



Nipah Virus and National Biosecurity: Assessing Indonesia's Readiness in a High-Risk Archipelago

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ABSTRACT

Indonesia has not reported a confirmed human case or a recognized livestock outbreak of Nipah virus (NiV), but serological and molecular studies have demonstrated evidence of NiV infection in *Pteropus* bat on several islands. This distinction is central to risk assessment: the reservoir hazard is present, whereas the pathways required for sustained spillover and amplification remain incompletely characterized. Indonesia does not necessarily reproduce the intensive pig–orchard system that amplified the 1998–1999 Malaysian outbreak, yet its heterogeneous livestock sector, wildlife trade, land-use change, and uneven surveillance create different and potentially under-recognized interfaces. Indonesia already has important preparedness foundations, including national NiV guidance, human syndromic and event-based surveillance, a national zoonoses information platform, the National Action Plan for Health Security 2025–2029 and the CARE-I One Health preparedness program. This Opinion argues that these broad capacities should now be translated into a NiV-specific operational framework combining longitudinal wildlife and veterinary surveillance, tiered laboratory confirmation, genomic analysis, interoperable data, community safeguards, and ASEAN coordination. Acting before a human outbreak would allow Indonesia to convert preparedness from a policy aspiration into regional One Health leadership.

Keywords: biosecurity, Indonesia, Nipah virus, One Health, pandemic preparedness

From reservoir evidence to a preparedness question

Nipah virus (NiV) is a bat-borne *Henipavirus* capable of causing severe respiratory and neurological disease. The World Health Organization estimates a case-fatality rate of approximately 40%–75%, and no licensed human vaccine or specific antiviral treatment is currently available (World Health Organization, 2026a). Human infection has followed several pathways: pig-to-human transmission in Malaysia and Singapore, contamination of food products by bats in Bangladesh and parts of India, horse-associated transmission in the Philippines, and person-to-person spread in families and healthcare settings (Ching et al., 2015; World Health Organization, 2026a, 2026b, 2026c). These distinct patterns demonstrate that the presence of infected bats alone does not determine the form or scale of an outbreak. Spillover depends on the ecological interface, susceptible intermediate hosts,

human behavior, and the capacity to detect early cases (Chatterjee et al., 2026).

NiV is a bat-borne *Henipavirus* capable of causing severe respiratory and neurological disease. The World Health Organization estimates a case-fatality rate of approximately 40%–75%, and no licensed human vaccine or specific antiviral treatment is currently available (World Health Organization, 2026a). Human infection has followed several pathways: pig-to-human transmission in Malaysia and Singapore, contamination of food products by bats in Bangladesh and parts of India, horse-associated transmission in the Philippines, and person-to-person spread in families and healthcare settings (Ching et al., 2015; World Health Organization, 2026a, 2026b, 2026c). These distinct patterns demonstrate that the presence of infected bats alone does not determine the form or scale

of an outbreak. Spillover depends on the ecological interface, susceptible intermediate hosts, human behavior, and the capacity to detect early cases. Indonesia also has human–bat interfaces that deserve explicit assessment (Nidom et al., 2025). Flying foxes are hunted, traded between provinces, sold in traditional markets, and consumed in parts of Indonesia, particularly North Sulawesi (Morcatty et al., 2022; Sheherazade & Tsang, 2015). Palm sap is also traditionally harvested in several Indonesian regions for sugar and beverages (Kurniawan et al., 2025). However, there is currently no evidence that NiV-contaminated sap, bat-contaminated fruit, or these food-production practices have caused human NiV infection in Indonesia. The Bangladesh and India experience should therefore be treated as a plausible exposure model to investigate in Indonesia.

Presently, Indonesia has not reported a confirmed human NiV case. Ministry of Health of the Republic of Indonesia surveillance data for 2024 through epidemiological week 22 of 2026 recorded 16 suspected cases across five provinces, all of which tested negative (Ministry of Health, Republic of Indonesia, 2026a). Nevertheless, repeated detection of NiV-related evidence in Indonesian bats means that the absence of recognized human disease should not be interpreted as the absence of a reservoir hazard. The relevant policy question is therefore not whether Indonesia should predict an inevitable outbreak, but whether it can identify and interrupt plausible spillover pathways before amplification occurs.

