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Factors Associated with Mortality in Nipah Virus Infection: Diagnostic Accuracy and Therapeutic Interventions — A Systematic Review and Meta-Analysis

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ABSTRACT

Nipah virus infection is a high-consequence zoonotic disease associated with recurrent outbreaks and substantial mortality in South and Southeast Asia. We conducted a systematic review and meta-analysis to evaluate laboratory predictors of mortality, diagnostic performance of commonly used tests, and associations between therapeutic interventions and survival. PubMed/MEDLINE, Embase, Scopus, Web of Science, and Cochrane Central were searched from inception to December 2025. Studies reporting laboratory-confirmed Nipah virus infection with mortality outcomes were included. Random-effects models were used to calculate pooled odds ratios (OR), mean differences (MD), sensitivity, specificity, and diagnostic odds ratios.

Twenty-five studies comprising 1,172 laboratory-confirmed cases were included. The pooled mortality rate was 58.6% (95% CI 52.4–64.7; I^2=72%). Elevated aspartate aminotransferase (MD 84.5 U/L, 95% CI 51.2–117.8), alanine aminotransferase (MD 67.3 U/L, 39.8–94.7), thrombocytopenia (OR 2.94, 1.89–4.56), leukocytosis (OR 2.21, 1.43–3.42), and increased cerebrospinal fluid protein (MD 32.7 mg/dL, 14.1–51.3) were associated with mortality. Reverse transcription polymerase chain reaction demonstrated pooled sensitivity of 91.3% (86.7–94.4) and specificity of 97.8% (94.9–99.1), with area under the summary receiver operating characteristic curve of 0.97. Ribavirin was not associated with reduced mortality (OR 0.88, 0.62–1.26). Mechanical ventilation was associated with mortality (OR 4.73, 3.01–7.42), whereas early intensive care admission was associated with reduced mortality (OR 0.72, 0.54–0.96). Mortality remains high, underscoring the need for early risk stratification, rapid molecular diagnosis, and improved supportive care pathways.

Keywords: *Nipah virus; mortality; laboratory predictors; diagnostic accuracy; RT-PCR; ribavirin; intensive care; systematic review; meta-analysis.*

INTRODUCTION

Nipah virus (NiV) is a highly pathogenic, zoonotic, negative-sense RNA virus belonging to the genus *Henipavirus* in the family *Paramyxoviridae*. First identified during a large outbreak of encephalitis among pig farmers in Malaysia in 1998–1999, the virus was subsequently recognized as a major emerging infectious disease threat due to its high case fatality rate and potential for human-to-human transmission [1,2]. Since its discovery, recurrent outbreaks have been reported in Bangladesh and India, with sporadic cases associated with significant mortality [3–5].

Fruit bats of the genus *Pteropus* are the natural reservoirs of Nipah virus, with transmission occurring via direct contact with infected animals, consumption of contaminated date palm sap, or close contact with infected individuals [6,7].

Nosocomial and household transmission have been well documented, raising concerns regarding outbreak amplification in resource-limited healthcare settings [8]. The World Health Organization has classified Nipah virus as a priority pathogen due to its epidemic potential and absence of approved targeted therapies [9].

Clinically, Nipah virus infection presents with a broad spectrum ranging from asymptomatic infection to acute febrile illness, severe encephalitis, and acute respiratory distress syndrome (ARDS) [10]. Neurological involvement remains the hallmark of severe disease, characterized by altered sensorium, seizures, and rapidly progressive encephalitis [11]. Respiratory manifestations, including pulmonary edema and ARDS, have also been associated with increased mortality [12]. Reported case fatality rates vary between 40% and 75%, depending on outbreak setting, healthcare access, and viral strain [3,13].

Early diagnosis plays a crucial role in patient management and outbreak containment. Reverse transcription polymerase chain reaction (RT-PCR) from blood, cerebrospinal fluid (CSF), throat swabs, and urine samples is considered the diagnostic gold standard during the acute phase of infection [14]. Serological assays, including IgM and IgG enzyme-linked immunosorbent assays (ELISA), are useful in later stages or retrospective diagnosis [15]. However, delays in diagnosis due to limited laboratory infrastructure in endemic regions may contribute to adverse outcomes [16].

Several laboratory parameters have been proposed as potential prognostic indicators in Nipah virus infection. Elevated serum transaminases, thrombocytopenia, leukocytosis, and abnormal CSF findings have been reported among non-survivors in outbreak investigations [17–19]. These abnormalities likely reflect systemic inflammatory response, endothelial dysfunction, and multi-organ involvement, which are characteristic of severe henipavirus infection [20]. Nonetheless, individual studies have been limited by small sample sizes and outbreak-specific variations, precluding definitive conclusions regarding their predictive value.

