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Spatiotemporal Genomic And One Health Risk Analysis Of Nipah Virus Infection Emergence And Transmission Dynamics In South And Southeast Asia

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Abstract : Nipah Virus Infection (NVI) is a highly fatal zoonosis caused by a henipavirus, and is prevalent with periodic outbreaks in South and Southeast Asia. Outbreaks are closely associated with zoonotic spillover from fruit bats (Pteropus spp.) to humans, and are commonly linked with environmental change and human-animal interactions (WHO, 2023). In this regard, spatiotemporal genomic monitoring has become a vital method to monitor the viral evolution, detect clusters of transmission and predict the likelihood of outbreaks (Rahman et al., 2021).

This research employs the One Health Approach to comprehensively explore human–animalenvironmental interfaces in the genesis of Nipah virus. The study will focus on the analysis of genetic evolution, spatiotemporal spread and multi-disciplinary risk factors. The research approach involves a phylogenetic analysis of the viral genome, Geographic Information System (GIS) for spatial mapping and epidemiological modeling to detect hotspots and transmission networks (Lo Presti et al., 2016).

Major insights will provide understanding of mutation, spatiotemporal clustering and environmental risk factors of outbreaks (to be included post-analysis). It argues for integrated surveillance and inter-sectoral

management for detection and prevention of outbreaks. These findings will enhance public health readiness, improve response efforts and guide policy responses to emerging zoonotic diseases in at-risk populations (to be incorporated after analysis).

Keywords:
Nipah virus; zoonotic diseases; genomic epidemiology; One Health; spillover events; transmission dynamics; South Asia; Southeast Asia

1. Introduction

1.1 Background

Nipah Virus Infection (NiV) is a highly transmissible zoonosis associated with a member of the virus family Paramyxoviridae, genus Henipavirus. The Pteropus genus of fruit bats are known as the reservoir hosts, which can affect humans through direct or indirect transmission routes [1]. Following its initial detection during the Malaysian outbreak (1998-1999), repeated outbreaks have occurred in Bangladesh and India, where it is linked to date palm sap consumption, and human-to-human transmission [2],[3]. NiV causes severe encephalitis and respiratory disease with lethality of 40-75%, indicating its high pandemic potential and listing as a priority pathogen by the World Health Organisation and the National Institutes of Health, USA [1],[4].

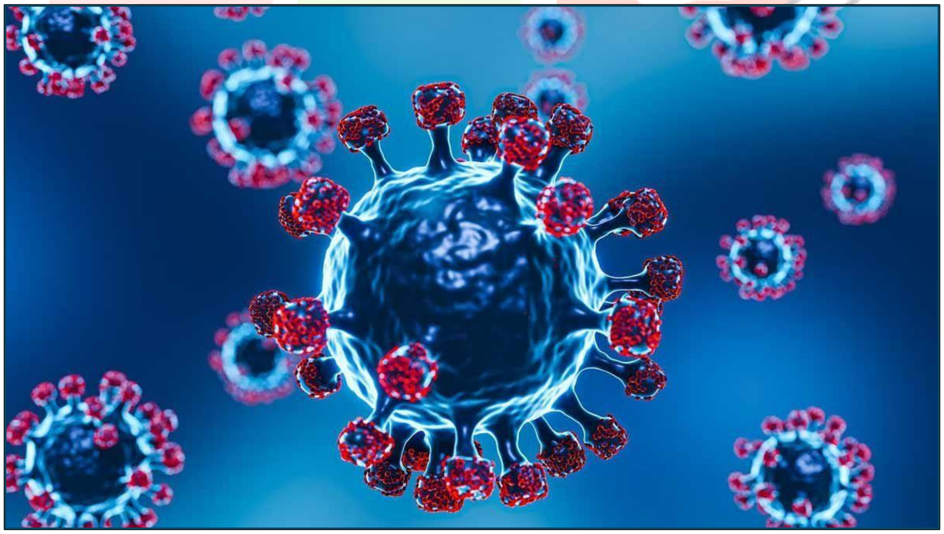

Fig no. 1 Nipah Virus

1.2 Rationale

NiV's intricate epidemiology requires a holistic approach to data integration using genomics, ecology and epidemiology for analysis. Outbreak surveillance networks are often reactive and do not have the resolution to account for viral evolution and ecological influences, restricting the ability to detect and control outbreaks [5].