What surveillance has established and what remains unknown

The Indonesian evidence base spans more than two decades but remains geographically and taxonomically incomplete. A 2006 survey detected NiV-neutralizing antibodies in *Pteropus vampyrus* bats sampled from Java and Sumatra, indicating exposure to NiV or a closely related cross-neutralizing *Henipavirus* (Sendow et al., 2006). In West Kalimantan, 19% of 84 *P. vampyrus* sera reacted in an enzyme-linked immunosorbent assay, whereas the 15 *Cynopterus brachyotis* bats examined were non-reactive. The same study found no serological evidence of NiV exposure among 610 pigs and no reported recent respiratory or encephalitic syndrome among participating farms (Sendow et al., 2010).

Molecular evidence was subsequently reported in 2013, when NiV RNA was detected in saliva and urine from *P. vampyrus* in North Sumatra (Sendow et al., 2013). A broader cross-sectional survey conducted from 2023 to 2024 tested 305 *P. vampyrus* samples from 13 locations across western, central, and eastern Indonesia and reported four RT-qPCR-positive samples from Kalimantan sampling sites (Nidom et al.,

2025). More recently, two of 64 *P. hypomelanus* bats sampled from animal markets in Central Java were positive by reverse-transcription PCR, and partial nucleocapsid sequences clustered with the Malaysian genotype (Putro et al., 2025).

These findings establish evidence of NiV infection or exposure in at least two *Pteropus* species, but they do not provide a national prevalence estimate. Several studies were cross-sectional, used convenience or market-derived samples, or covered limited locations or seasons. The negative pig survey was conducted in one province and is now more than a decade old. Published Indonesian data concerning NiV infection in horses, dogs, cats, goats, and other domestic mammals remain absent, although several of these species are susceptible elsewhere (World Organisation for Animal Health, 2026). Consequently, the evidence supports targeted vigilance rather than a claim that nationwide livestock spillover has already occurred.

The 2025 Central Java study is also an important institutional example because it involved the Environmental Health National Referral Laboratory, Directorate General of Public Health, Ministry of Health of the Republic of Indonesia and the National Research and Innovation Agency (BRIN) (Putro et al., 2025). It demonstrates practical collaboration between public-health and research institutions. However, it should be considered project-level evidence of collaboration rather than proof that a permanent, nationally coordinated NiV surveillance program is already operating.

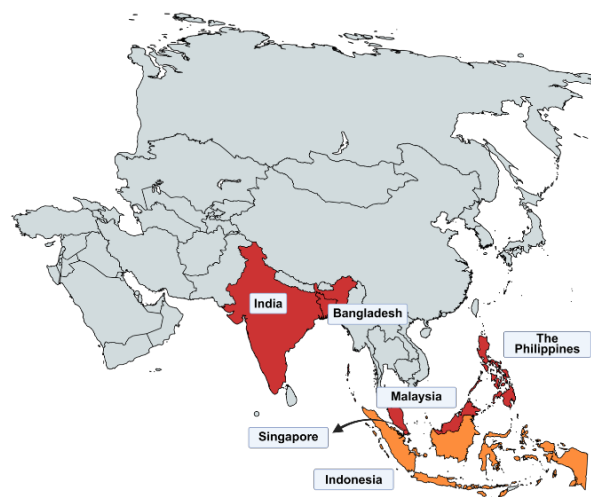


Figure 1 Regional geographic distribution of reported human NiV outbreaks and evidence of NiV in Indonesian bats. Countries with reported human NiV outbreaks, India, Bangladesh, Singapore, Malaysia, and the Philippines, are shown in red. Indonesian regions where evidence of NiV infection or exposure

has been reported in bats, Java, Sumatra, and Kalimantan, are shown in orange, based on studies conducted between 2013 and 2025 by Indonesian researchers (Sendow et al., 2013; Nidom et al., 2025; Putro et al., 2025). The single regional map preserves the geographic context between Indonesia and countries previously affected by NiV outbreaks. The map was prepared using MapChart (<https://www.mapchart.net>) and BioRender (<https://www.biorender.com/>).

Why has Indonesia not experienced Malaysia's pig-associated pattern?