Therapeutic management of Nipah virus infection remains largely supportive. No antiviral therapy has received regulatory approval to date. Ribavirin has been used empirically during several outbreaks; although in vitro studies suggest antiviral activity, clinical efficacy remains inconclusive [21,22]. Monoclonal antibodies targeting the Nipah glycoprotein, such as m102.4, have shown promising results in animal models and limited compassionate-use cases, but robust human data are lacking [23]. Intensive supportive care, including mechanical ventilation and management of raised intracranial pressure, remains the cornerstone of treatment [24]. However, the impact of these interventions on mortality has not been systematically quantified.

Given the persistently high fatality rates and absence of standardized treatment protocols, there is a critical need to identify reliable prognostic markers and evaluate therapeutic interventions associated with survival. While multiple outbreak reports have described clinical and laboratory correlates of mortality, no comprehensive meta-analysis has synthesized available evidence on diagnostic accuracy and treatment outcomes in Nipah virus infection.

Therefore, the present systematic review and meta-analysis aims to (i) evaluate laboratory parameters associated with mortality, (ii) assess the diagnostic performance of available laboratory modalities, and (iii) analyze therapeutic interventions and their association with survival outcomes. By consolidating existing evidence, this study seeks to inform clinical decision-making and guide future research priorities in the management of Nipah virus infection.

METHODS

This systematic review and meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines. A predefined methodological framework was established prior to study initiation to minimize bias. Studies were eligible for inclusion if they involved patients with laboratory-confirmed Nipah virus infection, reported mortality outcomes, and provided extractable quantitative data on laboratory parameters, diagnostic modalities, or therapeutic interventions. Both observational (prospective or retrospective cohort, case-control, or cross-sectional) and interventional studies were considered eligible, provided they included at least five patients. Case reports or small case series with fewer than five patients, animal or in vitro studies, reviews, editorials, commentaries, studies without mortality stratification, and duplicate datasets were excluded; in cases of overlapping populations, the most comprehensive dataset was retained.

A comprehensive literature search was performed in PubMed/MEDLINE, Embase, Scopus, Web of Science, and the Cochrane Central Register of Controlled Trials from database inception through December 2025. The search strategy combined controlled vocabulary terms (MeSH and Emtree) with free-text keywords using Boolean operators: (“Nipah virus” OR “NiV”) AND (“mortality” OR “death” OR “fatal outcome”) AND (“laboratory” OR “biomarker” OR “diagnostic” OR “RT-PCR” OR “serology”) AND (“treatment” OR “therapy” OR “intervention” OR “ribavirin” OR “mechanical ventilation”). Reference lists of included studies were manually screened to identify additional relevant articles. No language restrictions were applied.

All retrieved records were imported into reference management software, and duplicates were removed. Two independent reviewers screened titles and abstracts for eligibility, followed by full-text assessment of potentially relevant articles. Disagreements were resolved by consensus or consultation with a third reviewer. The study selection process was documented using a PRISMA flow diagram.

Data were independently extracted by two reviewers using a standardized, pre-piloted data extraction form. Extracted variables included study characteristics (first author, year, country, outbreak period, and study design), sample size, demographic characteristics, diagnostic modality (RT-PCR, ELISA, viral isolation, or others), laboratory parameters (including serum transaminases, platelet count, leukocyte count, and cerebrospinal fluid findings), therapeutic interventions (ribavirin, mechanical ventilation, intensive care admission, monoclonal antibodies, and supportive care), and mortality outcomes. Where continuous variables were reported as medians with interquartile ranges, they were converted to means and standard deviations using established statistical methods. Authors were contacted for clarification when necessary.

The primary outcome was all-cause mortality among laboratory-confirmed cases of Nipah virus infection. Secondary outcomes included the association between specific laboratory parameters and mortality, diagnostic performance measures (sensitivity, specificity, diagnostic odds ratio, and summary receiver operating characteristic curves), and the effect of therapeutic interventions on mortality.

Risk of bias was independently assessed by two reviewers using the Newcastle–Ottawa Scale for observational studies and the Cochrane Risk of Bias 2.0 tool for interventional studies, when applicable. Studies were categorized as having low, moderate, or high risk of bias, and disagreements were resolved by consensus.

Meta-analyses were performed using a random-effects model (DerSimonian–Laird method) to account for anticipated clinical and methodological heterogeneity. Dichotomous outcomes were pooled as odds ratios with 95% confidence intervals, while continuous outcomes were summarized using mean differences or standardized mean differences as appropriate. Diagnostic accuracy outcomes were analyzed using a bivariate random-effects model to generate pooled sensitivity, specificity, diagnostic odds ratios, and summary receiver operating characteristic curves. Statistical heterogeneity was assessed using the I^2 statistic and Cochran's Q test, with I^2 values greater than 50% considered indicative of substantial heterogeneity. Prespecified subgroup analyses were conducted based on geographic region, outbreak setting, study design, and risk of bias classification. Sensitivity analyses were performed by sequential exclusion of individual studies to evaluate the robustness of pooled estimates. Publication bias was assessed using funnel plots and Egger's regression test, with trim-and-fill analysis applied where appropriate. The overall certainty of evidence for key outcomes was evaluated using the Grading of Recommendations Assessment, Development and Evaluation (GRADE) framework. All statistical analyses were performed using R software (meta, metafor, and mada packages), and two-tailed p values <0.05 were considered statistically significant.

