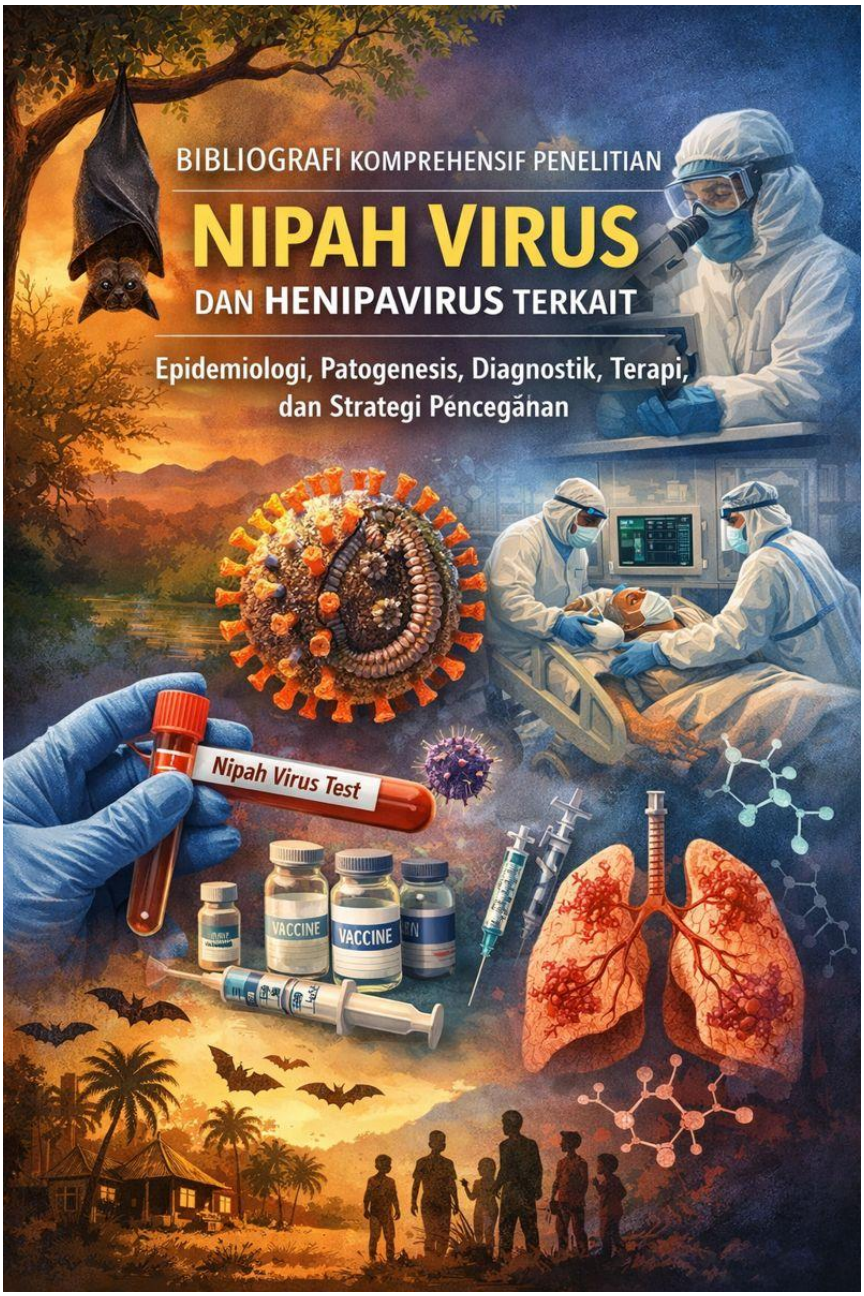
Bibliografi Komprehensif Penelitian Nipah Virus dan Henipavirus Terkait: Epidemiologi, Patogenesis, Diagnostik, Terapi, dan Strategi Pencegahan



PERPUSTAKAAN BALAI BESAR PERAKITAN DAN MODERNISASI VETERINER

BADAN PERAKITAN DAN MODERNISASI PERTANIAN

KEMENTERIAN PERTANIAN

2026

Kata Pengantar

Puji syukur ke hadirat Tuhan Yang Maha Esa, karena atas rahmat dan karunia-Nya, penyusunan bibliografi yang berjudul *"Bibliografi Komprehensif Penelitian Nipah Virus dan Henipavirus Terkait: Epidemiologi, Patogenesis, Diagnostik, Terapi, dan Strategi Pencegahan"* ini dapat diselesaikan dengan baik.

Bibliografi ini disusun sebagai upaya untuk menghimpun dan mendokumentasikan berbagai sumber ilmiah yang relevan mengenai Nipah virus serta henipavirus terkait lainnya. Kumpulan referensi yang tercantum mencakup beragam aspek penting, mulai dari epidemiologi dan tren wabah, interaksi inang–patogen, karakteristik klinis dan patogenesis penyakit, pengembangan metode diagnostik, hingga riset terkini mengenai terapi, vaksin, dan pendekatan pencegahan berbasis komunitas. Selain itu, bibliografi ini juga memuat kajian lintas disiplin, seperti analisis molekuler, bioinformatika, imunologi, serta faktor sosial dan perilaku yang memengaruhi risiko penularan.

Penyusunan bibliografi ini diharapkan dapat menjadi sumber rujukan yang bermanfaat bagi mahasiswa, peneliti, tenaga kesehatan, dan pihak-pihak lain yang tertarik atau terlibat dalam penelitian serta pengendalian penyakit zoonotik, khususnya Nipah virus. Dengan adanya kompilasi referensi ini, diharapkan pembaca dapat memperoleh gambaran menyeluruh mengenai perkembangan ilmu pengetahuan terkini dan tantangan yang masih dihadapi dalam penanganan penyakit yang memiliki potensi wabah dan dampak kesehatan global yang signifikan.

Akhir kata, penyusun menyadari bahwa bibliografi ini masih memiliki keterbatasan. Oleh karena itu, saran dan masukan yang bersifat membangun sangat diharapkan demi penyempurnaan di masa mendatang. Semoga bibliografi ini dapat memberikan kontribusi positif bagi pengembangan ilmu pengetahuan dan upaya kesehatan masyarakat.

Daftar Isi

1. Urvija Rani, Sachin Goel, Yatender Kumar, **Insights from comparative analysis of Nipah virus strains and identifying key host-pathogen interactions and their potential inhibitors**, In Silico Research in Biomedicine, Volume 2, 2026, 100198, https://doi.org/10.1016/j.insi.2026.100198.

ABSTRACT:

Nipah virus (NiV), a World Health Organization priority pathogen, was analyzed at the genome, gene, and protein levels. The Human-Nipah protein-protein interaction network enabled functional enrichment analysis of the host-pathogen interactome. Molecular docking and dynamics simulations investigated the binding behavior of Glycoprotein structures crystallized at pH 6.8 and pH 5.6 with Glutathione peroxidase 1 and identified potential inhibitors from the NPACT database. The NiV genome was confirmed to be AT-rich, and protein analysis revealed significant variability in the Glycoprotein's amino acid residues compared to other viral proteins like Fusion, Matrix, and Nucleocapsid. Docking studies showed pH-dependent differences in Glycoprotein binding residues interacting with GPX1. Among 519 screened compounds, Subtrifloralactone A, Subtrifloralactone B, and Limonin exhibited the strongest interactions with Glycoprotein. Subsequent molecular dynamics simulations over 100 nanoseconds demonstrated a stable trajectory for Subtrifloralactone A. Comparative Root-Mean-Square Deviation, Root Mean Square Fluctuation, Hydrogen bond and MMPBSA analysis confirmed that Subtrifloralactone A forms stable interactions with Glycoprotein, highlighting its potential as an inhibitor for NiV attachment. These findings suggest that Subtrifloralactone A could be further developed as a therapeutic candidate for Nipah virus infections.

Keywords: Nipah Virus; Strains; Glycoprotein; Bioinformatics; GPX1; Virtual screening; Molecular Dynamic Simulation

2. Md Zakiul Hassan, Susan Khader Ibrahim, Eli Harriss, Peter Horby, Piero Olliaro, Amanda Rojek, **Interpreting the natural history and pathogenesis of Nipah virus disease through clinical data, to inform clinical trial design: a systematic review,** The Lancet Microbe, 2026, 101295, https://doi.org/10.1016/j.lanmic.2025.101295.

ABSTRACT:

Nipah virus is a priority pathogen with high mortality and pandemic potential. Therapies for Nipah virus disease, such as monoclonal antibodies and antivirals, are under development and require clinical trials for evaluation. However, designing such trials is challenging due to the limited understanding of the clinical characteristics, pathogenesis, and current management of Nipah virus disease. In this Review, we gathered essential data from 59 studies reporting 717 Nipah virus disease cases, to inform trial design. Nearly all patients (618 [99%] of 624) had fever. Neurological symptoms included headache (419 [70%] of 601 patients), confusion (74 [65%] of 114), and altered consciousness (358 [62%] of 580); respiratory symptoms included cough (244 [45%] of 541) and difficulty in breathing (184 [58%] of 317). Imaging data revealed chest abnormalities (29 [80%] of 36) and brain involvement (40 [71%] of 56). Viral RNA was detectable early in illness across various sample types. The median case-fatality rate was 69% (IQR 31–88%), with 51 (26%) of 197 survivors presenting with persistent neurological deficits. Clinical management varied widely, with incomplete reporting limiting insights. Prospective observational studies are needed to generate actionable data on clinical case definitions, predictors of adverse outcomes, current standards of care, and standardised endpoints, to inform future trials.

3. Muralidharan Menon Arjun, Gopinathan Pillai Sreekanth, **Engineering Nipah virus: Reverse genetics as a gateway to novel drug discovery,** New Microbes and New Infections, Volume 69, 2026, 101682, https://doi.org/10.1016/j.nmni.2025.101682.

ABSTRACT:

Nipah virus (NiV) is a highly pathogenic and re-emerging virus that requires containment in biosafety level 4 (BSL-4) laboratories. The limited accessibility of these high-security facilities poses major obstacles to investigating immunopathogenesis and developing effective antiviral treatments. Reverse genetics allows manipulation of viral genomes without the need to handle the wild-type virus and has become instrumental in understanding NiV pathogenesis and advancing therapeutic research. These tools have proven vital for other high-containment viruses, notably during the SARS-CoV-2 pandemic, and have been adapted effectively for NiV. Reverse genetics-derived systems were used to evaluate the drug candidates in the preclinical studies of NiV, with several candidates in the development pipeline. This narrative review summarizes established reverse genetics and pseudotyping methodologies for NiV, highlighting their contributions to understanding viral pathogenesis and accelerating vaccine and therapeutic development.

Keywords: Nipah virus; Reverse genetics; Pseudotyped virus; Antivirals; Vaccines

4. Syed Moinuddin Satter, Sharmin Sultana, Shadman Sakib Choudhury, Wasik Rahman Aquib, Dewan Imtiaz Rahman, Mintu Chowdhury, Md Sazzad Hossain, Arifa Nazneen, Kamal Ibne Amin Chowdhury, Anika Farzin, Ayesha Siddika, Fateha Ema, Tonmoy Sarkar, Arifur Rahman Bablu, Muhammad Rashedul Alam, Mohammad Enayet Hossain, Md Taufiqur Rahman Bhuiyan, Trevor Shoemaker, Michael K. Lo, John D. Klena, Christina Spiropoulou, Mohammed Ziaur Rahman, Sayera Banu, Tahmina Shirin, Mahmuda Yasmin, Firdausi Qadri, Joel M. Montgomery, Chowdhury Rafiqul Ahsan, **Insights into the acute phase of Nipah virus infection: Clinical features, viral detection, and humoral immune response,** International Journal of Infectious Diseases, Volume 163, 2026, 108263, https://doi.org/10.1016/j.ijid.2025.108263.

ABSTRACT:

This study aimed to explore the humoral immune response and viral detection in the acute phase of Nipah virus (NiV) infection.

Methods

The study explored clinical and laboratory data from all 22 human NiV cases detected during the 2023, 2024 and 2025 outbreaks in Bangladesh. Oropharyngeal swabs and serum samples were tested for NiV genomic material by real-time reverse transcriptase polymerase chain reaction (RT-PCR); humoral immune response was detected by enzyme-linked immunosorbent assay (ELISA) for immunoglobulin M (IgM) and G (IgG).