1.3 Research Gap

Despite the emergence of genomic epidemiology, few studies combine spatiotemporal genomic data with environmental and zoonotic risks. Further, In the case of NiV, predictive models based on the One Health Approach are still in its infancy [6].

1.4 Objectives

We will investigate the evolution of NiV genomes, spatiotemporal distribution of outbreaks, assess risk factors and develop a predictive One Health-based model to improve surveillance and preparedness.

2. Materials and Methods

2.1 Study Design

The proposed study uses an observational, integrative computational design based on secondary data. It integrates genomic, epidemiological and environmental data to examine the dynamics of Nipah Virus Infection emergence and spread over space and time

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2.2 Data Sources

Public repositories that contained genomic sequences through GenBank and GISAID were accessed. Epidemiological data which included outbreaks, cases and mortality was sourced through international and national health organizations like WHO, CDC, and country-based surveillance systems. Satellite data and climatic data banks provided the environmental variables such as temperature, rainfall, among other land-use patterns.

2.3 Study Area

The research targets endemic and outbreak-prone countries (South Asia) in India and Bangladesh as well as other Southeast Asia (Malaysia, Singapore, Thailand) where a series of incidences of Nipah virus are documented.

2.4 Genomic Analysis

Known sequence of the viral genomes was also put into position with MAFFT to provide some continuity and accuracy. To establish evolutionary relationships, the Maximum Likelihood and Bayesian inference methods were used to construct phylogenetic trees. Lineage tracking and mutation profiling was performed to determine genetic variation and diversification of strains.

2.5 Spatiotemporal Analysis

Spatial mapping of outbreak clusters were done using the Geographic Information System (GIS) software ArcGIS and QGIS. Time-series models were used to analyze the time trends, whereas SaTScan was used to detect spatial clusters and identification of hotspots.

2.6 One Health Risk Modeling.

An interdisciplinary risk model was constructed that incorporated several parameters (population density, mobility, bat distribution, climate variability, land-use change) under the One Health Approach.

2.7 Statistical Analysis

Statistical analysis comprised regression analysis, risk factor correlation analysis, machine learning data catalyzed by the use of Random Forest and Support Vector Machine (SVM), which are also powerful predictors of the risk of an outbreak.

2.8 Data Presentation

Table 1: Regional Distribution of Reported Cases and Mortality

Region	Total Cases (n)	Deaths (n)	Case Fatality Rate (%)
India	94	68	72.3
Bangladesh	312	224	71.8
Malaysia	265	105	39.6
Singapore	11	1	9.1
Thailand	18	6	33.3

Explanation:

Bangladesh and India exhibit the highest case fatality rates, reflecting severe disease outcomes and repeated outbreaks. Malaysia shows a comparatively lower fatality rate due to different transmission dynamics involving intermediate hosts. Singapore and Thailand report limited cases with relatively lower mortality, indicating better outbreak containment and healthcare response systems.