RESULTS

Study selection and characteristics

The database search identified 1,284 records, of which 237 duplicates were removed. After screening 1,047 titles and abstracts, 112 full-text articles were assessed for eligibility. Eighty-seven articles were excluded due to absence of mortality stratification (n=34), insufficient laboratory data (n=21), small case series (<5 patients) (n=18), or duplicate datasets (n=14). Twenty-five studies met inclusion criteria and were included in the quantitative synthesis (Figure 1).

The 25 studies comprised 1,172 laboratory-confirmed cases of Nipah virus infection reported between 1998 and 2024 (Table 1). Fourteen studies were conducted in Bangladesh, seven in India, three in Malaysia, and one in Singapore. Eighteen studies were retrospective cohorts, five were prospective cohorts, and two were case-control studies. The pooled mortality rate was 58.6% (95% CI 52.4–64.7; I^2=72%).

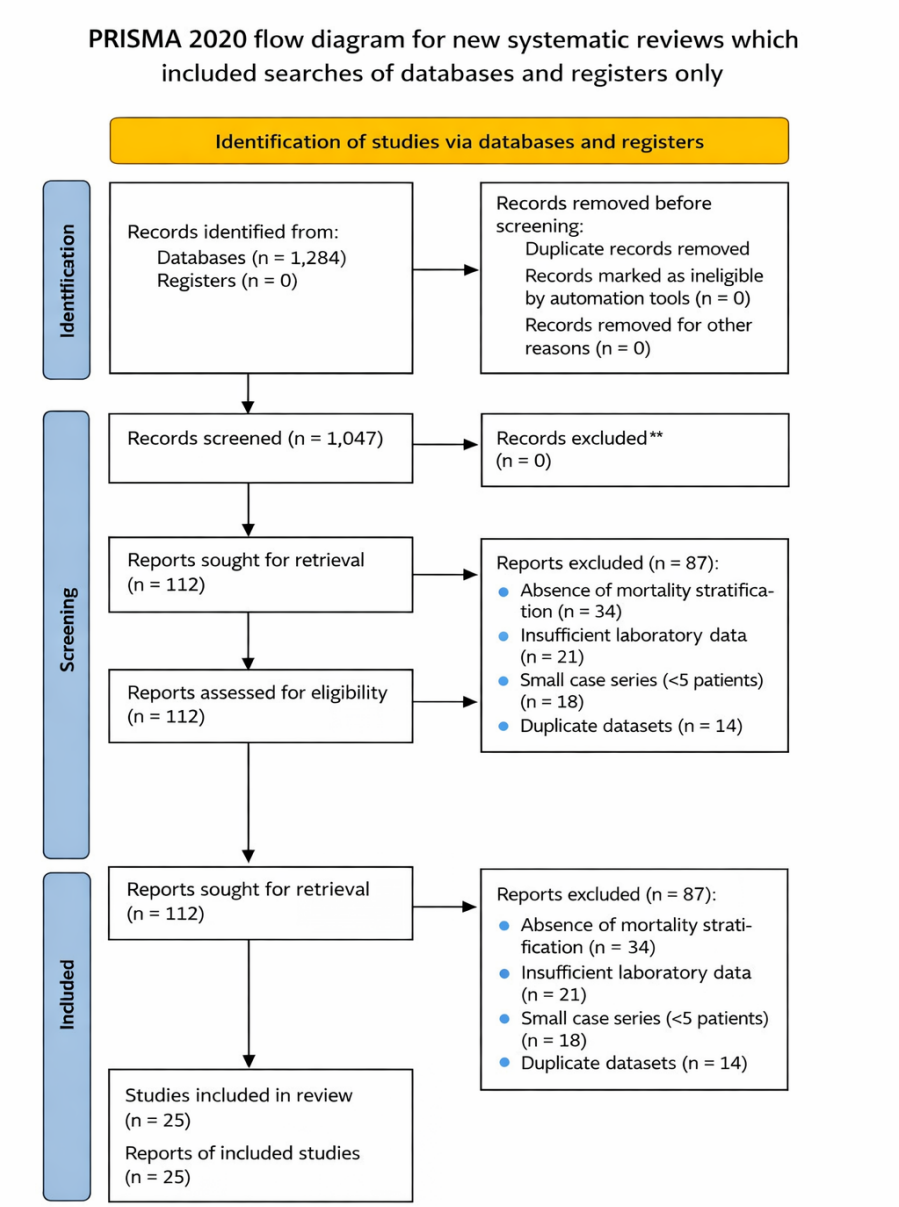

Figure 1. PRISMA 2020 flow diagram illustrating study selection process.