The apparent contrast with Malaysia is epidemiologically informative. The 1998–1999 Malaysian outbreak involved repeated viral introduction from flying foxes into a large commercial pig farm where fruit production and pig husbandry occurred in close proximity. Pigs were not merely susceptible hosts; the large and continually replenished pig population functioned as an amplifying host population, enabling within-farm transmission and increasing opportunities for human exposure. Movement of infected pigs then connected farms and extended the outbreak geographically (Pulliam et al., 2012). The outbreak was therefore not produced by bat infection alone; it emerged from a specific combination of bat access to cultivated fruit, a dense amplifying livestock population, herd turnover, and animal movement.

Indonesia's pig sector is heterogeneous. In parts of eastern Indonesia, pig production is dominated by smallholder systems with small herds, locally sourced feed, backyard slaughter, limited veterinary access, and weak biosecurity (Leslie et al., 2015). Such dispersed systems may be less likely than a large integrated commercial network to sustain the rapid regional amplification observed in Malaysia. This inference must remain cautious because evidence from eastern Indonesian smallholders cannot represent every Indonesian production system. Moreover, small herd size is not synonymous with low risk. Limited reporting, informal animal movement, backyard slaughter, and restricted veterinary contact may allow small clusters or unusual animal illnesses to remain undetected.

Other explanations are also plausible. The overlap among bat roosts, pig farms, fruit trees, and live-animal trade may differ among islands; viral shedding is intermittent; and existing surveys may have missed brief spillover events. Indonesia may also face pathways that do not require pigs. The Philippines illustrates horse-associated *Henipavirus* transmission, while Bangladesh and India demonstrate direct or food-associated bat-to-human spillover followed, in

some outbreaks, by person-to-person transmission (Ching et al., 2015; World Health Organization, 2026a, 2026b, 2026c). Indonesian wildlife-market studies have documented substantial trade and consumption of fruit bats, creating direct contact among bats, traders, processors, consumers, and other animals (Leslie et al., 2015). The absence of a documented pig outbreak therefore does not narrow overall NiV risk. Rather, it narrows only the hypothesis that Indonesia would reproduce Malaysia's pig-amplified outbreak pattern and strengthens the need to evaluate multiple alternative pathways, including wildlife handling and consumption, bat-contaminated food or sap, other susceptible domestic hosts, and subsequent person-to-person transmission.

Ecological and anthropogenic drivers of spillover

Land-use change can reshape NiV risk through several connected mechanisms. Deforestation, agricultural expansion, and habitat fragmentation may reduce or redistribute native food resources, alter bat roosting and foraging behavior, and increase the frequency with which bats use orchards, farms, or urban food sources. Livestock intensification can subsequently convert a rare wildlife-to-animal introduction into a larger amplification event. Research on bat-borne viruses demonstrates that spillover requires a sequence of enabling conditions, including pathogen shedding, environmental survival, recipient-host exposure, and recipient susceptibility (Plowright et al., 2015). Long-term *Henipavirus* research also shows that habitat loss and climate-driven food shortages can alter bat behavior and increase contact with domestic animals, although these findings should not be treated as direct evidence that such processes have already caused NiV spillover in Indonesia (Eby et al., 2023). Several relevant anthropogenic conditions are already present in Indonesia: substantial primary-forest loss has been documented, smallholder pig systems with limited biosecurity occur in parts of eastern Indonesia, and organized interprovincial flying-fox trade and consumption occur in Sulawesi and other markets (Sheherazade et al., 2015). These observations establish potentially relevant interfaces, but they do not demonstrate that land-use change or wildlife trade has caused NiV spillover in Indonesia.

Climate-related changes may modify flowering and fruiting phenology, seasonal bat movements, and nutritional stress. In Bangladesh, long-term ecological analyses have associated NiV spillover patterns with temperature, land-use history, persistent bat roosting near densely populated areas, and reliance on cultivated food resources (McKee et al., 2021). Comparable longitudinal data are not yet available for Indonesia. The key Indonesian gap is therefore not

whether ecological and anthropogenic drivers exist, but whether they coincide spatially and temporally with active NiV shedding and human or livestock exposure. Priority field studies should link bat roosts and movement, forest and agricultural land cover, fruiting and palm-sap production, livestock density and movement, wildlife-market supply chains, and human exposure practices. This would allow Indonesian risk assessment to distinguish documented interfaces from pathways that remain only biologically plausible. Prevention should include ecological as well as clinical measures. Risk reduction may involve protecting important bat-foraging habitats, preventing bat access to livestock feed and water, avoiding fruit trees directly above animal enclosures, and improving hygiene and

species separation in animal markets. Indiscriminate bat culling should be avoided because disturbing colonies may redistribute animals and increase contact elsewhere. Conservation-sensitive measures are more consistent with One Health than generalized wildlife removal (Eby et al., 2023).