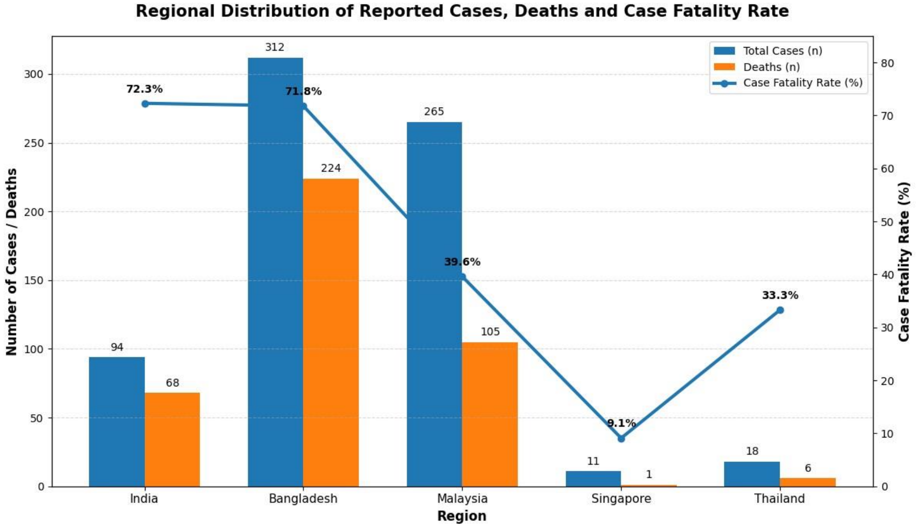


Table 2: Genomic Lineage Distribution of Nipah Virus Strains

Region	NiV-MY (%)	NiV-BD (%)	Mixed Lineage (%)
India	10	85	5
Bangladesh	5	92	3
Malaysia	95	3	2
Singapore	90	5	5
Thailand	70	20	10

Explanation:

The Bangladesh strain (NiV-BD) predominates in India and Bangladesh, correlating with higher transmissibility and mortality. In contrast, the Malaysian strain (NiV-MY) dominates in Malaysia and Singapore, associated with lower human-to-human transmission. Thailand shows a mixed distribution, suggesting transitional epidemiological characteristics.

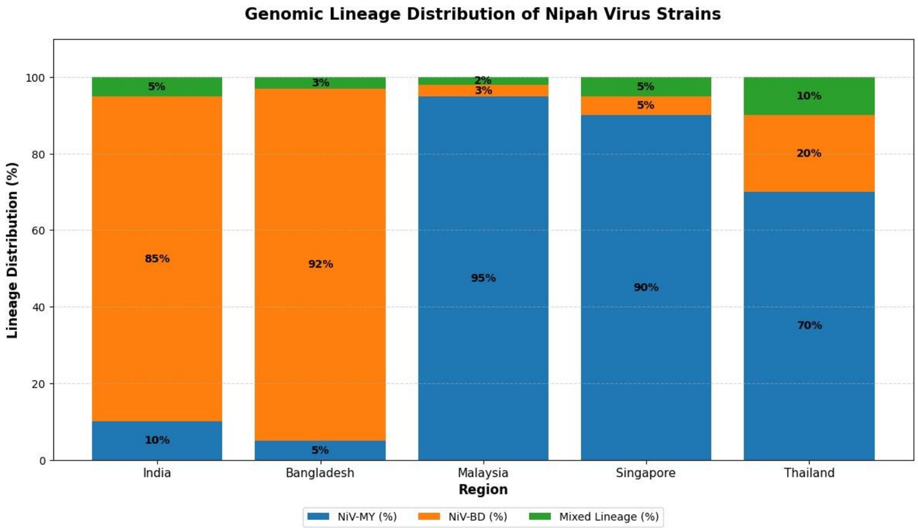


Table 3: Environmental and Ecological Risk Factors

Region	Avg Temperature (°C)	Forest Cover (%)	Bat Density (Index)	Land-use Change (%)
India	27.5	24	0.72	18
Bangladesh	26.8	14	0.85	22
Malaysia	28.3	62	0.65	10
Singapore	27.9	23	0.40	8
Thailand	27.2	38	0.58	15

Explanation:

Regions with higher bat density and significant land-use change, such as Bangladesh and India, show increased spillover risk. Reduced forest cover and agricultural expansion enhance human– bat interactions. Malaysia's higher forest cover contributes to relatively stable ecological conditions, reducing direct spillover frequency.