Results

A majority of cases were male (64%), and the overall median age of all cases was 21 (0-70) years. The case fatality rate (CFR) was 86% (19/22). 18 (82%) of the cases had evidence of primary infection (a history of recent consumption of raw date palm sap). Viremia on diagnosis resulted in 100% fatality, while CFR was 25% (1/4) in those without detectable viremia. All survivors tested IgG positive on diagnosis, compared to only a third of the fatal cases. Clearance of the virus from the oropharyngeal space started from the 16th to 20th day post-illness onset.

Conclusion

The study provides insights into the clinical indices, humoral immune response, and viral detection during NiV infection. This could aid in diagnostic schedules, prognosis, as well as inform isolation and containment strategies.

Keywords: Nipah virus; Immune response; Viral detection; Serology; Humoral immunity; Immunoglobulin

5. Jun-Sik Lim, Kyung-Duk Min, **Association between bat-predator species richness and Nipah virus spillover risk in Bangladesh,** One Health, Volume 21, 2025, 101274, https://doi.org/10.1016/j.onehlt.2025.101274.

Abstract: Species biodiversity is considered to reduce infectious diseases spillover from wildlife to human. However, despite the potential role of predator biodiversity in this process through trophic cascade, few studies have addressed this issue. In this study, we investigated the association between predator biodiversity and spillover risk, using Nipah virus infection in Bangladesh as an example, where spillover from bats to human has been reported since 2021. We defined counties of Bangladesh as epidemiological units. From three Orders (Strigiformes, Accipitriformes, and Falconiformes) known as bat-preying predators, we extracted 39 species occurrences data and then built species distribution model using MaxEnt algorithm with climate and environmental predictors, also incorporating a bias grid to account for reporting bias. Species presence and richness were estimated under varying classification thresholds and species subsets reported to prey bats to allow sensitivity analyses, yielding 12 measures of species richness for each Order. We then used spatial model to identify the association between the species richness and the counties with spillover event, while adjusting for confounders. Results showed that greater biodiversity of owls (Strigiformes) is likely to reduce the risk of Nipah virus spillover. In contrast, the biodiversity of eagles (Accipitriformes) and falcons (Falconiformes) have a potential of positive association, but evidence was insufficient. This result can be explained by the differences in activity rhythms. Owls share a nocturnal activity rhythm with bats, providing more opportunities to prey on bats and reduce their activity, thereby lowering spillover risk. In contrast, eagles and falcons are diurnal, and thus less likely to suppress bat activity directly. Instead, they may suppress species that compete with bats for food, inadvertently facilitating bat activity and increasing spillover risk. These results suggest that biodiversity should be more explicitly considered in public health governance and spillover prevention strategies.

Keywords: Biodiversity; Predator; Spillover; Nipah virus

6. Kerry Goldin, Bridget Brackney, Tessa Lutterman, Brandi N. Williamson, Manmeet Singh, Christopher Winski, Kathleen Cordova, Meaghan Flagg, Emmie de Wit, **Dexamethasone treatment does not alter mortality but reduces pulmonary pathology in Nipah virus-infected Syrian hamsters,** Antiviral Research, Volume 242, 2025, 106263, https://doi.org/10.1016/j.antiviral.2025.106263.

ABSTRACT:

Nipah virus (NiV) is an emerging zoonotic pathogen that causes severe respiratory and neurologic disease, and there are currently no licensed vaccines or approved treatments. The acute respiratory disease caused by NiV is associated with severe inflammation, similar to severe COVID-19.

Dexamethasone is an affordable and widely available synthetic glucocorticoid, that improved outcomes when administered to patients with severe COVID-19. To determine whether a similar beneficial effect could be achieved during NiV infection, we tested the effect of an anti-inflammatory or immunosuppressive dose of dexamethasone on NiV in the Syrian hamster model. We found that dexamethasone treatment produced the expected hematologic changes in uninfected animals in a dose-dependent manner. In NiV-infected animals, the anti-inflammatory dose of dexamethasone reduced pulmonary pathology, while the immunosuppressive dose had no effect. The anti-inflammatory dose did not increase virus replication in tissues or virus shedding from the respiratory tract, indicating the anti-inflammatory dose of dexamethasone does not result in increased virus replication. Despite reduced lung pathology, dexamethasone treatment did not increase survival after NiV challenge. When dexamethasone treatment was combined with the antiviral remdesivir, dexamethasone negated the increased survival observed in hamsters treated with remdesivir alone. Our study provides critical information on the effect of dexamethasone administration on the outcome of NiV infection and cautions against the use of dexamethasone in combination with other antivirals like remdesivir without preclinical validation.

Keywords: Nipah virus; Therapeutics; Animal model; Treatment efficacy; Immunopathogenesis; Immunomodulatory treatment

7. Dalia Yeasmin, Md Mosabber Hossain, Saleh Haider, Mahbubur Rahman, Md Zakiul Hassan, **The deadly drink: Nipah virus transmission through date palm sap, cultural practices and the evolution of behavioral interventions in Bangladesh over two decades,** Journal of Infection and Public Health, Volume 18, Issue 11, 2025, 102949, https://doi.org/10.1016/j.jiph.2025.102949.

ABSTRACT:

Nipah virus (NiV) has emerged as a significant public health threat, with recurring outbreaks in Bangladesh often linked to the consumption of raw date palm sap contaminated by fruit bats (Pteropus species). Over the past two decades, substantial efforts have been made to understand the cultural context of sap consumption, promoting behavior change and developing interventions to prevent NiV spillover. Despite these efforts, achieving sustainable change in sap consumption practices remains challenging due to deep-seated cultural practices, community perceptions of sap consumption, habitual behaviors, limited awareness of health risks and economic barriers. To prevent sap-borne transmission, future efforts should focus on affordable, community-led solutions while protecting local livelihoods. Promoting behavior change through trusted community education and safe harvesting practices must be supported by involving local health workers and community members in planning and evaluation. Long-term preparedness also requires investment in diagnostics, treatments and vaccines through inclusive, collaborative intersectoral research and one health approach.

Keywords: Nipah virus; date palm sap; behavior change communication; spillover; one health approach; outbreak; intervention; Bangladesh

8. Syed Moinuddin Satter, Dewan Imtiaz Rahman, Sharmin Sultana, Md. Mahfuzur Rahman, Wasik Rahman Aquib, Arifa Nazneen, Anika Farzin, Kamal Ibne Amin Chowdhury, Tonmoy Sarkar, Fateha Akther Ema, Shadman Sakib Choudhury, Ayesha Siddika, Muhammad Rashedul Alam, Faruq Abdulla, Probir Kumar Ghosh, Md. Omar Qayum, Md. Ferdous Rahman Sarker, Md Abdullah Omar

Nasif, Barnali Sen, Mintu Chowdhury, Md. Sazzad Hossain, Mahbubur Rahman, Ahmed Nawsher Alam, Mohammad Enayet Hossain, Trevor Shoemaker, Christina Spiropoulou, Emily S. Gurley, Stephen P. Luby, John D. Klena, Sayera Banu, Mohammed Ziaur Rahman, Joel M. Montgomery, Tahmina Shirin, **Epidemiology, clinical characteristics, and genetic diversity of Nipah virus strains from Bangladesh: 2016-2023,** International Journal of Infectious Diseases, Volume 159, 2025, 108010, https://doi.org/10.1016/j.ijid.2025.108010.

ABSTRACT:

Objectives

Nipah virus (NiV) causes deadly outbreaks in Bangladesh, with a fatality rate of 71%. Two sublineages, NiV-BD 1 and NiV-BD 2, have been identified. This study aimed to characterize their epidemiologic and clinical diversity.

Methods

This study analyzed 21 new (2016-2023) and 17 previously (2012-2015) reported NiV genome sequences and compared sublineages using descriptive and bivariate analysis.

Results

The median age of sequenced cases was 17 years (Interquartile Range (IQR): 9-30), 66% were male. Raw date palm sap consumption was main transmission pathway (92%). NiV-BD 2 showed a broader geographic distribution, including the southern region. The sublineages did not differ significantly in age, sex, or transmission modes. Both sublineages presented with fever, altered mental status, and unconsciousness. Respiratory distress was more frequent in NiV-BD 2 (23 of 29 cases), whereas hospitalization was longer for NiV-BD 1 (median: 3 days; IQR: 1-23). The overall mortality was 84%, with no significant difference between sublineages. Phylogenetic analysis demonstrated that NiV-BD 1 and NiV-BD 2 formed distinct clusters with 98.72-99.25% nucleotide and 99.98-99.99% amino acid identity. The structural nucleoprotein and matrix proteins remained conserved across sublineages.

Conclusions

This study highlights genetic, spatio-temporal, and clinical variation between sublineages, emphasizing continuous genomic surveillance to inform future vaccine and therapeutic strategies.

Keywords: Nipah virus; Nipah strain; Genetic diversity; Bangladesh

9. Laura Mazzola, Hanesh Chi Fru, Dounia Cherkaoui, Sophie Crettaz, Nsonghomanyi Fritz Roland Fonkeng, Audrey Albertini, Devy M. Emperador, Kavi Ramjeet, Emmanuel Agogo, **Diagnostic tests for Nipah virus: A landscape analysis,** Diagnostic Microbiology and Infectious Disease, Volume 114, Issue 1, 2026, 117101, https://doi.org/10.1016/j.diagmicrobio.2025.117101.

ABSTRACT:

Introduction: Nipah virus (NiV) is an emerging human pathogen with a high case fatality rate. The World Health Organization research and development roadmap for NiV published in 2019 highlighted a lack of validated and regulated Nipah virus (NiV) diagnostic tests, particularly those that can be used at the point of care (POC). This analysis assessed the current landscape of NiV diagnostics, including commercial tests and tests in development, to determine whether these gaps remain. Methods: Commercial tests for NiV diagnosis were identified through searches of diagnostic databases and news

platforms, targeted internet queries, and email exchanges with manufacturers. Non-commercial tests were identified through a literature search. Molecular tests, immunoassays and supportive protocols such as field-appropriate sample inactivation were included. Results: We identified 43 commercial NiV tests. Only six tests had national regulatory approval. Three molecular tests were designed for near POC and one lateral flow assay for true POC testing. Twenty-eight publications were identified by the literature search, of which 23 described test development and/or validation, three were independent evaluations or external quality assurance studies, and two were NiV inactivation protocols. Nine publications reported novel POC prototype development, of which seven were molecular assays, one an antigen test, and one a ribozyme biosensor. Clinical performance data on these prototypes were limited. Conclusions: Few commercial tests for NiV are available, especially POC tests suitable for use in remote settings where the virus is endemic. To address this gap, further evaluation and validation of tests in development with POC potential is required.

10. Brendan B. Larsen, Teagan McMahon, Jack T. Brown, Zhaoqian Wang, Caelan E. Radford, James E. Crowe, David Veesler, Jesse D. Bloom, **Functional and antigenic landscape of the Nipah virus receptor-binding protein,** Cell, Volume 188, Issue 9, 2025, Pages 2480-2494.e22, https://doi.org/10.1016/j.cell.2025.02.030.

ABSTRACT:

Nipah virus recurrently spills over to humans, causing fatal infections. The viral receptor-binding protein (RBP or G) attaches to host receptors and is a major target of neutralizing antibodies. Here, we use deep mutational scanning to measure how all amino-acid mutations to the RBP affect cell entry, receptor binding, and escape from neutralizing antibodies. We identify functionally constrained regions of the RBP, including sites involved in oligomerization, along with mutations that differentially modulate RBP binding to its two ephrin receptors. We map escape mutations for six anti-RBP antibodies and find that few antigenic mutations are present in natural Nipah strains. Our findings offer insights into the potential for functional and antigenic evolution of the RBP that can inform the development of antibody therapies and vaccines.

Keywords: Nipah; virus evolution; deep mutational scanning

11. Tao Li, Hua Xu, Mengyi Zhang, Jianhui Nie, Binfan Liao, Jingshu Xie, Yinan Jiang, Yawen Liu, Pingju Ge, Chunhui Zhao, Ziqi Sun, Yunbo Bai, Maoling Tang, Xiaodong Su, Youchun Wang, Weijin Huang, **A monoclonal antibody targeting conserved regions of pre-fusion protein cross-neutralizes Nipah and Hendra virus variants,** Antiviral Research, Volume 240, 2025, 106215, https://doi.org/10.1016/j.antiviral.2025.106215.

