG health targets encompass not just clinical treatment but also the social drivers of illness transmission [23,24].

Research cooperation constitutes another vital contribution of the UN. UN health programs promote SDG 3 by fostering global cooperation in the development of Nipah virus vaccines and therapeutic research's objectives include carrying out research and development for diseases predominantly impacting underdeveloped nations. This involves coordinating resources and expertise from several countries to combat a virus with pandemic potential. The UN's coordinated response to the Nipah virus demonstrates how tackling particular disease risks promotes overarching health goals. Enhancing health systems to address Nipah concurrently fortifies resilience against future emerging infectious illnesses, establishing sustainable infrastructure that fulfils many Sustainable Development Goal 3 targets. This strategy illustrates the UN's acknowledgment that effective disease management necessitates holistic health system enhancement rather than fragmented treatments [25].

5.0 African Tactical measures to Prevent and Fight the Nipah Virus

Africa enhances public health monitoring systems in accordance with the International Health Regulations (IHR) to promptly identify atypical viral infections. Numerous nations surveil viral haemorrhagic fevers and new zoonotic illnesses, including Nipah if it were to be

introduced [26,27].

Africa employs a One Health approach, unifying human, animal, and environmental health sectors. Monitoring of fruit bats, recognized reservoirs of the Nipah virus, is performed via wildlife research and ecological assessment initiatives [28].

Third, laboratory capacity has been enhanced via regional reference laboratories proficient in identifying high-risk diseases. Educating healthcare professionals in infection prevention and control (IPC) diminishes the likelihood of transmission within hospitals.

Fourth, border health protocols, including screening at entrance points, assist in identifying passengers exhibiting symptoms from impacted areas. Public health authorities restrict the trade of animals and the transportation of cattle to mitigate the dangers of zoonotic spillover. Africa collaborates with WHO Africa (AFRO), the Africa CDC, and international partners for risk assessment, preparedness planning, and quick response measures. These steps collectively enhance Africa's preparedness to prevent and address the Nipah virus [29-34].

6.0 Conclusion

The Nipah virus is a significant zoonotic hazard, necessitating coordinated global e orts and new disease management strategies. Since its identification in Malaysia in 1998, this lethal disease has exhibited exceptional resilience, disseminating throughout South and Southeast Asia with catastrophic e ects on both human and animal populations. The temporal spread of Nipah, originating from its original outbreak in Malaysian pig farms to subsequent clusters in Bangladesh, India, and the Philippines, highlights the virus's ability for global dissemination and its propensity to develop endemic patterns in novel regions.

Comprehending the transmission pathway from bats to humans has been essential in formulating preventative tactics. Pteropus fruit bats, as natural reservoir hosts, excrete the virus via saliva, urine, and partially consumed fruits, so establishing many exposure pathways for humans. Each transmission route contaminated date palm sap ingestion, direct contact with sick animals, or human-to-human transmission in hospital environments-poses distinct obstacles necessitating specific responses. This intricate epidemiology requires comprehensive strategies that consider both ecological and behavioural elements.

The digital transformation in Nipah virus management signifies a fundamental change in our approach to addressing new infectious illnesses. Advanced genetic sequencing facilitates swift strain identification, whilst artificial intelligence algorithms forecast outbreak areas by examining environmental and climatic data. Mobile health applications enable real-time monitoring, permitting healthcare professionals in remote locations to promptly report suspected instances. Geographic information systems delineate transmission patterns, pinpointing high-risk areas and directing resource distribution. These technological advancements have reduced response times from weeks to days, potentially preserving several lives through early detection and care.

The United Nations' incorporation of Nipah virus management into the Sustainable Development Goals framework signifies an acknowledgment that health security is intrinsically linked to overarching development aims. SDG 3's focus on health and well-being has prompted international organizations to allocate funding for monitoring infrastructure, enhance laboratory capabilities, and foster cross-border collaboration. The One Health approach, advocated by UN agencies, recognizes the interconnection of human, animal, and environmental health, necessitating coordinated measures that surpass conventional sectoral divisions.

African nations, while not yet substantially impacted by the Nipah virus, have proactively instituted preventive measures based on their experiences with previous haemorrhagic fevers such as Ebola. Improved border surveillance systems, fortified diagnostic capabilities, and community engagement initiatives equip the continent to respond swiftly in the event of a Nipah outbreak. The Africa CDC illustrates the significance of readiness over reaction through regional collaborations, with early warning systems and quick response teams prepared to manage any outbreaks before they intensify.

As climate change modifies bat habitats and human encroachment into wildlife regions escalates, the likelihood of future Nipah outbreaks is expected to rise. Preventing the next major epidemic necessitates persistent investment in surveillance, ongoing digital innovation, international collaboration, and community-level education. The insights gained from Nipah virus management highlighting readiness, technological integration, and global cooperation offer a framework for addressing the zoonotic risks that will surely arise in our linked world.

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Conflict of Interest Statement

Regarding the creation and submission of this work, the author asserts that there are no conflicts of interest. The author alone is the only creator of the content; no outside interests or undue influence might jeopardize the impartiality or integrity of the data. All references and sources used in the production of this content have been properly acknowledged and cited, guaranteeing that the original authors and their contributions receive due recognition. The author states that this work is an original invention and that no affiliations, financial interests, or personal ties have impacted the research, writing, or conclusions presented herein. The integrity of the submitted work and the accuracy of the material are entirely the author's responsibility.

Ethical Approval

Not reported

Guarantor

None

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