Regional experience and lessons for Indonesia

Regional experience demonstrates that NiV preparedness cannot be based on a single transmission model. **Table 1** summarizes the principal epidemiological patterns, selected preparedness features, and corresponding lessons for Indonesia.

Table 1. Regional Epidemiological Patterns and Preparedness Lessons Relevant to Indonesia

Setting	Dominant Epidemiological Pattern	Selected Preparedness Features	Priority Lesson for Indonesia
Indonesia	Bat serological or molecular evidence; no confirmed human case or recognized livestock outbreak (Ministry of Health, Republic of Indonesia, 2026a; Sendow et al., 2013; Nidom et al., 2025; Putro et al., 2025).	National NiV guideline, Early Awareness and Response System (SKDR), event-based surveillance, One Health information-sharing platform (SIZE), NAPHS 2025–2029, and CARE-I (Food and Agriculture Organization of the United Nations, 2026; Ministry of Health, Republic of Indonesia, 2021, 2025, 2026; SIZE, 2026; Sudarnika et al., 2026; World Health Organization, 2024, 2026d).	Convert broad national systems into a NiV-specific, multi-host operational pathway.
Malaysia	The 1998–1999 outbreak was amplified by intensive pig–orchard production and animal movement (Pulliam et al., 2012).	Culling, animal-movement controls, and stronger separation of fruit trees and bats from pig-production units (World Health Organization, 2026a; Pulliam et al., 2012).	Map pig–fruit–bat interfaces and prepare veterinary investigation and movement-control protocols before detection.
Bangladesh	Recurrent seasonal spillover, frequently associated with contaminated raw date-palm sap; person-to-person transmission can occur (World Health Organization, 2026b; McKee et al., 2021).	Hospital-based NiV surveillance, rapid-response teams, diagnostic testing, and seasonal risk communication (World Health Organization, 2026b).	Pair encephalitis and severe acute respiratory infection surveillance with detailed exposure histories, including raw or fermented palm sap, bat-contaminated fruit, bat hunting/handling or consumption, and household/healthcare contact; combine these with infection prevention and seasonal risk communication.
India	Recurrent outbreaks in Kerala and West Bengal, including healthcare-associated transmission (World Health Organization, 202698c).	Rapid response, contact tracing, laboratory confirmation, isolation, and targeted bat investigations (World Health Organization, 2026c).	Predefine referral, isolation, contact-management, and genomic workflows, while investigating direct bat-to-human and food-associated exposures that may be culturally and ecologically specific to Indonesian settings.
Philippines	A 2014 <i>Henipavirus</i> outbreak involved horses, slaughter exposure, and limited human-to-human transmission (Ching et al., 2015).	A joint health, agriculture, WHO investigation identified a multispecies transmission chain (Ching et al., 2015).	Include horses, unexplained animal deaths, slaughter practices, and occupational exposure in surveillance.

Indonesian's existing preparedness foundations

Indonesia is not starting from zero. The Ministry of Health issued national guidance for NiV prevention and control in 2021, covering epidemiological surveillance, clinical management, laboratory testing, risk-factor control, and risk communication. A national circular renewed NiV vigilance in 2026, while existing reporting employs syndromic and event-based systems, including surveillance for influenza-like illness, severe acute respiratory infection, pneumonia, and encephalitis (Ministry of Health, Republic of Indonesia, 2026a, 2026b; Sudarnika et al., 2026). These mechanisms provide an entry point for detecting cases but remain primarily oriented toward human health and depend on clinicians obtaining relevant animal, food, occupational, and travel histories (Sudarnika et al., 2026).