ABSTRACT:

Nipah virus (NiV) and Hendra virus (HeV) have an extremely high case fatality, leading to hundreds of deaths in several countries around the globe. Belonging to the same genus Henipavirus (HNV), the two species have a high degree of sequence similarity, resulting in cross-neutralizing immunity under favorable conditions. Here, we obtained ten anti-NiV-F monoclonal antibodies using hybridoma technology, and verified that these antibodies had potent neutralizing activities against epidemic NiV strains from different regions using a pseudovirus assay, and the neutralizing concentration reached the nanogram per milliliter level. Moreover, two of the antibodies, NiF03-3C9 and NiF03-2F6, were found to have cross-neutralizing activity against HeV, which was even stronger than that against NiV.

Epitope competition analysis revealed two classes of epitopes for these antibodies. Cryo-electron microscopy showed that NiF03-3C9 binds to lateral residues of the prefusion F protein trimer, highly conserved in both Nipah and Hendra. The protective potency of the antibodies was also validated using in vivo pseudovirus infection models of Nipah and Hendra viruses. The mAbs developed in this study and their conserved cross-neutralizing epitopes elucidated by structural analysis may contribute to the control of highly pathogenic HNV outbreaks.

Keywords: Nipah; Hendra; Cross-neutralization; Conserved epitope

12. Muhammad Aqib Shabbir, Ammara Amin, Ammarah Hasnain, Ayesha Shakeel, Ambreen Gul, **Immunoinformatics-driven design of a multi-epitope vaccine against nipah virus: A promising approach for global health protection,** Journal of Genetic Engineering and Biotechnology, Volume 23, Issue 2, 2025, 100482, https://doi.org/10.1016/j.jgeb.2025.100482.

ABSTRACT:

This study focuses on developing a multi-epitope vaccine against the highly pathogenic Nipah virus using immunoinformatics. It aims to design a vaccine targeting the viral nucleoprotein to elicit robust immune responses. The approach integrates epitope prediction, vaccine construction, and validation through computational tools to address the lack of effective vaccines and mitigate global health threats posed by Nipah virus outbreaks. Immunoinformatics approaches have been utilized for epitope prediction, focusing on B-cell and T-cell epitopes of the Nipah virus nucleoprotein. The multi-epitope vaccine was constructed using linkers and adjuvants to enhance immunogenicity. Structural refinement, molecular docking with human ephrin B2 receptor, and immune simulations were performed to validate the vaccine's stability, binding efficiency, and immune response potential. The designed multi-epitope vaccine exhibited high antigenicity (0.56), non-allergenicity, and non-toxicity. Docking analysis showed a strong binding affinity with the ephrin B2 receptor (binding energy: −920 kcal/mol). Immune simulations indicated significant immune responses with high IgG and IgM levels and memory B-cell activation. Population coverage analysis revealed a global coverage of 88.3 %, supporting its potential for broad immunization. The designed vaccine against the Nipah virus demonstrates promising antigenicity, stability, and strong binding with the ephrin B2 receptor. With global population coverage and a robust immune response, it holds potential for clinical development. Further experimental validation and in vitro studies are recommended to confirm its efficacy as a viable vaccine candidate for the Nipah virus.

Keywords: Nipah Virus; Multi-Epitope Vaccine; Immunoinformatics; Epitope Prediction; Docking Analysis

13. Nazmun Nahar, Shahana Parveen, Emily S. Gurley, Probir Kumar Ghosh, Ishrat Jabeen, Md. Rifat Haidar, Farhat Jahan, Mohammad Saeed Munim, Md. Wazed Ali, Tahmina Shirin, Sayera Banu, Atique Iqbal Chowdhury, Asraful Alam, Brian E. Dawes, Joan Fusco, Thomas P. Monath, Gray Heppner, Stephen P. Luby, **Community interpretation of a consent form and willingness to participate in a Nipah virus vaccine trial in Bangladesh,** Vaccine, Volume 68, 2025, 127953, https://doi.org/10.1016/j.vaccine.2025.127953

ABSTRACT:

Introduction

Clinical trials conducted in low resource settings of vaccines against unlikely pandemics generate practical barriers to achieving genuine informed consent. Uncertainty over the likelihood of the occurrence of emerging disease threats complicates risk-benefit considerations. We explored how people interpreted the language of a draft consent form for a Phase II trial of a vaccine against Nipah virus (NiV), a lethal bat-borne zoonosis, and assessed their willingness to participate after learning about the trial procedures.

Methods

We conducted a mixed-methods study collecting data from residents of Dhaka city, and Faridpur District between December 2021 and November 2022. Our qualitative team revised a draft consent form with input from the community, while the quantitative team conducted face-to-face interviews of 978 household heads making vaccine and treatment decisions.

Results

We presented the consent form to 20 respondents. They expressed a desire to learn more about NiV disease and sought clarification on the vaccine trial process, use of a placebo, privacy and confidentiality, potential side effects, and compensation procedures. During the quantitative survey, among 328 respondents who indicated a willingness to participate in the vaccine trial, only 1 % (3/328) were familiar with the concept of a placebo. After the quantitative data collection team explained the meaning of a placebo, 61 % (199/328) expressed their willingness to participate in the trial.

Conclusion

Our data suggest that obtaining informed consent for vaccine trials against pathogen with pandemic potentials is feasible but requires a commitment to eliciting study participants' perspectives and tailoring study materials to address their concerns and gaps in understanding.

Keywords: Vaccine trial; Informed consent; Placebo; Nipah virus infection; Bangladesh

14. Muhammad Hassan Hafeez, Hafsa Ajmal, Amna Nadeem, Shehroze Tabassum, Aymar Akilimali, **Navigating Nipah virus: Insights, challenges, and recommendations,** New Microbes and New Infections, Volume 64, 2025, 101575, https://doi.org/10.1016/j.nmni.2025.101575.

ABSTRACT:

Nipah virus (NiV), a zoonotic pathogen with global implications, poses multifaceted challenges. Highlighting the virus's diverse strains and recurrent outbreaks, we explore the rapid course of infections, diagnostic limitations, and the pressing need for therapeutic advancements. Emphasizing the complex dynamics of viral transmission; the urgency for comprehensive biosecurity measures and early detection systems is highlighted. This advocates for a robust global response to address the evolving landscape of NiV, emphasizing the need for collaborative efforts to mitigate its impact on public health.

Keywords: Nipah virus; Epidemiology; Zoonotic pathogen; Public health

15. Muaz Faruque, Md Afjalus Siraj, Md Nazmul Hasan Zilani, Asish Kumar Das, Md Anisuzzman, Md Monirul Islam, **Investigating small molecules in propolis as Nipah virus glycoprotein (NiV-G) inhibitors through molecular interaction studies,** Heliyon, Volume 11, Issue 4, 2025, e42595, https://doi.org/10.1016/j.heliyon.2025.e42595.

ABSTRACT:

Despite the significant fatality rates associated with Nipah virus (NiV) outbreaks in South Asia, including Bangladesh, and India, till today, there is no approved medications to treat it. In this context, small molecules in propolis were computationally screened through pharmacokinetic and toxicity studies followed by molecular docking and dynamics simulation with Nipah virus glycoprotein (NiV-G protein) to assess their anti-Nipah potential. A thorough literature analysis was performed to identify antiviral compounds in propolis from a pool of 84 experimental articles. Following ADMET analysis, 27 molecules out of 34 were docked against NiV-G and compared with a control ligand, ribavirin, which is an investigational drug against Nipah. The molecular docking revealed that bauer-7-en-3β-yl acetate (BA) and moronic acid (MA) bound more strongly to the active site of NiV-G than ribavirin and other ligands. Investigation of root-mean-square deviation (RMSD), root mean square fluctuations (RMSF), radius of gyration (Rg), solvent accessible surface area (SASA), molecular surface area (MolSA), binding free energy (MM-PBSA), the complexity of hydrogen bonds (HBs), and secondary structure of ligand-target interactions for 100 ns by molecular dynamics (MD) simulation study further supported the docked complex's stability and compactness. Therefore, the in silico molecular interaction analysis reports that both molecules may be the possible candidates against Nipah infection.

16. Stephen R. Welch, Jessica R. Spengler, Jessica R. Harmon, JoAnn D. Coleman-McCray, Sarah C. Genzer, Katherine A. Davies, Teresa E. Sorvillo, Florine E.M. Scholte, Sergio E. Rodriguez, Joel M. Montgomery, Stuart T. Nichol, Christina F. Spiropoulou, **Prophylactic protection from lethal henipavirus disease mediated by Nipah-derived defective interfering particles is influenced by challenge virus strain and viral species,** eBioMedicine, Volume 119, 2025, 105897, https://doi.org/10.1016/j.ebiom.2025.105897.

ABSTRACT:

Background

Henipaviruses, including Nipah and Hendra viruses, are zoonotic pathogens that can cause severe respiratory and neurological diseases with high mortality rates in humans. Due to the severity of the disease, the high pandemic potential of these viruses, and the lack of approved treatments, the development of safe and effective medical countermeasures against henipaviruses is a critical priority.

Methods

Here, we evaluate treatment efficacy of defective interfering particles (DIPs)—naturally occurring virus-like particles that lack substantial portions of the viral genome—against henipaviruses in the Syrian hamster model of disease.

Findings

Prophylactic DIP treatment markedly reduced clinical signs and lethality in Syrian hamsters. Single or repeated pre-exposure regimens, starting up to 3 days before challenge, provided protection, while post-exposure treatment was ineffective. DIPs derived from NiV strain Malaysia were most effective against NiV Malaysia but also provided strong protection against the closely related NiV Bangladesh

with certain regimens. However, these DIPs offered minimal or no protection against lethality from the more distantly related Hendra virus.

Interpretation

Our data indicate efficacy of DIPs as a pre-exposure prophylactic for henipavirus infection and support a direct mechanism of viral inhibition.

Funding

This work was partially supported by the DARPA INTERfering and Co-Evolving Prevention and Therapy (INTERCEPT) program (DARPA-BAA-16-35), CDC Emerging Infectious Disease Research Core Funds, an appointment to the Research Participation Program at the Centers for Disease Control and Prevention (CDC) administered by the Oak Ridge Institute for Science and Education through an interagency agreement between the U.S. Department of Energy and CDC (K.A.D., S.E.R.), and by NIAID 1R01AI151006 (T.E.S).

Keywords: Nipah virus; Hendra virus; Henipavirus; Viral zoonoses; Defective interfering viruses; Mesocricetus; Syrian hamsters; Models; Animal; Antiviral agents; Administration; Intranasal

17. Md. Mahfuzur Rahman, Mojnu Miah, Mohammad Enayet Hossain, Samiur Rahim, Sharmin Sultana, Syed Moinuddin Satter, Ariful Islam, Shannon L. M. Whitmer, Jonathan H. Epstein, Christina F. Spiropoulou, John D. Klena, Tahmina Shirin, Joel M. Montgomery, Maria E. Kaczmarek, Mohammed Ziaur Rahman, Iqbal Kabir Jahid, **Development of a culture-independent whole-genome sequencing of Nipah virus using the MinION Oxford Nanopore platform,** Microbiology Spectrum, Volume 13, Issue 6, 2025, https://doi.org/10.1128/spectrum.02492-24.

ABSTRACT:

Nipah virus (NiV) is a deadly zoonotic pathogen in Southeast Asia causing severe respiratory and encephalitis symptoms with a high fatality rate. Whole-genome sequencing (WGS) is crucial for tracking transmission, conducting epidemiological analyses, and understanding NiV's adaptive evolution. WGS is essential for analyzing genomes, particularly in understanding pathogen nature, and pathogenesis and aiding in the development of therapeutics. However, sequencing this highly contagious virus directly from samples is challenging in low- and middle-income countries lacking BSL-4 facilities. This study developed and optimized a culture-independent, high-throughput multiplex PCR-based third-generation sequencing protocol for NiV using the Oxford Nanopore Technology platform and a proposed bioinformatics pipeline to generate consensus genome sequences directly from environmental and clinical specimens. We amplified 12 NiV RT-PCR-positive specimens (11 clinical, one environmental) to produce 60 amplicons, each approximately 400 bp, covering the entire ~18.2 kb genome. Using a two-step reverse transcriptase PCR approach, libraries were prepared with a ligation sequencing kit. Raw sequence data were then analyzed using bioinformatics tools. A minimum of 10,000 total reads per sample provided a nearly complete coverage (>95%) of the NiV genome, even with low virus concentrations (Ct ≤ 32), with an average quality score of 10.2. The WGS of 12 NiV-positive samples achieved coverage between 95.71% (Ct 29.54) and 99.3% (Ct 22.34). The entire process, from RNA extraction to finished sequences, took only 24 h. We developed a portable, culture-independent, high-throughput sequencing workflow suitable for resource-limited settings, aiding in real-time monitoring, outbreak investigation, and detection of new NiV strains and genetic evolution.