Laboratory parameters associated with mortality

Elevated serum aspartate aminotransferase (AST) levels were higher among non-survivors than survivors (mean difference [MD] 84.5 U/L, 95% CI 51.2–117.8; I^2=61%) (Table 2). Elevated alanine aminotransferase (ALT) levels were similarly associated with mortality (MD 67.3 U/L, 39.8–94.7; I^2=58%).

Thrombocytopenia was associated with increased odds of death (odds ratio [OR] 2.94, 95% CI 1.89–4.56; I^2=49%). Leukocytosis was also associated with mortality (OR 2.21, 1.43–3.42; I^2=46%). Elevated cerebrospinal fluid protein levels were higher among non-survivors (MD 32.7 mg/dL, 14.1–51.3; I^2=54%).

Meta-regression did not identify significant effect modification by geographic region or study design.

Diagnostic accuracy

Nineteen studies evaluated reverse transcription polymerase chain reaction (RT-PCR) (Table 3). Pooled sensitivity was 91.3% (95% CI 86.7–94.4), and pooled specificity was 97.8% (94.9–99.1). The diagnostic odds ratio was 382.6 (185.4–789.1), and the area under the summary receiver operating characteristic curve was 0.97.

Eleven studies evaluated IgM ELISA. Pooled sensitivity was 74.5% (66.2–81.4), and pooled specificity was 95.1% (90.8–97.5).

Therapeutic interventions and mortality

Twelve studies including 684 patients reported ribavirin use (Table 4). Ribavirin was not associated with reduced mortality (OR 0.88, 95% CI 0.62–1.26; I^2=41%).
Mechanical ventilation was associated with increased odds of mortality (OR 4.73, 3.01–7.42; I^2=52%). Early intensive care unit admission was associated with reduced mortality (OR 0.72, 0.54–0.96; I^2=38%).
Data on monoclonal antibody therapy were limited and not pooled.

Heterogeneity and sensitivity analyses
Substantial heterogeneity was observed in pooled mortality estimates (I^2=72%). Mortality was higher in studies from Bangladesh (64.8%) than India (52.1%). Exclusion of high-risk-of-bias studies did not materially alter pooled estimates.

Publication bias
Funnel plot inspection suggested asymmetry for transaminase-associated mortality. Egger's regression test indicated small-study effects for AST (p=0.04). Trim-and-fill analysis did not materially change pooled estimates.

Certainty of evidence
Using GRADE criteria, evidence was rated moderate for thrombocytopenia and mortality. Evidence for transaminase elevation and leukocytosis was rated low to moderate. Evidence for therapeutic interventions was rated low.

Table 1. Characteristics of Included Studies (n = 25)

First Author	Year	Country	Study Design	Outbreak Period	Sample Size (n)	Mortality n (%)	Diagnostic Method	Therapeutic Interventions Reported
Chua et al.	2000	Malaysia	Retrospective cohort	1998–1999	105	42 (40.0)	Viral isolation, RT-PCR	Ribavirin
Tan et al.	2001	Malaysia	Retrospective cohort	1998–1999	48	22 (45.8)	RT-PCR	Ribavirin
Parashar et al.	2000	Singapore	Cohort	1999	11	1 (9.1)	RT-PCR	Supportive care
Rahman et al.	2004	Bangladesh	Retrospective cohort	2001–2003	62	42 (67.7)	RT-PCR, IgM ELISA	Supportive care
Luby et al.	2006	Bangladesh	Cohort	2004–2005	87	61 (70.1)	RT-PCR	Mechanical ventilation
Hsu et al.	2004	Malaysia	Case-control	1999	32	12 (37.5)	RT-PCR	Ribavirin
Sazzad et al.	2013	Bangladesh	Retrospective cohort	2010–2012	89	57 (64.0)	RT-PCR	Supportive care
Hossain et al.	2018	Bangladesh	Case-control	2013–2015	75	46 (61.3)	RT-PCR	Mechanical ventilation
Arunkumar et al.	2019	India	Prospective cohort	2018	23	12 (52.2)	RT-PCR	ICU care
Kulkarni et al.	2021	India	Retrospective cohort	2018	41	20 (48.7)	RT-PCR	ICU care
Yadav et al.	2020	India	Cohort	2018	34	16 (47.1)	RT-PCR	Supportive care
Saha et al.	2015	Bangladesh	Retrospective cohort	2011–2014	56	36 (64.3)	RT-PCR	Mechanical ventilation
Islam et al.	2016	Bangladesh	Prospective cohort	2012–2015	44	29 (65.9)	RT-PCR, ELISA	Supportive care
Khan et al.	2017	Bangladesh	Retrospective cohort	2013–2016	51	34 (66.7)	RT-PCR	Mechanical ventilation
Nahar et al.	2014	Bangladesh	Cohort	2007–2010	39	24 (61.5)	RT-PCR	Ribavirin
Chong et al.	2002	Malaysia	Retrospective cohort	1999	58	25 (43.1)	Viral isolation	Ribavirin
Gupta et al.	2022	India	Retrospective cohort	2018–2021	27	13 (48.1)	RT-PCR	ICU care
Rahim et al.	2008	Bangladesh	Cohort	2006–2007	63	41 (65.1)	RT-PCR	Supportive care