The National Zoonoses and Emerging Infectious Diseases Information System, known as SIZE, is a concrete One Health asset. Launched in December 2023 and operational from April 2024, SIZE links the Ministry of Health's Early Awareness and Response System (SKDR), the Ministry of Agriculture's iSIKHNAS, and the wildlife-health information system formerly managed by the Ministry of Environment and Forestry. Its initial integrated diseases include rabies, leptospirosis, anthrax, and avian influenza (Food and Agriculture Organization of the United Nations, 2026; Ministry of Health, Republic of Indonesia, 2021, 2025, 2026; SIZE, 2026; Sudarnika et al., 2026; World Health Organization, 2024, 2026d). NiV is not currently listed among these routine integrations. Adding a risk-based NiV alert pathway to SIZE would be more practical than constructing a parallel data platform.

Broader policy frameworks could support this extension. Indonesia has adapted the One Health Joint Plan of Action to its national context through multisectoral participation involving health, agriculture, environmental, home-affairs, and development-planning stakeholders (World Health Organization, 2024). The National Action Plan for Health Security 2025–2029 provides a current whole-of-government roadmap for prevention, detection, notification, and response (Ministry of Health, Republic of Indonesia, 2025).

In 2026, the Government launched the three-year Collaborative Approach for Resilient Surveillance and Pandemic Preparedness in Indonesia (CARE-I). The program aims to establish One Health laboratory and surveillance networks, improve interoperability, train the workforce, and strengthen emergency response at national and subnational levels (Food and Agriculture Organization, 2026; World Health Organization, 2026d). CARE-I brings together the Ministries of Health, Agriculture, and Forestry, BRIN, and

international partners. Although CARE-I is broader than NiV, it provides an institutional structure through which NiV-specific preparedness could be operationalized.

Operational priorities and research gaps for an Indonesian NiV system

Laboratory decentralization should be functional rather than indiscriminate. Frontline facilities require case-recognition capacity and safe protocols for specimen collection, packaging, and referral. Selected regional laboratories could perform validated molecular testing on appropriately inactivated material, supported by biosafety training, external quality assessment, reliable reagent supplies, and referral contingencies. National reference capacity should provide confirmation, sequencing, and interpretation. Work involving infectious-virus isolation or propagation requires specialized maximum-containment facilities; simply distributing additional BSL-3 laboratories would not, by itself, create a safe or complete NiV network (European Centre for Disease Prevention and Control, 2026). Point-of-care or near-patient assays should be deployed only after appropriate analytical and clinical validation.

Because no licensed human NiV vaccine is currently available, preparedness plans should emphasize early detection, patient isolation, infection prevention and control, contact management, and veterinary containment rather than ring vaccination (Afnani et al., 2026; Chatterjee et al., 2026).

Veterinary surveillance should focus on interfaces where evidence suggests plausible exposure. Sentinel surveillance could prioritize pig farms, abattoirs, horse populations, wildlife markets, and fruit-production areas that overlap with *Pteropus* roosts or feeding sites.

Triggers should include unexplained respiratory or neurological disease, clusters of animal deaths, and concurrent illness among animal handlers. This does not require continuous testing of every domestic animal. The WHO regional strategy supports adaptable, risk-based animal surveillance informed by epidemiological evidence (World Health Organization Regional Office for South-East Asia, 2023).

Wildlife surveillance should become longitudinal and multispecies, incorporating repeated sampling, bat demographics, season, reproductive status, roost movement, land cover, and food-resource availability. Surveillance should distinguish serological evidence of previous exposure from molecular evidence of active infection and should avoid extrapolating findings from one market, province, or island to the entire country.

Genomic surveillance should accompany every

confirmed molecular detection for which sample quality is adequate. Partial gene sequences have helped establish regional relationships, but full-genome or broader genomic data are required to characterize viral diversity, evaluate diagnostic-assay compatibility, and investigate possible links among bat, livestock, and future human infections. Standardized metadata and rapid sequence sharing would strengthen national interpretation and cross-border risk assessment. Genomics should therefore be embedded within the laboratory network rather than treated as a separate research activity.