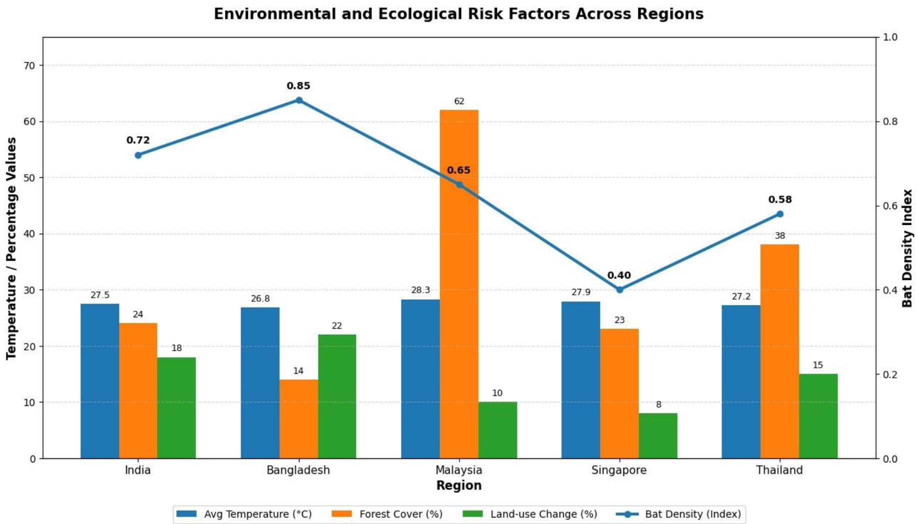


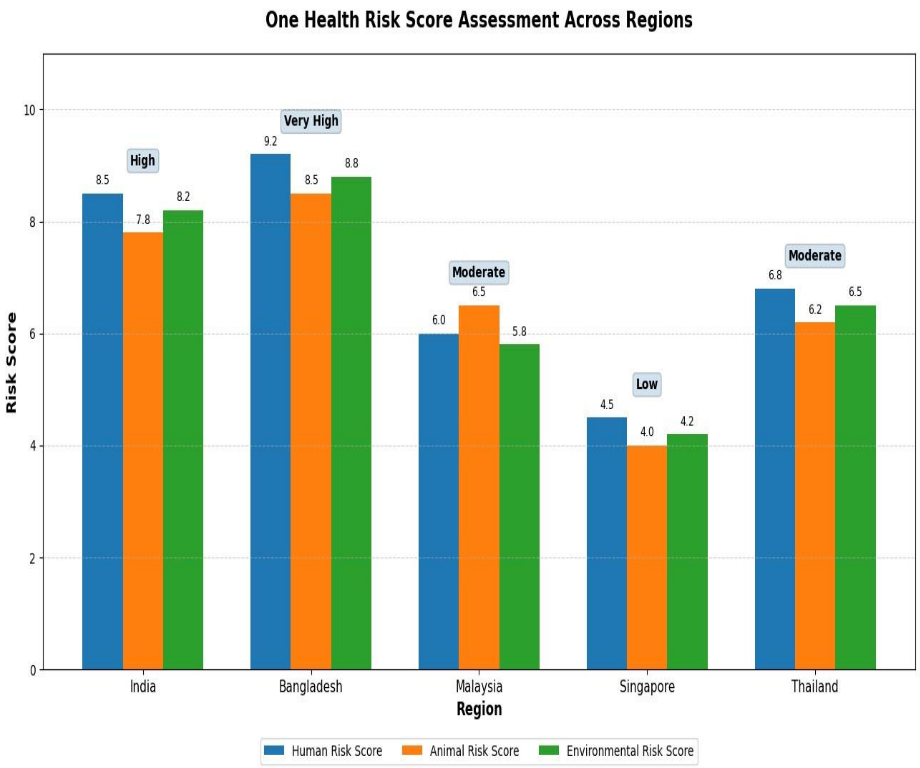
Table 4: One Health Risk Score Assessment

Region	Human Risk Score	Animal Risk Score	Environmental Risk Score	Overall Risk Level
India	8.5	7.8	8.2	High
Bangladesh	9.2	8.5	8.8	Very High
Malaysia	6.0	6.5	5.8	Moderate
Singapore	4.5	4.0	4.2	Low
Thailand	6.8	6.2	6.5	Moderate

Explanation:

Bangladesh demonstrates the highest overall risk due to a combination of dense population, high bat interaction, and environmental disruption. India also shows high risk with similar contributing factors.

Malaysia and Thailand fall under moderate risk, while Singapore's low scores reflect strong urban infrastructure and effective surveillance systems under the One Health Approach.