Importance

The development of a culture-independent, high-throughput whole-genome sequencing (WGS) protocol for Nipah virus (NiV) using the Oxford Nanopore MinION technology marks a significant advancement in outbreak response, surveillance, and genomic analysis of NiV. NiV is an RG4 category C pathogen; working with the NiV virus is a deep concern of biosafety and biosecurity. It demands the development of biologically safe procedures to get genetic information. This protocol utilizes biologically safe samples that were collected into recommended lysis solution, multiplex PCR, and third-generation sequencing, effectively addressing challenges in sequencing NiV. This optimized workflow achieved over 95% genome coverage without the need for virus culture. It is a cost-effective, rapid, and efficient approach to the WGS of NiV, making it suitable for resource-limited settings like Bangladesh. The method enhances the capacity for outbreak investigations, epidemiological analyses, and monitoring virus, aiding in detecting emerging strains. This work contributes significantly to global pandemic preparedness and response efforts.

The development of a culture-independent, high-throughput whole-genome sequencing (WGS) protocol for Nipah virus (NiV) using the Oxford Nanopore MinION technology marks a significant advancement in outbreak response, surveillance, and genomic analysis of NiV. NiV is an RG4 category C pathogen; working with the NiV virus is a deep concern of biosafety and biosecurity. It demands the development of biologically safe procedures to get genetic information. This protocol utilizes biologically safe samples that were collected into recommended lysis solution, multiplex PCR, and third-generation sequencing, effectively addressing challenges in sequencing NiV. This optimized workflow achieved over 95% genome coverage without the need for virus culture. It is a cost-effective, rapid, and efficient approach to the WGS of NiV, making it suitable for resource-limited settings like Bangladesh. The method enhances the capacity for outbreak investigations, epidemiological analyses, and monitoring virus, aiding in detecting emerging strains. This work contributes significantly to global pandemic preparedness and response efforts.

Keywords: Nipah virus; Oxford Nanopore MinION; culture independent; whole-genome sequencing; clinical and environmental specimen

18. Xin Hui S Chan, Ilsa L Haeusler, Bennett J K Choy, Md Zakiul Hassan, Junko Takata, Tara P Hurst, Luke M Jones, Shanghavie Loganathan, Elinor Harriss, Jake Dunning, Joel Tarning, Miles W Carroll, Peter W Horby, Piero L Olliaro, **Therapeutics for Nipah virus disease: a systematic review to support prioritisation of drug candidates for clinical trials,** The Lancet Microbe, Volume 6, Issue 5, 2025, 101002, https://doi.org/10.1016/j.lanmic.2024.101002.

ABSTRACT:

Nipah virus disease is a bat-borne zoonosis with person-to-person transmission, a case-fatality rate of 38–75%, and well recognised potential to cause a pandemic. The first reported outbreak of Nipah virus disease occurred in Malaysia and Singapore in 1998, which has since been followed by multiple outbreaks in Bangladesh and India. To date, no therapeutics or vaccines have been approved to treat Nipah virus disease, and only few such candidates are in development. In this Review, we aim to assess the safety and efficacy of the therapeutic options (monoclonal antibodies and small molecules) for Nipah virus disease and other henipaviral diseases to support prioritisation of drug candidates for further evaluation in clinical trials. At present, sufficient evidence exists to suggest trialling 1F5, m102.4, and remdesivir (alone or in combination) for prophylaxis and early treatment of Nipah virus disease. In addition to well designed clinical efficacy trials, in-vivo pharmacokinetic–pharmacodynamic

studies are needed to optimise the selection and dosing of therapeutic candidates in animal challenge and natural human infection.

19. Gunner P. Johnston, Fikret Aydemir, Haewon Byun, Emmie de Wit, Kristie L. Oxford, Jennifer E. Kyle, Jason E. McDermott, Brooke L. Deatherage Kaiser, Cameron P. Casey, Karl K. Weitz, Heather M. Olson, Kelly G. Stratton, Natalie C. Heller, Viraj Upadhye, I. Abrrey Monreal, J. Lizbeth Reyes Zamora, Lei Wu, D.H. Goodall, David W. Buchholz, Joeva J. Barrow, Katrina M. Waters, Ruth N. Collins, Heinz Feldmann, Joshua N. Adkins, Hector C. Aguilar, **Multi-platform omics analysis of Nipah virus infection reveals viral glycoprotein modulation of mitochondria,** Cell Reports, Volume 44, Issue 3, 2025, 115411, https://doi.org/10.1016/j.celrep.2025.115411.

ABSTRACT:

The recent global pandemic illustrates the importance of understanding the host cellular infection processes of emerging zoonotic viruses. Nipah virus (NiV) is a deadly zoonotic biosafety level 4 encephalitic and respiratory paramyxovirus. Our knowledge of the molecular cell biology of NiV infection is extremely limited. This study identified changes in cellular components during NiV infection of human cells using a multi-platform, high-throughput transcriptomics, proteomics, lipidomics, and metabolomics approach. Remarkably, validation via multi-disciplinary approaches implicated viral glycoproteins in enriching mitochondria-associated proteins despite an overall decrease in protein translation. Our approach also allowed the mapping of significant fluctuations in the metabolism of glucose, lipids, and several amino acids, suggesting periodic changes in glycolysis and a transition to fatty acid oxidation and glutamine anaplerosis to support mitochondrial ATP synthesis. Notably, these analyses provide an atlas of cellular changes during NiV infections, which is helpful in designing therapeutics against the rapidly growing Henipavirus genus and related viral infections.

Keywords: Nipah virus; paramyxovirus; proteomics; omics; transcriptomics; lipidomics; metabolomics; host; metabolism; infection

20. Elijah Kolawole Oladipo, James Akinwumi Ogunniran, Oluwaseyi Samuel Akinpelu, Tosin Omoboyede Omole, Boluwatife Ayobami Irewolede, Glory Jesudara Oluwasanya, Esther Moradeyo Jimah, Bamidele Abiodun Iwalokun, Olatunji Matthew Kolawole, Tosin Yetunde Senbadejo, Titilayo Marbel Olotu, Elukunbi Hilda Awoyelu, Helen Onyeaka, **Designing next-generation mRNA vaccines against nipah virus using predictive immunoinformatics frameworks,** In Silico Research in Biomedicine, Volume 1, 2025, 100036, https://doi.org/10.1016/j.insi.2025.100036.

ABSTRACT:

The Nipah virus (NiV) is a zoonotic pathogen designated as a priority disease by the World Health Organization. Currently, there are no approved vaccines specifically available for NiV infection in either humans or animals. In this study, we employed immunoinformatics approaches to design an mRNA vaccine candidate targeting five proteins from the Nipah virus. Viral protein sequences were retrieved and analyzed, and antigenic sequences were selected for further evaluation. The vaccine construct was developed using linear B-cell epitopes, cytotoxic T lymphocyte (CTL) epitopes, and helper T lymphocyte (HTL) epitopes capable of inducing interleukin-4 (IL-4), interleukin-10 (IL-10), and interferon-gamma (IFN-γ) responses, as predicted using various bioinformatics tools. The final

construct comprised fifteen epitopes, an adjuvant, an MHC class I-targeting domain (MITD), a Kozak sequence, 5′ and 3′ untranslated regions (UTRs), and a 5′ cap, all linked using appropriate peptide linkers. The vaccine was predicted to be antigenic, non-toxic, and non-allergenic, with favorable physicochemical properties, including a molecular weight of 129.23 kDa, an aliphatic index of 74.42, a GRAVY score of −0.483, and an isoelectric point (pI) of 8.61. Molecular docking simulations demonstrated strong binding affinities with Toll-like receptors 3 and 4 (TLR3 and TLR4). These findings suggest that the designed vaccine construct has the potential to elicit a protective immune response against the Nipah virus. However, further experimental validation is required to assess its efficacy and safety.

Keywords: Nipah virus; mRNA vaccine; Immunoinformatics; Epitope prediction; Toll-like receptors (TLRs)

21. Awnon Bhowmik, Mahmudul Hasan, Md. Mehedi Hasan Redoy, Goutam Saha, **Nipah virus outbreak trends in Bangladesh during the period 2001 to 2024: a brief review,** Science in One Health, Volume 4, 2025, 100103, https://doi.org/10.1016/j.soh.2024.100103.

ABSTRACT:

Nipah virus (NiV) is a zoonotic threat that has caused recurrent outbreaks in Bangladesh since 2001, raising significant public health concerns. This study provides a descriptive analysis of NiV outbreaks from 2001 to 2024, examining trends in infection and death rates and their correlation with climatic factors such as temperature, humidity, and rainfall. The findings highlight significant spikes in NiV cases during specific years, with environmental factors, particularly temperature and precipitation, showing solid correlations with outbreak patterns. The study also explores the impact of population dynamics on transmission risks, including urbanization and density. By focusing on these factors, this research supports the development of targeted public health interventions in high-risk areas, particularly in Bangladesh's northwestern and central districts, where recurrent outbreaks have been observed. These insights improve surveillance and preventive strategies for mitigating future NiV outbreaks.

Keywords: Nipah virus; Bangladesh outbreaks; Infection trends; Mortality rates; Climatic factors; Northwestern high-risk regions; Public health interventions

22. Mobin Ibne Mokbul, Shuvajit Saha, Samiha Nahar Tuli, Fatema Binte Nur, A.M. Khairul Islam, Tariful Islam, Shirsho Shreyan, Alok Bijoy Bhadra, Golam Dastageer Prince, Irfath Sharmin Eva, Mustari Nailah Tabassum, Ferdous Wahid, Md Irfan Bin Kayes, Nazim Hassan Ziad, Mohammad Delwer Hossain Hawlader, **Assessment of the general population knowledge about the emergence of Nipah virus outbreak in Bangladesh: A nationwide cross-sectional study,** Journal of Virus Eradication, Volume 11, Issue 1, 2025, 100585, https://doi.org/10.1016/j.jve.2025.100585.

ABSTRACT:

The emergence of the Nipah virus (NiV) poses a significant global health threat, particularly in South-East Asian countries. This cross-sectional nationwide study is a pioneer in assessing knowledge levels of NiV outbreak among the general population in Bangladesh. It was conducted among the general population of Bangladesh from 15th January to 10th February 2024. A conveniently selected sample

of individuals participated in the assessment of their knowledge about NiV. A semi-structured questionnaire was used as the data collection tool. After data curation, a total of 2121 responses that met the inclusion criteria were retained for analysis. Among 2121 participants, 69.38 % were aware of NiV. Overall, 62 % demonstrated good knowledge of the virus. The main sources of information were social media (29.9 %), television (25.41 %), educational institutions (18.95 %), newspapers (13.65 %), friends (6.39 %), and workplaces (5.91 %). Multivariate logistic regression analysis showed that participants aged 31–40 years had lower odds of poor knowledge (OR = 0.57, 95 % CI: 0.39–0.82, $p < 0.01$) compared to those aged 21–30. Females had higher odds of poor knowledge (OR = 1.38, 95 % CI: 1.05–1.81, $p = 0.02$) than males. Lower education levels were associated with higher odds of poor knowledge. Moreover, non-healthcare workers also had higher odds of poor knowledge compared to healthcare workers. There were regional differences, with varying odds in Rangpur (OR = 0.43, 95 % CI: 0.26–0.70, $p < 0.01$), Khulna (OR = 1.70, 95 % CI: 1.10–2.61, $p = 0.01$), and Mymensingh (OR = 2.77, 95 % CI: 1.70–4.53, $p < 0.01$) compared to Dhaka. The current study underscores the importance of evidence-based educational strategies, and may guide government and policymakers to design future targeted interventions to enhance public health literacy and mitigate the spread of NiV in Bangladesh as well as in its neighbouring countries.

Keywords: Nipah virus; Bangladesh; Knowledge; Public health; Awareness; Education

23. Mingqing Lu, Yanfeng Yao, Hang Liu, Yun Peng, Xuejie Li, Ge Gao, Miaoyu Chen, Xuekai Zhang, Lingjing Mao, Peipei Yang, XiaoYu Zhang, Jing Miao, Zhiming Yuan, Jiaming Lan, Chao Shan, **Single-dose intranasal AdC68-vectored vaccines rapidly protect Syrian hamsters against lethal Nipah virus infection,** Molecular Therapy, Volume 33, Issue 7, 2025, Pages 3270-3285, https://doi.org/10.1016/j.ymthe.2025.03.032.