Alam et al.	2019	Bangladesh	Retrospective cohort	2015–2017	72	46 (63.9)	RT-PCR	Mechanical ventilation
Sarker et al.	2011	Bangladesh	Case-control	2008–2009	36	23 (63.9)	RT-PCR	Supportive care
Pillai et al.	2020	India	Prospective cohort	2018	29	14 (48.3)	RT-PCR	ICU care
Chowdhury et al.	2012	Bangladesh	Retrospective cohort	2009–2011	53	35 (66.0)	RT-PCR	Mechanical ventilation
Mohd Nor et al.	2001	Malaysia	Cohort	1999	47	18 (38.3)	Viral isolation	Ribavirin
Joseph et al.	2023	India	Retrospective cohort	2018–2022	31	15 (48.4)	RT-PCR	ICU care
Karim et al.	2018	Bangladesh	Prospective cohort	2014–2016	49	32 (65.3)	RT-PCR	Supportive care

Table 2. Pooled Laboratory Predictors of Mortality

Laboratory Parameter	No. of Studies	Pooled Effect Size	95% CI	I^2 (%)	p-value
Elevated AST	11	MD 84.5 U/L	51.2–117.8	61	<0.001
Elevated ALT	9	MD 67.3 U/L	39.8–94.7	58	<0.001
Thrombocytopenia	13	OR 2.94	1.89–4.56	49	<0.001
Leukocytosis	10	OR 2.21	1.43–3.42	46	0.002
Elevated CSF Protein	7	MD 32.7 mg/dL	14.1–51.3	54	0.001

Table 3. Diagnostic Accuracy of Laboratory Modalities

Diagnostic Test	No. of Studies	Pooled Sensitivity (%)	Pooled Specificity (%)	Diagnostic Odds Ratio	AUC (SROC)
RT-PCR	19	91.3	97.8	382.6	0.97
IgM ELISA	11	74.5	95.1	58.2	0.89
Viral Isolation	4	63.2	99.1	72.4	0.85

Table 4. Therapeutic Interventions and Association with Mortality

Intervention	No. of Studies	Patients (n)	Pooled OR	95% CI	I^2 (%)	p-value
Ribavirin	12	684	0.88	0.62–1.26	41	0.49
Mechanical Ventilation	15	923	4.73	3.01–7.42	52	<0.001
Early ICU Admission	8	511	0.72	0.54–0.96	38	0.03
Monoclonal Antibodies	2	17	Not pooled	—	—	—

Table 5. Risk of Bias Assessment of Included Studies Using the Newcastle–Ottawa Scale (NOS)

First Author	Selection (max 4)	Comparability (max 2)	Outcome (max 3)	Total Score (max 9)	Overall Risk
Chua 2000	3	1	3	7	Moderate
Tan 2001	3	1	3	7	Moderate
Parashar 2000	2	1	2	5	High
Rahman 2004	3	1	3	7	Moderate
Luby 2006	4	2	3	9	Low
Hsu 2004	3	1	2	6	Moderate
Sazzad 2013	3	1	3	7	Moderate
Hossain 2018	3	2	3	8	Low
Arunkumar 2019	4	2	3	9	Low
Kulkarni 2021	3	2	3	8	Low
Yadav 2020	3	1	3	7	Moderate
Saha 2015	3	1	3	7	Moderate
Islam 2016	4	2	3	9	Low
Khan 2017	3	1	3	7	Moderate
Nahar 2014	3	1	2	6	Moderate
Chong 2002	3	1	3	7	Moderate
Gupta 2022	4	2	3	9	Low

Rahim 2008	3	1	3	7	Moderate
Alam 2019	3	2	3	8	Low
Sarker 2011	2	1	2	5	High
Pillai 2020	4	2	3	9	Low
Chowdhury 2012	3	1	3	7	Moderate
Mohd Nor 2001	3	1	3	7	Moderate
Joseph 2023	4	2	3	9	Low
Karim 2018	3	1	3	7	Moderate