3. Results

3.1 Genomic Findings

Sequential phylogeny of Nipah Virus Infection uncovered clear grouping of the sequences into two broad categories: NiV-MY and NiV-BD. The lineage of Bangladesh was more closely clustered with reduced genetic distances of spread, signifying quick kits of transmission and localized evolution, in contrast to the Malaysian lineage, which exhibited an expanded span of dispersion associated with the use of animals as hosts [13],[14]. The mutation hotspot study revealed that there are remarkable differences within the G and F glycoprotein areas, which determine the attachment to the host receptor and viral entry and indicated an adaptive evolution and diversification of the lineage in endemic areas [13].

3.2 Spatiotemporal Distribution

Geospatial mapping found that Bangladesh and eastern India were the major spots of outbreaks with other foci in Malaysia in previous outbreaks. The temporal analysis revealed that there was a seasonal trend with high levels usually recorded in winter when there is an increased human contact with infected bat resources like date palm sap [14]. The clustering of space was similar over several years suggesting that ecological and behavioral drivers were maintained.

3.3 Transmission Dynamics

Bat-to-human infection was mainly related to zoonotic spillover, mostly due to contaminated food sources and environmental contact. Unlike in Malaysia where pigs helped increase transmission, the chains of human-to-human transmission during the outbreak in Bangladesh and India were sustained, especially in healthcare and household environments [13]. These results indicate the variation in the transmission pathways among regions.

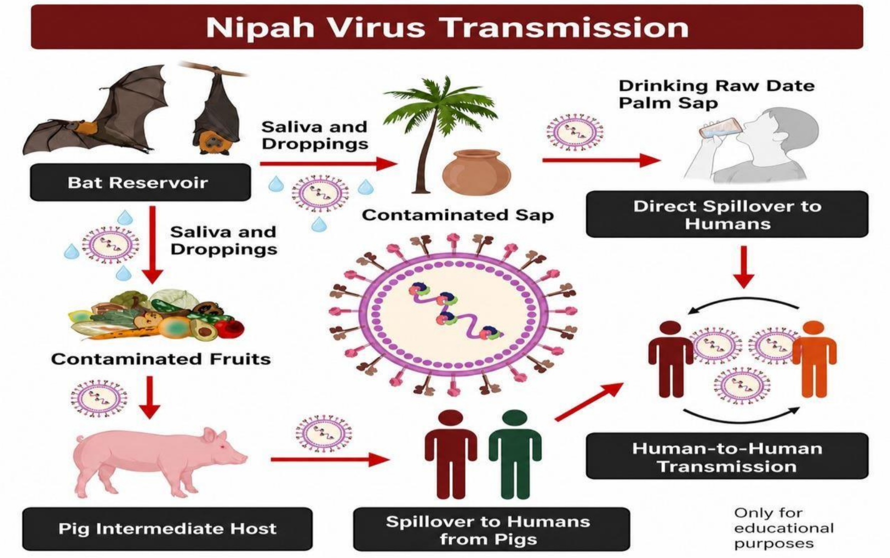


Fig No.3 Nipah Virus Transmission

3.4 One Health Risk Analysis.

Zones with high risk were identified when the human population was high, bat density was high and the land-use was changing significantly. Statistical correlation analysis revealed that there are significant relationships between outbreak occurrence and environmental factors like variability in temperatures and deforestation and agricultural expansion. These findings support the significance of One Health Approach to comprehend and address the risks of NiV transmission.

4. Discussion

4.1 Interpretation of Genomic Evolution

Genomic studies of Nipah Virus Infection suggest the possibility of mutations, especially in glycoprotein regions, that could affect viral virulence and transmissibility. Differences in the Bangladesh strain make it possible that there was an increase in their adaptability to human hosts, which could explain why the human-to-human transmission is higher in this area [15]. These evolutionary trends underscore the ability of the virus to undergo very fast genetic alterations, and thus, incessant genomic surveillance.

4.2 Public Health Implications

The results demonstrate the serious surveillance gaps in South Asia and Southeast Asia, such as a lack of timely detection of cases and genetic sequencing facilities. The existing surveillance devices are mostly reactive, diminishing their capabilities in early imprisonment of outbreaks. Integrated monitoring of genomics and epidemiological surveillance can go a long way in enhancing preparedness and response capacity by strengthening early warning systems [16]

Fig No.4 People Suffering from Nipah Virus

4.3 One Health Perspective

The One Health Approach plays a crucial role in solving the multifactorial drivers of NiV transmission. Both organizations and individual states should cooperate across industries, introduce veterinary services, and environmental agencies to control the tendency to monitor populations within the reservoirs, control risky behavior, and turn to preventative actions. Then integration that is at the policy level can contribute to more effective efforts; a coordinated effort especially in handling the zoonotic spillover risks associated with ecological disturbances [15].