ABSTRACT:

Nipah virus (NiV) infection is highly lethal in humans, and the development of vaccines that provide rapid protection is critical for addressing NiV outbreaks. In this study, we demonstrate that a single intranasal immunization with the chimpanzee adenoviral-vectored NiV vaccine, AdC68-F, induced robust and sustained cellular and humoral responses in BALB/c mice, and provided complete protection against challenge with the NiV-Malaysia strain (NiV-M) in Syrian hamsters. Notably, AdC68-F, administered at a dose of 5 × 109 viral particles, offered a complete prophylactic protection window as few as 7 days before exposure to a lethal NiV-M challenge. Furthermore, passive transfer of sera from AdC68-F or AdC68-G immunized animals conferred complete protection against NiV-M infection in naive hamsters. These findings underscore the pivotal role of antigen-specific immunity in controlling NiV infection and highlight the potential of single-dose intranasal AdC68-based NiV vaccines for rapid protection during outbreaks. By providing rapid and effective protection, these vaccines could help reduce human-to-human transmission and aid in curbing NiV outbreaks.

Keywords: Nipah virus; AdC68; hamsters; passive transfer; rapid protection

24. Side Hu, Heesu Kim, Pan Yang, Zishuo Yu, Barbara Ludeke, Shawna Mobilia, Junhua Pan, Margaret Stratton, Yuemin Bian, Rachel Fearns, Jonathan Abraham, **Structural and functional analysis of the Nipah virus polymerase complex,** Cell, Volume 188, Issue 3, 2025, Pages 688-703.e18, https://doi.org/10.1016/j.cell.2024.12.021.

ABSTRACT:

Nipah virus (NiV) is a bat-borne, zoonotic RNA virus that is highly pathogenic in humans. The NiV polymerase, which mediates viral genome replication and mRNA transcription, is a promising drug target. We determined the cryoelectron microscopy (cryo-EM) structure of the NiV polymerase complex, comprising the large protein (L) and phosphoprotein (P), and performed structural, biophysical, and in-depth functional analyses of the NiV polymerase. The L protein assembles with a long P tetrameric coiled-coil that is capped by a bundle of α-helices that we show are likely dynamic in solution. Docking studies with a known L inhibitor clarify mechanisms of antiviral drug resistance. In addition, we identified L protein features that are required for both transcription and RNA replication and mutations that have a greater impact on RNA replication than on transcription. Our findings have the potential to aid in the rational development of drugs to combat NiV infection.

Keywords: Nipah virus; RNA virus; polymerase; emerging viruses; RNA replication; RNA transcription

25. Nazmun Nahar, Shahana Parveen, Emily S. Gurley, Probir Kumar Ghosh, Ishrat Jabeen, Md. Rifat Haidar, Farhat Jahan, Mohammad Saeed Munim, Kanij Fatema Chanda, Md. Wazed Ali, Zubair Akhtar, Tahmina Shirin, Sayera Banu, Atique Iqbal Chowdhury, Asraful Alam, Brian E. Dawes, Joan Fusco, Thomas P. Monath, Gray Heppner, Stephen P. Luby, **Community willingness to participate in a Nipah vaccine trial in Bangladesh,** Vaccine, Volume 62, 2025, 127578, https://doi.org/10.1016/j.vaccine.2025.127578.

ABSTRACT:

Nipah virus (NiV) is a deadly zoonotic disease with pandemic potential, prioritized by the World Health Organization for research and vaccine development. Since Bangladesh has faced annual NiV outbreaks and repeated spillovers since 2001, it is likely to be the site of a Phase II vaccine trial. This study explored people's knowledge about NiV and their willingness to participate in a NiV vaccine trial in Bangladesh.

Methods

We conducted a mixed methods study, collecting qualitative and quantitative data from Mirpur township, Dhaka, and NiV-affected Faridpur District. From December 2021 to November 2022, the team interviewed adult male and female respondents responsible for household treatment and vaccination decisions.

Results

The team conducted 66 in-depth interviews and 978 survey interviews. Many in-depth interviewees were aware of NiV and, when asked if they would participate in a NiV vaccine trial, responded with one of three options: willing, unwilling, or would decide later. They were concerned about vaccine safety and side effects when making a decision about participation. In the survey, more respondents from Mirpur township, Dhaka, had heard about a disease transmitted from bats to people (57 %, 272/478 vs. 52 %, 262/500) and were willing to participate in a vaccine trial (45 %, 217/478 vs. 22 %, 111/500) than those from Faridpur. A high number expressed willingness to take an investigational NiV vaccine during an outbreak (Dhaka 75 %, 205/272 vs. Faridpur 81 %, 398/491 Faridpur). We did not find any association between knowledge about NiV and willingness to participate in a NiV vaccine trial.

Conclusion

Many respondents expressed willingness to participate in a NiV vaccine trial, especially during an outbreak, suggesting that such a trial may be feasible in Bangladesh. Given concerns about safety and side effects, clear communication on these issues may support informed participation.

Keywords: Vaccine trial; Investigational vaccine; Nipah virus infection; Bangladesh

26. Md Zakiul Hassan, Amanda Rojek, Piero Olliaro, Peter Horby, **Improving clinical care of patients in Nipah outbreaks: moving beyond 'compassionate use',** The Lancet Regional Health - Southeast Asia, Volume 33, 2025, 100527, https://doi.org/10.1016/j.lansea.2024.100527.

ABSTRACT:

The 2024 Nipah outbreak in Kerala, India—its fifth in six years—and the recurring annual outbreaks in Bangladesh underscore the persistent threat posed by the Nipah virus (NiV) in the region. With a high mortality rate, human-to-human transmission potential, and the widespread presence of Pteropus bats, the natural reservoir, NiV remains a significant epidemic threat. Despite being a WHO priority pathogen, there has been no systematic effort to improve patient care for NiVD, leading to consistently poor outcomes. Current care relies on supportive measures and the 'compassionate use' of unapproved drugs like ribavirin and remdesivir. Drugs used 'off-label' during outbreaks can become the 'standard of care' without robust evidence of their safety or efficacy, complicating the testing of new therapies and perpetuating uncertainty about their true effectiveness. To improve NiVD care, we propose four key strategies: 1) Enhance early case detection, 2) optimize supportive care to improve outcomes and create a standard for future trials, 3) adopt a syndromic approach centered on encephalitis, and 4) explore innovative trial designs tailored to low case numbers as an alternative to 'compassionate use'. By integrating these strategies, healthcare systems in NiV-endemic regions will be better equipped to manage both current and future outbreaks.

Keywords: Nipah virus; Outbreak; Compassionate drug use; Epidemic; Pandemic; Southeast Asia; Clinical trials; Encephalitis; Therapeutics

27. Hui Ming Ong, Puteri Ainaa S. Ibrahim, Chee Ning Chong, Chong Tin Tan, Jie Ping Schee, Michael Selorm Avumegah, Raúl Gómez Román, Neil George Cherian, Won Fen Wong, Li-Yen Chang, **Malaysia outbreak survivors retain detectable Nipah antibodies and memory B cells after 25 years,** Journal of Infection, Volume 90, Issue 2, 2025, 106398, https://doi.org/10.1016/j.jinf.2024.106398.

ABSTRACT:

Objective

To evaluate the long-term humoral immune response to Nipah virus (NiV) in a cohort of 25 survivors after 25 years of post-infection.

Methods

A total of 25 survivors of NiV infection from the 1998 outbreak were recruited for sample collection. The serum IgG antibody response to NiV antigens, specifically nucleocapsid (N), fusion glycoprotein

(F) and attachment glycoprotein (G) was evaluated using ELISA. Additionally, the samples were tested for neutralizing antibodies and memory B cell responses.

Results

Detection rates of anti-NiV-F and anti-NiV-G were 56% and 60%, respectively, among the survivors at a 1:100 dilution, whereas only 20% were specifically reactive to rNiV-N. Notably, all samples that tested positive for NiV-F and NiV-G at this dilution also exhibited neutralizing antibodies, highlighting the specificity of these assays. Live virus neutralization assay showed that 72% of survivors had detectable neutralizing antibodies, with varying titers, indicating long-lasting immune memory. Furthermore, memory B cell responses specific to NiV-F and NiV-G were observed in six randomly selected survivors, suggesting the presence of enduring immunological memory.

Conclusions

These findings highlight the potential of NiV-F and NiV-G as reliable markers for NiV exposure and underscore the need for continuous surveillance and research. Such efforts are crucial for advancing vaccine development and improving preparedness for future NiV outbreaks.

Keywords: Nipah virus; ELISA; IgG; Neutralizing antibodies; Memory B cells

28. Olivier Reynard, Mathieu Iampietro, Claire Dumont, Sandrine Le Guellec, Stephanie Durand, Marie Moroso, Elise Brisebard, Kévin P. Dhondt, Rodolphe Pelissier, Cyrille Mathieu, Maria Cabrera, Deborah Le Pennec, Lucia Amurri, Christopher Alabi, Sylvain Cardinaud, Matteo Porotto, Anne Moscona, Laurent Vecellio, Branka Horvat, **Development of nebulized inhalation delivery for fusion-inhibitory lipopeptides to protect non-human primates against Nipah-Bangladesh infection,** Antiviral Research, Volume 235, 2025, 106095, https://doi.org/10.1016/j.antiviral.2025.106095.

ABSTRACT:

Nipah virus (NiV) is a lethal zoonotic paramyxovirus that can be transmitted from person to person through the respiratory route. There are currently no licensed vaccines or therapeutics. A lipopeptide-based fusion inhibitor was developed and previously evaluated for efficacy against the NiV-Malaysia strain. Intraperitoneal administration in hamsters showed superb prophylactic activity and promising efficacy, however the intratracheal delivery mode in non-human primates proved intractable and spurred the development of an aerosolized delivery route that could be clinically applicable. We developed an aerosol delivery system in an artificial respiratory 3D model and optimized the combinations of flow rate and particle size for lung deposition. We characterized the nebulizer device and assessed the safety of lipopeptide nebulization in an African green monkey model that mimics human NiV infection. Three nebulized doses of fusion-inhibitory lipopeptide were administered every 24 h, resulting in peptide deposition across multiple regions of both lungs without causing toxicity or adverse hematological and biochemical effects. In peptide-treated monkeys challenged with a lethal dose of NiV-Bangladesh, animals retained robust levels of T and B-lymphocytes in the blood, infection-induced lethality was significantly delayed, and 2 out of 5 monkeys were protected from NiV infection. The present study establishes the safety and feasibility of the nebulizer delivery method for AGM studies. Future studies will compare delivery methods using next-generation fusion-inhibitory anti-NiV lipopeptides to evaluate the potential role of this aerosol delivery approach in achieving a rapid antiviral response.

Keywords: Nipah virus; Nebulization; Virus-cell-fusion; Inhibitory lipopeptides; Non-human primates; Antivirals

29. Celeste Huaman, Caitlyn Clouse, Madeline Rader, Allison M. Strazzella, Jocelyn King, Elise M. Santorella, Lianying Yan, Shuangyi Bai, Bronwyn M. Gunn, Moushimi Amaya, Christopher C. Broder, Brian C. Schaefer, **A recombinant Cedar virus preclinical model that recapitulates neurological features of henipavirus disease,** iScience, Volume 28, Issue 10, 2025, 113571, https://doi.org/10.1016/j.isci.2025.113571.

ABSTRACT:

Nipah virus (NiV) and Hendra virus (HeV) are members of the henipavirus genus that cause severe respiratory and/or neurological disease in humans. Because NiV and HeV can only be handled under BSL-4 containment, there are significant practical barriers to the study of pathogenicity and the evaluation of therapeutic countermeasures. However, Cedar virus (CedV) is a non-pathogenic henipavirus that can be used in a BSL-2 setting. Here, we demonstrate that recombinant CedVs that express the F and G glycoproteins of NiV or HeV display an in vivo tissue tropism that better emulates authentic NiV and HeV. Moreover, by severely impairing interferon signaling through the use of STAT1-deficient mice, we show that rCedVs expressing NiV/HeV F and G cause neurological disease signs and mortality in most animals. Thus, this BSL-2 mouse model represents a powerful tool for pre-clinical investigation of candidate therapeutics and studies of henipavirus pathogenesis mechanisms.

Keywords: Virology; Neuroscience; Immunology

30. Celeste Huaman, Caitlyn Clouse, Madeline Rader, Allison M. Strazzella, Jocelyn King, Elise M. Santorella, Lianying Yan, Shuangyi Bai, Bronwyn M. Gunn, Moushimi Amaya, Christopher C. Broder, Brian C. Schaefer, **A recombinant Cedar virus preclinical model that recapitulates neurological features of henipavirus disease,** iScience, Volume 28, Issue 10, 2025, 113571, https://doi.org/10.1016/j.isci.2025.113571.