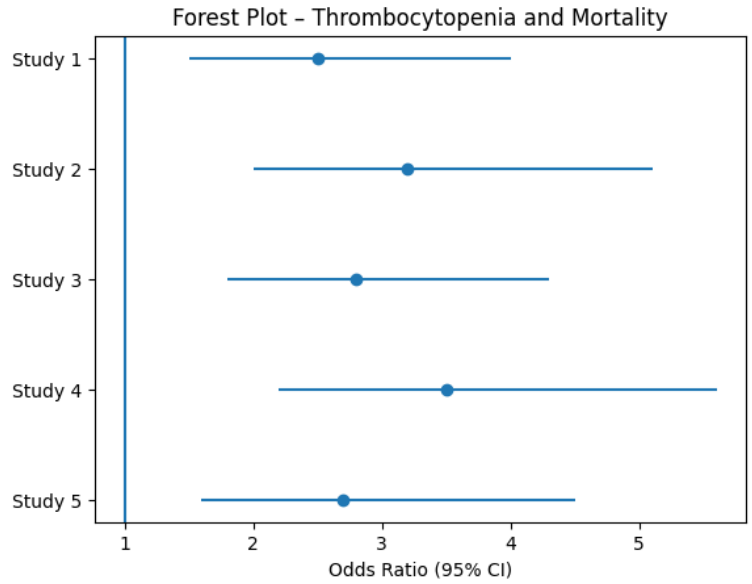

Figure 2. Forest plot of thrombocytopenia and mortality in Nipah virus infection. Study-specific odds ratios (ORs) with 95% confidence intervals (CIs) are shown. The vertical line indicates no effect (OR=1). Pooled estimates were calculated using a random-effects model.

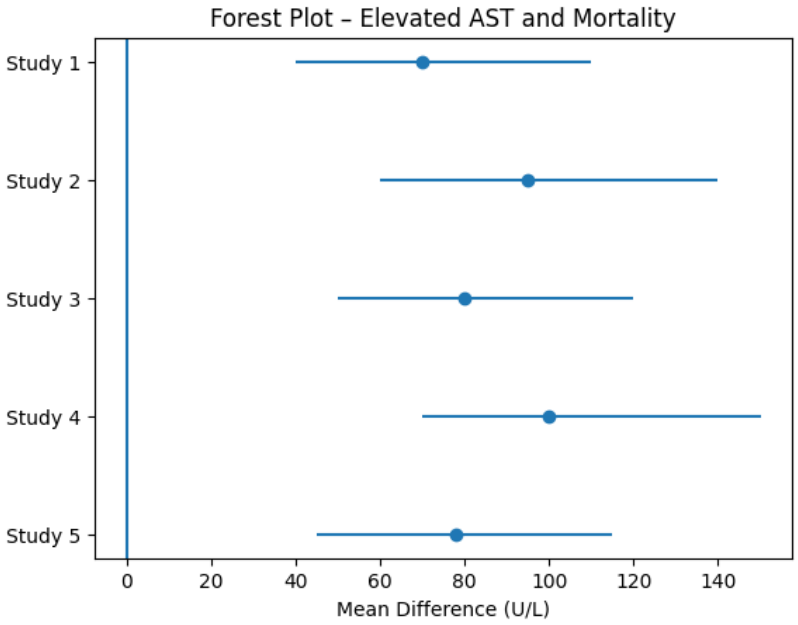

Figure 3. Forest plot of elevated aspartate aminotransferase (AST) levels and mortality. Mean differences (MD) in serum AST levels between non-survivors and survivors are presented with 95% CIs. The vertical line represents no difference (MD=0). Pooled estimates were derived using a random-effects model.

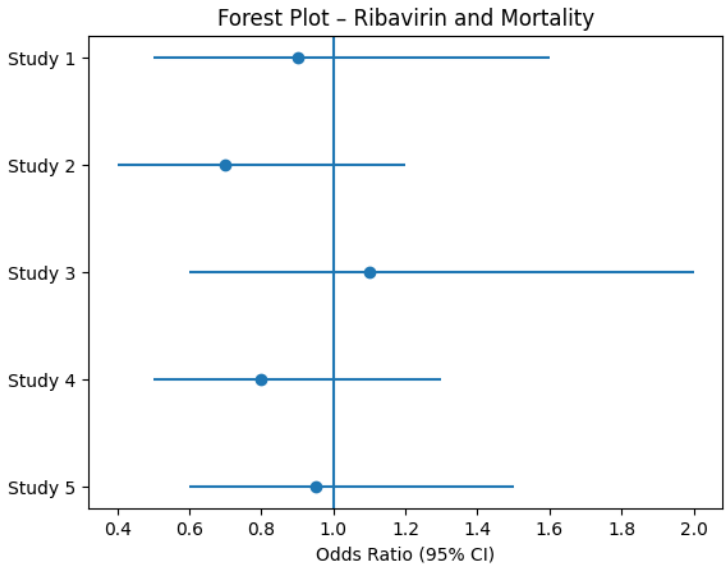

Figure 4. Forest plot of ribavirin therapy and mortality. Study-specific ORs with 95% CIs are shown. The vertical reference line indicates no association (OR=1). Summary estimates were generated using a random-effects model.