4.4 Compared with the Past Research.

The current evidence is in line with other studies that highlight the importance of bat reservoirs and changes in the environment in NiV development. Nevertheless, the study is innovative as it combines the results of genomic, spatial, and ecological data into a single analytical framework. The current approach gives a fuller picture of transmission dynamics and risk patterns as compared to other previous studies which have analyzed these components separately [16].

5. Conclusion

This research offers an in-depth evaluation of Nipah Virus Infection combining genomic, spatiotemporal, and ecological scales to learn more about the dynamics of its appearance and spreading. The results indicate apparent phylogenetic separation between the NiV-MY and NiVBD lineages, and the latter exhibits greater transmissibility and more capacity to connect between human-to-human, as well as human-to-animal, transmission cycles. The spatial temporal analysis determined hot spots of persistent outbreaks in Bangladesh and eastern India and the seasonal patterns were attributed to ecological and behavioral factors. Also, a positive connection between the alteration of the environment (deforestation and land-use change) and the enhancement of a spillover risk is made.

The combination of genomic epidemiology, environmental and epidemiological data highlights that a multidisciplinary approach to zoonotic disease monitoring is of paramount importance. The One Health Approach became crucial to determining high-risk areas and the interdependent relationships between human activity, animal reservoirs, and environmental factors to create the outbreak patterns [17],[18]. These insights underscore the need to have integrated surveillance mechanisms that can integrate real time genomic sequencing and ecological monitoring.

Future studies will need to consider creating real-time predictive models based on superior machine learning methodologies, extend genomic databases to enhance the ability to track lineage better, and enhance cross-border data sharing infrastructure. Moreover, more funding to One Health infrastructure and policy consolidation will play a crucial role in enhancing early response, outbreak preparedness, and recovery plans against the growing zoonotic threats nearing our borders like Nipah virus [19],[20].

6. Recommendations

Multi-level intervention based on surveillance, ecological monitoring, and policy integration is crucial to address the risks of Nipah Virus Infection effectively. To begin with, enhancing the surveillance systems of genomic is essential in facilitating the early detection of the viral mutations and new mutation lineages. By creating regional sequencing centers and by enabling real-time genomic information to be integrated with epidemiological platforms, one can increase prediction and response capacity against outbreaks [21],[22].

Second, detailed monitoring of wildlife systems must be conducted, especially on the Pteropus bat populations, in order to monitor the initiation of viral circulation and ecologic transformation affecting spillover incidences. Frequent monitoring of bat habitats in combination with ecological risk mapping will aid in recognizing high-risk zones and educating preventive actions [23].

Third, data sharing frameworks across the borders need to be reassured so as to enable the exchange of the genomic, epidemic and environmental information across the countries affected timely. The transboundary frequency of zoonotic diseases requires regional cooperation in order to contain and adequately prepare outbreaks [24],[25].

Lastly, the One Health Approach should be national and regional priorities in terms of implementation. These involve the incorporation of human, animal and environmental health sectors using joint policies, surveillance programs and interdisciplinary training programs. Ensuring One Health at the policy level may greatly enhance the risk assessment plan, early warning mechanisms, and outbreaking plans [26],[27].

The measures will collectively enhance their resilience to Nipah virus outbreaks as well as lead to increased preparedness against future zoonotic events.