ABSTRACT:

Nipah virus (NiV) and Hendra virus (HeV) are members of the henipavirus genus that cause severe respiratory and/or neurological disease in humans. Because NiV and HeV can only be handled under BSL-4 containment, there are significant practical barriers to the study of pathogenicity and the evaluation of therapeutic countermeasures. However, Cedar virus (CedV) is a non-pathogenic henipavirus that can be used in a BSL-2 setting. Here, we demonstrate that recombinant CedVs that express the F and G glycoproteins of NiV or HeV display an in vivo tissue tropism that better emulates authentic NiV and HeV. Moreover, by severely impairing interferon signaling through the use of STAT1-deficient mice, we show that rCedVs expressing NiV/HeV F and G cause neurological disease signs and mortality in most animals. Thus, this BSL-2 mouse model represents a powerful tool for pre-clinical investigation of candidate therapeutics and studies of henipavirus pathogenesis mechanisms.

Keywords: Virology; Neuroscience; Immunology

31. Yiru Wang, Lixia Zhao, Yi Zhang, Xiuxia Gao, Yannan Wang, Wenping Shi, Roger D. Kornberg, Heqiao Zhang, **Structures of the measles virus polymerase complex with non-nucleoside inhibitors and mechanism of inhibition,** Cell, Volume 188, Issue 18, 2025, Pages 4913-4923.e13, https://doi.org/10.1016/j.cell.2025.06.017.

ABSTRACT:

The measles virus (MeV), a highly contagious non-segmented negative-sense RNA virus in the Paramyxoviridae family, causes millions of infections annually, with no approved antivirals available. The viral polymerase complex, comprising the large (L) protein and the tetrameric phosphoprotein (P), is a key antiviral target. We determined the cryo-electron microscopy structures of the MeV polymerase complex alone and bound to two non-nucleoside inhibitors, ERDRP-0519 and AS-136A. Inhibitor binding induces a conformational change in the catalytic loop, allosterically locking the polymerase in an inactive "GDN-out" state. These findings led to the proposal that ERDRP-0519 would also be effective against Nipah virus (NiV), a highly pathogenic virus with no available antivirals. This proposal was confirmed by structure determination of the NiV polymerase complex and by inhibition of transcription.

Keywords: measles virus; Nipah virus; non-nucleoside inhibitor; cryo-EM; polymerase complex; ERDRP-0519; AS-136A; L-P complex

32. Maryam Shafaati, Milad Zandi, **Langya henipavirus (LayV) as an emerging zoonotic disease: a mini-review,** New Microbes and New Infections, Volume 68, 2025, 101643, https://doi.org/10.1016/j.nmni.2025.101643.

ABSTRACT:

Henipavirus is one of the genera in the Orthoparamyxovirinae subfamily, which includes several emerging viruses that pose a major public health threat. The predominant members of the virus genus, Hendra and Nipah viruses, are extremely virulent zoonotic viruses that cause neurological and respiratory infections and outbreaks in humans. The recently discovered Langya henipavirus, a new henipavirus phylogenetically related to Mojiang henipavirus (MojV), has been associated with febrile illness in patients from China who are mainly agricultural workers. Active surveillance must be conducted worldwide in an open and collaborative manner to reduce the likelihood of this new virus causing a health crisis. More research is needed to address the remaining difficulties.

Keywords: Langya henipavirus; Henipavirus; Zoonotic

33. Attila J. Trájer, **The role of Denisovan paleohabitats in shaping modern human genetic resistance to viral, bacterial, and parasitic infections,** Journal of Human Evolution, Volume 207, 2025, 103746, https://doi.org/10.1016/j.jhevol.2025.103746.

ABSTRACT:

Denisovans contributed notably to the genomes of present-day East and Southeast Asians. However, the relationship between the inhabited paleohabitats and the adaptive genetic traits related to infections in modern humans remains underexplored. This study uses geospatial techniques to analyze climatic factors associated with three Denisovan archaeological sites linked to nine specimens. Additionally, past and present climates and biomes, as well as the geographic distributions of eight infectious agents and disease vector groups, were modeled and compared with the modern genetic heritage of Denisovans. Findings reveal that the identified Denisovans inhabited subarctic and monsoon-influenced temperate climates, occupying boreal and seasonal forest biomes in the three

studied archaeological sites. Sites such as Denisova Cave and Baishiya Karst Cave exhibited low climatic suitability for Ascaris lumbricoides, visceral leishmaniasis, and Nipah virus. Plasmodium vivax– and Aedes albopictus–like vectors plausibly were also not present. Conversely, Denisova Cave and Baishiya Karst Cave exhibit high climatic suitability for Ixodes persulcatus and Lyme borreliosis when Denisovans inhabited these sites. The paleoenvironment of the Laotian Cobra Cave site—with the exception of Nipah henipavirus—was suitable for all modeled pathogens and vectors. From the studied vectors and diseases, I. persulcatus and Lyme borreliosis are missing from Melanesia, where the region's humans have the highest Denisovan legacy. This suggests that Denisovans from humid continental climates, such as those near Cobra Cave, may have contributed alleles providing adaptive advantages against ascariasis and mosquito-borne diseases in environments where modern human populations with high Denisovan genetic legacy reside.

Keywords: Hominin; Ecology; Paleoenvironment; Prehistoric disease susceptibility

34. Jakub Hantabal, F. Javier Salguero, Miles W. Carroll, **Current knowledge on the host-pathogen interactions of henipaviruses and novel platforms to enable further characterisation,** eBioMedicine, Volume 123, 2026, 106110, https://doi.org/10.1016/j.ebiom.2025.106110.

ABSTRACT:

Henipaviruses, particularly the species Nipah (NiV) and Hendra (HeV), are emerging viral threats with potential to cause a public health emergency of international concern due to their high virulence and absence of approved preventative and therapeutical countermeasures. Consequently, research of NiV and HeV is restricted to high-containment laboratories and relies heavily on in vitro models. Despite NiV and HeV initial characterisation >25 years ago, significant gaps remain in the knowledge of the host-pathogen interactions, which are an important research focus for design of therapeutics and supportive care modalities. This review summarises current knowledge in the host-pathogen interactions of henipaviruses and critically assesses the current and emerging in vivo and in vitro models for henipavirus research.

Keywords: Henipavirus; Nipah; Hendra; Pathogenesis; Host-pathogen interactions; Infection; Immunity; Model

35. Leon Schrell, Hannah L. Fuchs, Antje Dickmanns, David Scheibner, Judith Olejnik, Adam J. Hume, Wencke Reineking, Theresa Störk, Martin Müller, Annika Graaf-Rau, Sandra Diederich, Stefan Finke, Wolfgang Baumgärtner, Elke Mühlberger, Anne Balkema-Buschmann, Matthias Dobbelstein, **Inhibitors of dihydroorotate dehydrogenase synergize with the broad antiviral activity of 4'-fluorouridine,** Antiviral Research, Volume 233, 2025, 106046, https://doi.org/10.1016/j.antiviral.2024.106046.

ABSTRACT:

RNA viruses present a constant threat to human health, often with limited options for vaccination or therapy. Notable examples include influenza viruses and coronaviruses, which have pandemic potential. Filo- and henipaviruses cause more limited outbreaks, but with high case fatality rates. All RNA viruses rely on the activity of a virus-encoded RNA-dependent RNA polymerase (RdRp). An antiviral nucleoside analogue, 4'-Fluorouridine (4'-FlU), targets RdRp and diminishes the replication of several RNA viruses, including influenza A virus and SARS-CoV-2, through incorporation into nascent

viral RNA and delayed chain termination. However, the effective concentration of 4′-FlU varied among different viruses, raising the need to fortify its efficacy. Here we show that inhibitors of dihydroorotate dehydrogenase (DHODH), an enzyme essential for pyrimidine biosynthesis, can synergistically enhance the antiviral effect of 4′-FlU against influenza A viruses, SARS-CoV-2, henipaviruses, and Ebola virus. Even 4′-FlU-resistant mutant influenza A virus was re-sensitized towards 4′-FlU by DHODH inhibition. The addition of uridine rescued influenza A virus replication, strongly suggesting uridine depletion as a mechanism of this synergy. 4′-FlU was also highly effective against SARS-CoV-2 in a hamster model of COVID. We propose that the impairment of endogenous uridine synthesis by DHODH inhibition enhances the incorporation of 4′-FlU into viral RNAs. This strategy may be broadly applicable to enhance the efficacy of pyrimidine nucleoside analogues for antiviral therapy.

Keywords: Influenza a virus; SARS-CoV-2; Ebolavirus; Cedar virus; Nipah virus; Henipavirus; 4′-Fluorouridine; EIDD-2749; N4-hydroxycytidine; Molnupiravir; Dihydroorotate dehydrogenase (DHODH); Teriflunomide; Brequinar; Pyrimidine analogues; RNA polymerase

36. Jian-Di Li, Yu-Qing Liu, Rong-Quan He, Zhi-Guang Huang, Wan-Ying Huang, Hong Huang, Zhi-Hong Liu, Gang Chen, **Understanding and addressing the global impact: A systematic review and cross-sectional bibliometric analysis of Langya henipavirus and pre-existing severe henipaviruses,** Journal of Infection and Public Health, Volume 18, Issue 2, 2025, 102631, https://doi.org/10.1016/j.jiph.2024.102631.

ABSTRACT:

In 2022, Langya henipavirus was identified in patients with fever in eastern China. This study provides an overview of the scientific landscape, highlights research focus areas, and outlines potential future investigations. The relevant scientific literature was systematically searched and reviewed via advanced bibliometric techniques. Over the past two decades, henipavirus research has increased at an annual rate of 8.82 %. The United States leads in research output, with the Australian Animal Health Laboratory as the top institution. Most articles are published in the Journal of Virology, identified as the most influential journal along with researcher Wang LF. Current research focuses on “zoonosis,” “vaccine,” and “pathogenesis,” whereas future areas may include “molecular docking,” “immunoinformatics,” “climate change,” “antibodies,” “vaccines,” “glycoprotein,” and “ephrin-b2.” This study details henipavirus research, highlighting key players, trends, and future directions. These insights will guide future efforts to address the risks posed by novel Henipaviruses, such as Langya.

Keywords: Langya henipavirus; Hendra virus; Nipah virus; Bibliometric analysis; Vaccine

37. Juwan Kim, Su J Lee, Dae-Gyun Ahn, Ji-Seung Yoo, **Immune evasion and pathogenesis of henipaviruses,** Current Opinion in Virology, Volume 74, 2026, 101509, https://doi.org/10.1016/j.coviro.2026.101509.

ABSTRACT:

Zoonotic viruses pose an escalating threat to global health, driven by climate change, deforestation, urbanization, and increased human-wildlife interactions. Among these threats, Henipaviruses — particularly Hendra virus and Nipah virus — have emerged as priority pathogens due to their severe clinical manifestations, broad host range, and pandemic potential. Naturally maintained in asymptomatic Pteropus fruit bats, Henipaviruses periodically spill over into humans via

intermediate hosts, causing outbreaks characterized by acute respiratory and neurological syndromes and high fatality rates. Despite the increasing frequency of spillover events linked to environmental disruptions, no licensed antivirals or human vaccines currently exist. This review summarizes recent advances in Henipavirus virology, pathogenesis, host interactions, and the innate immune evasion mechanisms. An integrated understanding of these key aspects is critical for the design of effective preventive strategies within a unified One Health approach.

38. David J. Williamson, Cecilia Zaza, Irene Carlon-Andres, Tobias Starling, Alessia Gentili, Joseph W. Thrush, Audrey Le Bas, Ravi Teja Ravi, Stuart Neil, Ray J. Owens, Maud Dumoux, Sabrina Simoncelli, Sergi Padilla-Parra, **Single-molecule localisation microscopy approaches reveal envelope glycoprotein clusters in single-enveloped viruses: a potential functional role?,** Biochemical Society Transactions, Volume 53, Issue 3, 2025, Pages 643-652, https://doi.org/10.1042/BST20240769.