Emergency preparedness also requires operational agreements before a case is detected. Joint protocols should define which institution leads multisectoral risk assessment, how human and animal alerts are linked, when farms or markets are investigated, how specimens move safely, and how results are communicated. Tabletop exercises should test patient isolation, healthcare-worker protection, contact tracing, animal-movement restrictions, safe carcass management, and surge logistics. Compensation and social-protection mechanisms are essential if livestock destruction or market closure becomes necessary; without credible safeguards, farmers and traders may delay reporting.

At the regional level, Indonesia can use the ASEAN One Health Network and the ASEAN One Health Joint Plan of Action 2023–2030 as platforms for standardized notification, joint risk assessment, laboratory referral, genomic data sharing, and coordinated communication. The ASEAN Emergency Operations Centre Network could complement these arrangements through rapid public-health information exchange. Cross-border collaboration is especially important because flying foxes and animal trade do not follow national boundaries. Preparedness should therefore connect Indonesian surveillance with Malaysia, Singapore, the Philippines, and other neighboring states rather than rely primarily on visible border or airport screening.

Key knowledge gaps and research priorities for NiV in Indonesia

Representative longitudinal surveillance

Indonesia needs repeated, seasonally structured surveillance across western, central, and eastern regions, including *P. vampyrus*, *P. hypomelanus*, and other sympatric bat species. Sampling should distinguish previous serological exposure from active viral detection and should not extrapolate results from one island or market to the entire country.

Risk-based multihost studies

Updated pig surveillance is warranted where pig

production, fruit crops, and bat activity overlap. Horses and other susceptible domestic mammals should be included where local ecology or unexplained syndromes justify investigation. Retrospective examination of selected unexplained human encephalitis or severe respiratory cases could help assess under-detection, subject to appropriate ethical approval, biosafety arrangements, and specimen availability.

Integrated risk mapping

National risk maps should combine information on bat distributions and roosts, land-use change, flowering and fruiting patterns, livestock density and movement, animal markets, human populations, and access to health services. Their purpose should be to guide sentinel placement and prevention resources rather than label entire provinces as uniformly high risk.

Genomic and diagnostic readiness

Research should characterize Indonesian viral diversity, determine whether existing assays reliably detect locally circulating lineages, establish quality-assured sequencing workflows, and define safe referral routes for confirmatory testing. Biobanking and interoperable metadata standards should be developed across human, animal, and environmental sectors.

Behavioral and socioeconomic evidence

Studies should examine bat hunting, interprovincial trade, slaughter and food preparation, farm biosecurity, fruit harvesting and handling, palm-sap collection and consumption practices, illness reporting, trust in authorities, and acceptable compensation mechanisms. Particular attention should be given to whether bats can access sap-collection vessels, harvested fruit, livestock feed, or other foods that are consumed or processed by people. These practices should be mapped empirically rather than assumed to reproduce the Bangladesh or India pathway. Preparedness measures may fail if technically sound interventions conflict with livelihoods or encourage concealment.

Conclusion

Indonesia's NiV risk profile is characterized by an important epidemiological paradox, evidence of viral circulation or exposure has been documented in fruit bats, yet no confirmed human cases or recognized livestock outbreaks have been reported. This apparent gap should not be interpreted as evidence of negligible risk, nor should it support speculative or alarmist projections. Rather, it represents a critical window for preparedness. The most defensible approach is a risk-based One Health framework that integrates wildlife ecology, veterinary surveillance, human syndromic surveillance, laboratory confirmation, genomic epidemiology, and community-level risk reduction.

Indonesia already has substantial policy and institutional foundations on which such a framework could be built, including national NiV guidance, the National Zoonoses and Emerging Infectious Diseases Information System (SIZE), the National Action Plan for Health Security, the Indonesia One Health agenda, and CARE-I. The central challenge is therefore not the absence of policy instruments, but their operationalization for NiV preparedness. This will require clearly defined surveillance and response triggers, accountable institutional responsibilities, interoperable data-sharing mechanisms, recurrent simulation and preparedness exercises, and sustained financing. Establishing and evaluating such an integrated system before the emergence of human cases would strengthen national preparedness while also positioning Indonesia to contribute to regional NiV prevention and response across ASEAN, where transboundary reservoir hosts, ecological connectivity, and shared patterns of human–animal interaction create common vulnerabilities.

Conflicts of interest statement

The authors declared no conflicts of interest.

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