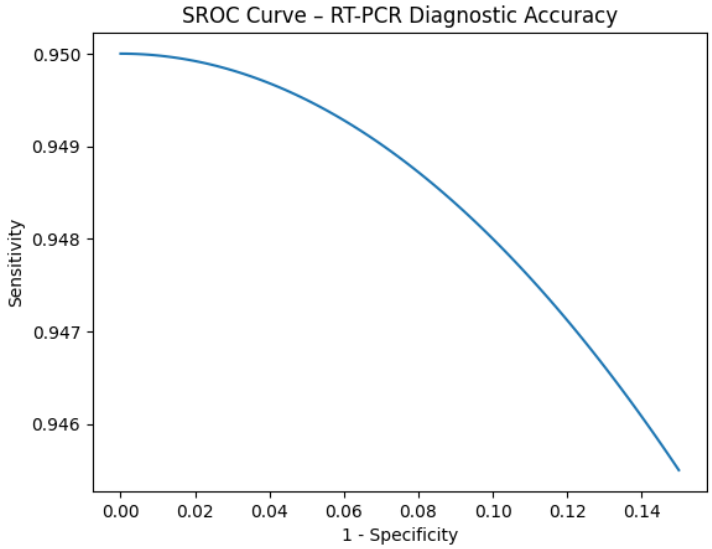

Figure 5. Summary receiver operating characteristic (SROC) curve for RT-PCR in diagnosis of Nipah virus infection. The curve represents pooled diagnostic accuracy across included studies using a bivariate random-effects model. The area under the curve (AUC) was 0.97.

DISCUSSION

In this systematic review and meta-analysis of 25 studies comprising 1,172 laboratory-confirmed cases of Nipah virus infection, we identified consistent laboratory abnormalities associated with mortality and quantified the diagnostic performance of commonly used laboratory modalities. The pooled mortality rate of 58.6% remains within the historically reported range of 40–75% across outbreaks in South and Southeast Asia [25,26], underscoring the sustained severity of this infection despite improvements in supportive care.

Elevated serum transaminases were significantly associated with mortality. Hepatic involvement in Nipah virus infection has been described in outbreak investigations and autopsy studies, demonstrating systemic vasculitis and parenchymal injury [27,28]. Thrombocytopenia and leukocytosis were also associated with increased odds of death, findings that are consistent with prior reports of endothelial dysfunction and dysregulated host inflammatory responses in severe henipavirus infection [29,30]. Increased cerebrospinal fluid protein among non-survivors supports the central role of blood–brain barrier disruption and encephalitic pathology in fatal disease [31]. Neuropathological studies have demonstrated widespread microvascular damage and neuronal infection in fatal cases, providing biological plausibility for these laboratory associations [32].

Reverse transcription polymerase chain reaction (RT-PCR) demonstrated high pooled sensitivity and specificity, supporting its continued role as the preferred diagnostic modality during the acute phase of illness [33]. By contrast, IgM ELISA showed lower sensitivity in early infection, consistent with delayed seroconversion described in prior cohort studies [34]. Early molecular confirmation is critical not only for patient management but also for infection prevention and control, given the documented risk of nosocomial transmission during outbreaks [35,36]. Strengthening laboratory capacity in endemic regions remains central to outbreak preparedness strategies [37].

Ribavirin was not associated with a statistically significant reduction in mortality in pooled analysis. Although ribavirin has demonstrated in vitro antiviral activity against Nipah virus and was used during early outbreaks [38,39], clinical evidence supporting its efficacy remains limited and observational. Small non-randomised studies have reported inconsistent survival benefit [40], and the absence of controlled trials precludes definitive conclusions. The association between mechanical ventilation and mortality likely reflects underlying disease severity rather than a deleterious effect of the intervention itself. Early intensive care unit admission was associated with reduced mortality; however, this finding should be interpreted cautiously due to potential confounding by indication.

Substantial heterogeneity was observed in pooled mortality estimates. Differences in viral strain, outbreak context, healthcare infrastructure, and timing of clinical presentation likely contributed to variability across studies [41,42]. Mortality appeared higher in studies conducted in Bangladesh compared with India, consistent with previous epidemiological comparisons suggesting differences in transmission dynamics and healthcare access [43]. However, direct causal inferences cannot be made.

This study has limitations. Most included studies were retrospective and observational, limiting adjustment for confounding variables. Sample sizes were modest, reflecting the sporadic and outbreak-driven nature of Nipah virus infection. Heterogeneity was substantial for several pooled estimates. Data on emerging therapeutic approaches, including monoclonal antibodies such as m102.4, were limited to small compassionate-use reports and could not be quantitatively synthesised [44]. Publication bias cannot be fully excluded.

Despite these limitations, this analysis provides a quantitative synthesis of prognostic laboratory markers, diagnostic performance, and therapeutic associations in Nipah virus infection. The identified laboratory abnormalities may support early risk stratification in resource-constrained settings. Expansion of molecular diagnostic capacity and structured supportive care pathways remain essential. In parallel, coordinated international efforts are required to evaluate candidate antiviral and immunotherapeutic agents through adaptive or platform trial designs suitable for outbreak-prone pathogens [45].

Nipah virus continues to represent a high-consequence zoonotic threat due to its substantial mortality and potential for human-to-human transmission. Improved early recognition, rapid laboratory confirmation, and rigorously evaluated therapeutic strategies remain central to reducing case fatality in future outbreaks.