ABSTRACT:

Understanding how viruses enter and fuse with host cells is crucial for developing effective antiviral therapies. The process of viral entry and fusion involves a series of complex steps that allow the virus to breach the host cell membrane and deliver its genetic material inside, with viral fusogens often co-operating to attain the required energy for successful membrane fusion. This co-operative clustering of fusogens in viral envelopes is similar to receptor clustering in cellular systems, where receptors aggregate to initiate signalling cascades. Single-molecule localisation microscopy (SMLM) approaches have emerged as powerful tools to study these intricate mechanisms, allowing the observation of proteins with unprecedented levels of detail. These technologies provide unparalleled insights into the dynamics of viral entry and fusion at a molecular level, revealing how the co-ordinated action of fusogens facilitates membrane fusion. By employing the newest advances in SMLM techniques, such as DNA-PAINT and MINFLUX, we anticipate that precise information on the key steps of viral fusion can be revealed with high spatial and temporal resolutions, identifying critical points in the process that can be targeted by antiviral strategies.

Keywords: biophysics; envelope glycoprotein; fusion; microscopy; single molecule

39. Chandhu Balachandran, Sakib Akther Pattassery, Babasaheb V. Tandale, Vijay Parashramji Bondre, Veetilakath Jithesh, Mohammed Asharu Jaman, Bhavya Fernandez, S. Harikumar, R. Balasubramanian, Anisha Pulinchani, B.M. Prema, Datta K. Butte, Abhijeet V. Jadhav, **A community-based focal serosurvey for West Nile virus infection following a surge in cases in 2024 in Kerala, India: a cross-sectional analysis,** New Microbes and New Infections, Volume 69, 2026, 101698, https://doi.org/10.1016/j.nmni.2026.101698.

ABSTRACT:

Background

From January to May of 2024, 27 cases of neuroinvasive disease due to West Nile Virus (WNV) were confirmed from Kerala. The number of cases were more than those seen over past three years combined. Cases were not clustered geographically and were primarily reported from four districts, viz, Kozhikode, Thrissur, Malappuram and Ernakulum. To understand the circulation of WNV, a focal serosurvey was conducted in the regions from where cases were reported.

Methods

A cross-sectional study was done in four districts of Kerala. Patients, family members and immediate neighbours were recruited at each case location. From 27 clusters across 26 villages/localities, 751 blood samples were collected. Due to cross-reactivity of WNV antibodies and that of Japanese Encephalitis (JE) virus, a micro-neutralization assay was done against both these viruses for all the samples.

Results

The seropositivity of WNV infection was found to be 29.96 % (26.68–33.24). Males had higher seropositivity than females, though the difference was not statistically significant. The overall seropositivity was higher compared to previously published studies. There was no significant difference in seropositivity across age-groups and sex. Seropositivity of JE infection was 1.86 % (0.90–2.83).

Discussion

Though a smaller proportion of infected get neurological involvement, WNV seropositivity among considerable number of people in a wide geography of the state is a public health concern.

Conclusion

To deal with this concern, more studies on bird-human interaction and larger serosurveys might be needed. Close monitoring and intervention planning are warranted to control possible future WNV spread.

Keywords: West Nile virus; One health; Emerging infections; Focal serosurvey; Outbreak investigation

40. Rajkapoor Balasubramanian, Naina Mohamed Pakkir Maideen, Arun Shanmugam, Narayanaswamy Harikrishnan, **A Review of Pre-clinical Data on the Pharmacotherapeutic Potential of Black Seeds (Nigella sativa) against Influenza Virus Infection,** Current Traditional Medicine, Volume 12, 2026, https://doi.org/10.2174/0122150838352681250404051446.

ABSTRACT:

Background and Objective

Influenza is a respiratory virus, and certain patients with some chronic conditions and other risk factors are vulnerable to severe infection requiring hospitalizations and further fatal complications. Few antiviral drugs are approved for the management of patients with influenza infection. Since N. sativa supplementation significantly reduces all-cause mortality, improves viral clearance, and diminishes viral loads in patients with SARS-CoV-2 infection and other viruses, including hepatitis C virus, our review focuses on the antiviral efficacy of black seeds (N. sativa) against influenza viruses.

Methods

The databases, including Medline/PMC/PubMed, Scopus, Web of Science, Google Scholar, ScienceDirect, and reference lists, were searched to identify relevant publications using keywords, such as Nigella sativa, black seeds, black cumin seeds, kalonji, and influenza virus. This review included only English publications, while duplicates were excluded.

Results

supplementation with N. sativa improved clinical symptoms, enhanced cytokine gene expression, labelpressed H9N2 virus pathogenesis, increased antibody titers against the H9N2 influenza virus, significantly reduced mortality, decreased virus shedding, promoted weight gain, boosted both cell-mediated and humoral immune responses, and facilitated early viral clearance in several preclinical studies involving H9N2-infected turkeys. Furthermore, a number of preclinical and clinical investigations showed that N. sativa has antiviral properties against other viruses. Furthermore, N. sativa has several pharmacotherapeutic potentials, including antiviral, immunomodulatory, antioxidant, and anti-inflammatory qualities that may be helpful in the treatment of influenza virus infection, according to multiple meta-analyses. Additionally, N. sativa's pharmacological properties, including its antihistaminic, bronchodilatory, antidiabetic, antiobesity, antihypertensive, antihyperlipidemic, and anticancer properties, may help to alleviate the signs, symptoms, and complications associated with influenza virus infection.

Conclusion

To prevent further complications, patients at higher risk of developing complications from influenza virus infection could be managed with specific antivirals and black seeds (N. sativa) as adjunctive therapy in the early stages of infection. Future clinical studies would establish the effectiveness of black seeds (N. sativa) against influenza infection.

Keywords: Black seeds; Nigella sativa ; kalonji; thymoquinone; antiviral; anti-inflammatory; antioxidant

41. Abel E. Quispe, Renzo Vera, Josimar Quiñones, José Angulo-Tisoc, César Lázaro, Alberto Manchego, Milagros Lostaunau, Edgar Valdez, Miguel Rojas, Dennis A. Navarro-Mamani, **Molecular detection of zoonotic RNA viruses in guinea pigs (Cavia porcellus) from small-scale family farming in the region of Cusco-Peru,** One Health, Volume 22, 2026, 101335, https://doi.org/10.1016/j.onehlt.2026.101335.

ABSTRACT:

Emerging zoonotic diseases are frequently associated with close human-animal interactions in small-scale farming systems. Guinea pigs (Cavia porcellus) are widely raised for food in the Andean region, often under poor sanitary conditions; however, little is known about their role as reservoirs of enteric viruses with zoonotic potential. This study aimed to detect zoonotic RNA viruses in intestinal samples from guinea pigs raised on small-scale family farms in the Cusco region of Peru. A total of 34 intestinal tissue samples from adult guinea pigs showing gastrointestinal lesions were analyzed by reverse transcription polymerase chain reaction (RT-PCR) and nested PCR for the molecular detection of Coronavirus (CoV), Rotavirus A (RVA), Mammalian orthoreovirus (MRV), and Kobuvirus (KoV). Positive amplicons were sequenced and analyzed phylogenetically to confirm the PCR assays. Overall, 91.18% (31/34) of samples tested positive for at least one virus. RVA was the most frequently detected (58.82%), followed by CoV (29.41%), MRV (23.53%), and KoV (23.53%). Single-virus infections accounted for 20 cases and co-infections were identified in 11 cases. RVA was the most frequently detected, both in single (n = 9) and co-infections (n = 11). KoV detection was predominantly associated with co-infections rather than single infections. These findings provide the first molecular evidence of multiple zoonotic RNA viruses in guinea pigs from small-scale farming in Peru, highlighting their

potential role as reservoirs in zoonotic transmission cycles. Enhanced surveillance and improved farm-level biosecurity are essential to mitigate risks of viral emergence in these traditional farming systems.

Keywords: Guinea pig; Cavia porcellus; Zoonotic RNA viruses; Andean region; Peru

42. Alexandre Lalande, Lola Canus, Amélie Bourgeais, Cyrille Mathieu, Eva Ogire, **The liver as a potential gate to the brain for encephalitic viruses,** Current Opinion in Virology, Volume 71, 2025, 101463, https://doi.org/10.1016/j.coviro.2025.101463.

ABSTRACT:

To model infection of viruses targeting the liver and the central nervous system, two-dimensional in vitro cultures rapidly show their limitations. Conversely, in vivo models do not easily allow the investigation of early events of the infection process. In between, ex vivo models, comprising mainly organoids and organotypic cultures, mimic or retain the cytoarchitecture of the organ while being relatively simple to handle and analyze. Here, we summarize the main features of brain and liver ex vivo models and pinpoint examples of their utilization for studying encephalitogenic and hepatotropic viruses. We highlight a gap of development and application of liver compared to ex vivo models in virology. Many hepatotropic viruses can also infect and/or have impacts on the central nervous system. In this sense, we sought to present these ex vivo models while providing a conceptual framework for the modeling of the hepatocerebral axis in the context of viral infections.

43. Bahram Zargar, Syed A. Sattar, Julie McKinney, M. Khalid Ijaz, **The stability and elimination of mammalian enveloped and non-enveloped respiratory and enteric viruses in indoor air: Testing using a room-sized aerobiology chamber,** Journal of Virological Methods, Volume 335, 2025, 115144, https://doi.org/10.1016/j.jviromet.2025.115144.

ABSTRACT:

We assessed the viability of aerosolized human betacoronavirus OC43 (HCoV-OC43; ATCC VR-1558), human rhinovirus-14 (RV-14; ATCC VR-284) and feline calicivirus (FCV; ATCC VR-782) as representative enveloped and non-enveloped respiratory and enteric viruses of mammals in indoor air under ambient conditions (relative humidity 50 ± 10 % and air temperature 22 ± 2°C) using a room-sized (25 m3; 900 ft3) aerobiology chamber. All virus suspensions contained a soil load to simulate the presence of body fluids and they were separately aerosolized into the chamber using a six-jet Collison nebulizer. A muffin fan was used to uniformly mix the air inside the chamber and to keep the aerosols airborne. A slit sampler with Petri plates containing 3 % (wt./vol) gelatin was used to collect the air samples. The gelatin was liquefied in an incubator and assayed for infectious virus as plaque-forming units (PFU). The rates of biological decay of HCoV-OC43, RV-14 and FCV were 0.0052 ± 0.00026, 0.0034 ± 0.0027 and 0.0081 ± 0.0031 (as log10 PFU/m3/min), respectively. We also assessed a HEPA filter-based stand-alone air purifier against the experimentally aerosolized viruses and the device could demonstrate > 3-log10 reductions in the viability of the three viruses in 46, 62 and 41 minutes, respectively. Therefore, we can now investigate the stability of mammalian viruses in indoor air as well as air decontamination technologies against them under field-relevant conditions.

Keywords: Air decontamination; Indoor air; Mammalian viruses; Human coronavirus; Feline calicivirus; Human rhinovirus; Aerobiology chamber

44. Yaohui Li, Xiaoyan Huang, Xiaodong Zai, Chenfeng Mao, Ruihua Li, Yamei Feng, Yue Zhang, Zhang Zhang, Jun Zhang, Junjie Xu, **Antigenic and structural insights into Langya henipavirus attachment glycoprotein,** Virologica Sinica, Volume 40, Issue 5, 2025, Pages 769-777, https://doi.org/10.1016/j.virs.2025.08.005.

ABSTRACT:

The invasion of host cells by the henipavirus is facilitated through the interaction between viral attachment (G) and fusion (F) glycoproteins with receptors on the cell surface. Langya henipavirus (LayV) was newly identified in China in 2022. The G proteins of LayV and Mojiang virus (MojV) exhibit high amino acid homology (86%), while they are located in a unique evolutionary clade within the Henipavirus genus. In this study, the crystal structure of the LayV G protein was resolved at a 3.37 Å resolution, revealing a head domain with six β-propeller-like domains distinct from other henipavirus G proteins, such as those of Nipah virus (NiV) and Hendra virus (HeV). Furthermore, the prominent loop in the center cavity of the LayV G protein showed unique structural features. In the ELISA and SPR assays, the LayV G protein was unable to bind to the existing henipavirus-neutralizing antibodies or the ephrin-B2 receptor. Immunogenicity studies in mice demonstrated robust antibody responses elicited by the LayV G protein. These antibodies exhibited strong reactivity against both LayV and MojV G proteins. However, only weak cross-reactivity was observed with other henipaviruses. Moreover, eight monoclonal antibodies targeting the LayV G protein were generated, two of which exhibited broad binding activity across different henipavirus G proteins. These findings underscore the need for tailored vaccines and therapeutics for LayV and related novel henipaviruses

Keywords: Langya henipavirus (LayV); Attachment glycoprotein; Crystal structure; Glycosylation; Immunogenicity; Monoclonal antibodies

45. Lipi Akter, Junna Kawasaki, Tofazzal Md. Rakib, Takashi Okura, Fumihiro Kato, Shohei Kojima, Kosuke Oda, Yusuke Matsumoto, **Functional analysis of promoter element 2 within the viral polymerase gene of an emerging paramyxovirus-Sosuga virus,** Microbiology Spectrum, Volume 13, Issue 5, 2025, https://doi.org/10.1128/spectrum.00534-25.