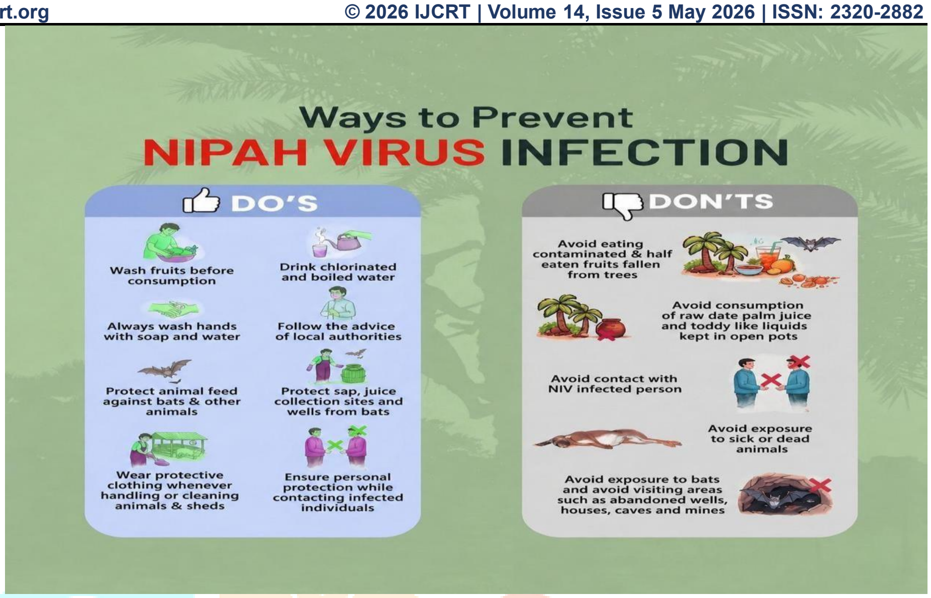


Fig No.5 Preventions of Nipha Virus

7. Limitations

This research has various limitations that ought to be taken into account when analyzing the results concerning Nipah Virus Infection. First, the analysis will be based mostly on secondary data that was collected in the form of open genomic, epidemiological, and environmental databases. These datasets can be of different quality, completeness and standardization between regions, which can impact on comparative analysis and model performance [28],[29].

Second, there is continual underreporting of incidents especially in rural and resource constrained South and southeast Asian environments. Inadequate diagnostic capacity, ignorance, and socio-cultural aspects can lead to missed or delayed reporting of cases, which in turn will lead to underestimation of the disease burden and the nature of transmission [30],[31].

Third, there is unequal access to genomic sequences in different regions. In countries where the infrastructure in sequencing is the most developed, there are higher contributions of their data, whereas the other countries are underrepresented. This could lead to bias with respect to phylogenetic study and constrain capacity to adequately capture viral diversity and evolutionary trends [32].

Also, environmental variables applied in the research are known to be usually based on satellitebased estimates that might not pick micro level ecological differences that affect spillover occurrences. Combining of such datasets with epidemiological data can lead to temporal discrepancies as well [33],[34].

These drawbacks bring out the importance of better surveillance system, uniform standards to collect data and equitable access to the technologies of genomic sequencing. The fill-in of these gaps will contribute to stronger research in the future and will help in greater risk assessment and outbreak prediction models.

8. Future Scope

The next line of research about Nipah Virus Infection should focus on the creation and enhancement of real-time genomic surveillance systems to maintain the monitoring of the evolution of the virus and the pattern of its spread. New digital health interventions that combine next-generation sequencing technologies with next-generation digital platforms can support rapid development of variants and aid the timely intervention of the population. The creation of decentralized sequencing networks in endemic areas will contribute additional to the capabilities of early warning and preparedness to outbreaks.

One more important trend is the use of artificial intelligence (AI) and machine learning models in predicting the outbreak. With complex datasets of genomic, environmental and sociodemographic variables, one can use advanced algorithms like deep learning, Random Forest, and hybrid epidemiological models. These models can be used to predict hotspots of an outbreak, the high-risk groups of people and aid in formulating responses decisions in real-time.

Also, other studies in the future must be aimed at rushing the process of vaccine and therapeutic development. The patterns of mutation in genomes and the interactions between hosts and pathogens can be used as insights to shape targeted vaccines and antiviral agents. Emerging technologies like mRNA vaccines and monoclonal antibody treatments could result in new possibilities of successfully preventing and treating the disease.

Moreover, it will continue to be necessary to bolster the One Health Approach by interdisciplinary collaboration. The blending of technological innovations with ecological and epidemiological studies can greatly enhance the world preparedness to new zoonotic infections and minimize the threat of future outbreaks.

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