ABSTRACT:

Paramyxovirus genomes carry bipartite promoters at the 3′ ends of both their genome and antigenome, thereby initiating RNA synthesis, which requires the viral polymerase to recognize two elements: the primary promoter element 1 (PE1) and the secondary promoter element 2 (PE2). We have previously shown that the antigenomic PE2 (agPE2) in many viruses in the Rubulavirinae subfamily is located within the coding region of the viral RNA polymerase L gene. Sosuga virus (SOSV), belonging to the Rubulavirinae subfamily, is highly pathogenic to humans, thus necessitating high-level containment facilities for infectious virus research. The use of a minigenome system permits studies of viral RNA synthesis at lower biosafety levels. Because minigenomes of negative-strand RNA viruses generally comprise only the untranslated regions, agPE2 within the L coding region—such as those found in Rubulavirinae like SOSV—is typically omitted. However, generating an SOSV minigenome that retains agPE2 led to a pronounced increase in activity, enabling a detailed examination of the role of agPE2 in SOSV replication. In many Rubulavirinae, the agPE2 not only acts as a promoter but also encodes part of the L protein, resulting in a distinct motif at the C-terminus of the L protein. We have further shown that this motif is preserved even in Rubulavirinae that no longer

contain the agPE2 within the L gene. IMPORTANCE Paramyxoviruses are classified into three major subfamilies: Orthoparamyxovirinae, Avulavirinae, and Rubulavirinae. All paramyxovirus genomes and antigenomes possess bipartite promoters, comprising two elements: promoter element 1 (PE1) at the 3′ end and promoter element 2 (PE2) located internally. We previously revealed that, in many Rubulavirinae, the antigenomic PE2 lies within the coding region of the viral RNA polymerase L gene. In this study, we used Sosuga virus, a member of the Rubulavirinae subfamily, to elucidate the role of antigenomic PE2 in viral replication. Because the PE2 region encodes part of the L protein, its presence leads to a distinctive motif at the C-terminus of L protein. Notably, this motif is conserved in all Rubulavirinae, including those that do not harbor the antigenomic PE2 within their L gene, indicating its importance in viral propagation.

Paramyxoviruses are classified into three major subfamilies: Orthoparamyxovirinae, Avulavirinae, and Rubulavirinae. All paramyxovirus genomes and antigenomes possess bipartite promoters, comprising two elements: promoter element 1 (PE1) at the 3′ end and promoter element 2 (PE2) located internally. We previously revealed that, in many Rubulavirinae, the antigenomic PE2 lies within the coding region of the viral RNA polymerase L gene. In this study, we used Sosuga virus, a member of the Rubulavirinae subfamily, to elucidate the role of antigenomic PE2 in viral replication. Because the PE2 region encodes part of the L protein, its presence leads to a distinctive motif at the C-terminus of L protein. Notably, this motif is conserved in all Rubulavirinae, including those that do not harbor the antigenomic PE2 within their L gene, indicating its importance in viral propagation.

Keywords: negative-strand RNA virus; paramyxovirus; promoters; RNA polymerases; viral replication

46. Anna L. Bula, Raitis Bobrovs, Pavel Arsenyan, Teodors Pantelejevs, **Consequences of Peptide Macrocyclization Revealed by Virus-Inspired β-Hairpin Mimetics,** ACS Chemical Biology,2026, https://doi.org/10.1021/acschembio.5c00834.

ABSTRACT:

Mimicry of protein secondary structure elements, such as α-helices and β-sheets, using conformationally constrained peptide macrocycles, can be utilized to disrupt native protein–protein and protein-nucleic acid interactions. Although α-helical stapled peptides have been extensively studied as pharmacological probes, the application of β-sheet and β-hairpin mimetics remains comparatively limited. Less is known about the structural and biophysical consequences of β-hairpin macrocyclization in the context of target binding. In this work, we use a poxvirus immune antagonist protein 018 as a template for the structure-based design of β-hairpin mimetic macrocyclic peptides targeting the STAT1 transcription factor. We demonstrate that successive orthogonal cyclizations have additive effects on the thermodynamic and kinetic properties of peptide binding, most notably slowing the dissociation from the target. We elucidate the structural and dynamic consequences of interstrand and head-to-tail cross-linking and propose a kinetic model explaining the gains in target residence. Finally, we highlight the pharmacological potential of these peptides by competitive inhibition of STAT1 binding to its cognate interferon receptor docking site. These data suggest that β-hairpin macrocyclization may represent a general strategy to extend target engagement, with implications for peptidic probe design.

47. Bugude Laxmi, Palempalli Uma Maheswari Devi, Thanjavur Naveen, Viswanath Buddolla, **Virus-like particles: Innovative strategies for combatting emerging and re-emerging viral threats,** The Microbe, Volume 7, 2025, 100351, https://doi.org/10.1016/j.microb.2025.100351.

ABSTRACT:

Virus-like particles (VLPs) are non-infectious nanostructures that closely mimic the architecture and surface features of native viruses while lacking genetic material. This structural resemblance, combined with their inherent safety, positions VLPs as powerful tools in addressing the growing challenges posed by emerging and re-emerging viral threats. This review highlights their significant contributions in three key areas: vaccine development, viral diagnostics, and environmental surveillance. In the field of vaccinology, VLPs have shown remarkable potential to elicit robust immune responses, making them suitable for designing multivalent and broad-spectrum vaccines, particularly against zoonotic and vector-borne viruses. In diagnostics, their use in assay development has significantly improved the sensitivity and specificity of viral detection, offering promise for rapid and accurate identification of pathogens. Moreover, VLPs are being increasingly explored in environmental monitoring systems, where they contribute to the early detection of viral pathogens in water and other ecological matrices. These applications not only enhance our understanding of virus transmission dynamics but also support public health preparedness. VLPs also serve as valuable tools for studying viral immune evasion mechanisms and host-pathogen interactions, contributing to our understanding of viral evolution. Their adaptability and multifunctionality suggest that VLPs will play an increasingly important role in global virology research, disease prevention, and pandemic preparedness.

Keywords: Virus-like particles; Emerging viruses; Re-emerging viruses; Zoonotic viruses; Multivalent vaccines

48. Arwa Ahmed Zehairy, Sayed Sartaj Sohrab, Awatif Abid Al-Judaibi, Esam Ibraheem Azhar, **Rift Valley Fever Virus: An update on current status and future prospects,** Revista Argentina de Microbiología, 2025, https://doi.org/10.1016/j.ram.2025.09.002.

ABSTRACT:

Rift Valley fever is a mosquito-borne disease caused by the Rift Valley Fever Virus (RVFV) belonging to the genus Phlebovirus. This virus causes febrile or hemorrhagic illness in humans and ruminants, such as abortion, and death; especially in young sheep, cattle, and goats resulting in devastating epidemics in Africa and the Arabian Peninsula. The WHO has included this virus in Bluepoint's list of eight pathogens. This virus is a crucial health concern in the Kingdom of Saudi Arabia (KSA), as the Kingdom is regularly exposed to this virus from the original source of East African countries. A complete understanding of viral pathogenesis, epidemiology, antiviral therapeutics, and human vaccines is still lacking. This review aims to provide an update on the status, pathogenesis, prevalence, challenges, and future prospects of RVFV in the KSA. The information provided will aid in the design and development of disease management strategies and novel prophylactic and therapeutic measures to control the infection and disease progression of RVFV in both humans and animals.

Resumen

La fiebre del Valle del Rift es una enfermedad transmitida por mosquitos, y causada por el virus de la fiebre del Valle del Rift (RVFV, por sus siglas en inglés), perteneciente al género Phlebovirus. Este virus causa enfermedades febriles o hemorrágicas en humanos y rumiantes, como abortos, y puede

ocasionar la muerte. Especialmente en ovejas jóvenes, ganado vacuno y cabras, el RVFV ha provocado epidemias devastadoras en África y la Península Arábiga. La OMS ha incluido este virus en la lista de los ocho patógenos de Bluepoint. En el Reino de Arabia Saudita, el RVFV es un problema sanitario crucial debido a su regular ingreso desde su fuente original: los países del este de África. Todavía falta una comprensión completa de muchos aspectos de esta afección, incluidas la patogénesis viral, la epidemiología, las terapias antivirales y las vacunas humanas. Esta revisión busca ser una actualización sobre el estatus, la patogénesis y la prevalencia del RVFV en Arabia Saudita, y dar cuenta de los desafíos y las perspectivas futuras. La información proporcionada ayudará en el diseño y desarrollo de estrategias de manejo de enfermedades, y de nuevas medidas profilácticas y terapéuticas para controlar la infección y la progresión de la enfermedad causada por el RVFV tanto en humanos como en animales.

Keywords: Rift Valley fever; RVFV; Vectors; Humans; Livestock; KSA; Fiebre del Valle del Rift; RVFV; Vectores; Humanos; Ganado; Arabia Saudita

49. Xinping Fu, Tomasz Benedyk, Shaun Xiaoliu Zhang, **Strategically engineering an oncolytic herpes simplex virus to improve systemic delivery,** Molecular Therapy Oncology, Volume 34, Issue 1, 2026, 201132, https://doi.org/10.1016/j.omton.2026.201132.

ABSTRACT:

Oncolytic virotherapy (OV) has emerged as a promising cancer treatment strategy, utilizing viruses to selectively infect and destroy tumor cells while simultaneously stimulating anti-tumor immunity. OV has also been shown to modulate the tumor immune microenvironment, enhancing the efficacy of immunotherapy. Despite the recent regulatory approvals of oncolytic viruses such as T-VEC (JS1/34.5-/47-/GM-CSF), Oncorine (H101), and Teserpaturev (G47Δ), the clinical impact of OV remains limited by its reliance on intratumoral administration. Systemic delivery is essential for effectively treating metastatic and inaccessible tumors but is hindered by two major challenges: rapid clearance by the mononuclear phagocyte system (MPS) and neutralization by antiviral antibodies. To overcome these barriers, we developed FusOn-SD, an enhanced version of FusOn-H2 engineered for systemic delivery. Our strategy integrates both genetic and adaptive modifications: (1) incorporating the extracellular domain (ECD) of CD47 to evade MPS-mediated clearance and (2) serially passaging the virus in immune sera to enhance resistance to neutralizing antibodies. Preclinical studies demonstrate that FusOn-SD efficiently reaches tumor sites following systemic administration, exhibiting enhanced immune evasion and oncolytic potency. These findings position FusOn-SD as a promising candidate for advancing OV beyond localized injections, with the potential to transform virotherapy into a viable treatment for metastatic cancer.

Keywords: oncolytic virus; herpes simplex virus; virotherapy; systemic delivery; CD47

50. Hudson A Smith, Shatabdi Chakraborty, Paul R Gooley, Gregory W Moseley, Stephen M Rawlinson, **New directions in the multifunctionality of RNA viruses: insights from the rabies virus P-protein,** Current Opinion in Virology, Volume 73, 2025, 101496, https://doi.org/10.1016/j.coviro.2025.101496.

ABSTRACT:

RNA viruses have compact genomes that typically encode only a few proteins, but these viruses orchestrate complex replication cycles while concurrently exercising control over multiple aspects of the biology of the infected host cell, including the evasion of antiviral responses. Central to this functional diversity is the evolution of multifunctional proteins, which integrate diverse roles in replication and host subversion through structural, regulatory, and spatial versatility. The rabies virus P-protein exemplifies these principles. In addition to serving as an essential cofactor and chaperone in viral transcription and replication, the P-protein also antagonizes type I interferon responses, modulates intranuclear processes, and targets multiple host membrane-less organelles via liquid–liquid phase separation. These diverse functions are mediated by a combination of mechanisms, including expression as multiple isoforms, modular domain architecture, intrinsic disorder, dynamic subcellular trafficking, post-translational modifications, conformational plasticity, and RNA binding. In this review, we discuss established and recently emerging mechanisms underlying P-protein multifunctionality, which is likely to provide a model for understanding the multifunctionality of other viral, and likely cellular proteins. We also highlight how similar strategies are employed across RNA viruses to overcome genomic constraints, and discuss how these mechanisms may represent promising targets for future antiviral interventions.