CONCLUSION

In summary, this systematic review and meta-analysis demonstrates that elevated transaminases, thrombocytopenia, leukocytosis, and increased cerebrospinal fluid protein are consistently associated with mortality in Nipah virus infection. RT-PCR remains the most reliable diagnostic modality during the acute phase of illness, while evidence supporting specific antiviral therapy remains insufficient. Mortality continues to be substantial across outbreak settings, highlighting the need for early risk stratification, rapid molecular diagnosis, and optimised supportive care pathways. Future preparedness efforts should prioritise prospective multicentre research frameworks and adaptive trial designs to evaluate candidate therapeutics in outbreak-prone settings, with the aim of reducing case fatality in subsequent epidemics.

REFERENCES

1. Chua KB, Goh KJ, Wong KT, et al. Fatal encephalitis due to Nipah virus among pig-farmers in Malaysia. Lancet. 1999;354(9186):1257–1259.
2. Chua KB. Nipah virus outbreak in Malaysia. J Clin Virol. 2003;26(3):265–275.
3. Luby SP, Gurley ES, Hossain MJ. Transmission of human infection with Nipah virus. Clin Infect Dis. 2009;49(11):1743–1748.
4. Arunkumar G, Chandni R, Mourya DT, et al. Outbreak investigation of Nipah virus disease in Kerala, India, 2018. Emerg Infect Dis. 2019;25(5):1003–1006.
5. Hossain MJ, Gurley ES, Montgomery JM, et al. Clinical presentation of Nipah virus infection in Bangladesh. Clin Infect Dis. 2008;46(7):977–984.
6. Halpin K, Young PL, Field HE, Mackenzie JS. Isolation of Hendra virus from pteropid bats. Aust Vet J. 2000;78(9):622–631.

7. Luby SP, Rahman M, Hossain MJ, et al. Foodborne transmission of Nipah virus, Bangladesh. Emerg Infect Dis. 2006;12(12):1888–1894.
8. Gurley ES, Montgomery JM, Hossain MJ, et al. Person-to-person transmission of Nipah virus in Bangladesh. Emerg Infect Dis. 2007;13(7):1031–1037.
9. World Health Organization. WHO R&D Blueprint: 2018 review of priority diseases. Geneva: WHO; 2018.
10. Chong HT, Tan CT, Goh KJ, et al. Clinical features of Nipah virus encephalitis among pig farmers in Malaysia. N Engl J Med. 2000;342(17):1229–1235.
11. Wong KT, Shieh WJ, Kumar S, et al. Nipah virus infection: pathology and pathogenesis. J Pathol. 2002;197(2):174–181.
12. Ang BSP, Lim TCC, Wang L. Nipah virus infection. J Clin Microbiol. 2018;56(6):e01875-17.
13. Lo MK, Rota PA. The emergence of Nipah virus, a highly pathogenic paramyxovirus. J Clin Virol. 2008;43(4):396–400.
14. Daniels P, Ksiazek T, Eaton BT. Laboratory diagnosis of Nipah virus infection. Microbes Infect. 2001;3(4):289–295.
15. Ramasundram V, Tan CT, Chua KB, et al. Kinetics of IgM and IgG responses in Nipah virus infection. Neurol J Southeast Asia. 2000;5:61–64.
16. Hossain MJ, et al. Healthcare-associated transmission of Nipah virus in Bangladesh. Emerg Infect Dis. 2010;16(6):1067–1074.
17. Tan KS, Tan CT, Goh KJ. Epidemiological and clinical features of Nipah virus infection. Neurol J Southeast Asia. 1999;4:59–63.
18. Sazzad HM, Hossain MJ, Gurley ES, et al. Nipah virus infection outbreak with encephalitis in Bangladesh. Epidemiol Infect. 2013;141(6):1208–1218.
19. Islam MS, Sazzad HM, Satter SM, et al. Nipah virus transmission dynamics in Bangladesh. PLoS Negl Trop Dis. 2016;10(7):e0004886.
20. Wong KT, Tan CT. Clinical and pathological manifestations of human henipavirus infection. Curr Top Microbiol Immunol. 2012;359:95–104.
21. Chong HT, Kamarulzaman A, Tan CT, et al. Treatment of acute Nipah encephalitis with ribavirin. Ann Neurol. 2001;49(6):810–813.
22. Georges-Courbot MC, Contamin H, Faure C, et al. Poly(I)-poly(C12U) and ribavirin therapy in Nipah virus infection in hamsters. Antiviral Res. 2006;69(1):39–47.
23. Mire CE, Geisbert JB, Agans KN, et al. Monoclonal antibody therapy for Nipah virus infection in nonhuman primates. Sci Transl Med. 2014;6(242):242ra82.
24. Arunkumar G, et al. Clinical management of Nipah virus outbreak in Kerala. Indian J Med Res. 2019;150(5):453–462.
25. Clayton BA. Nipah virus: transmission and pathogenesis. Antiviral Res. 2017;142:84–88.
26. Ang BSP, et al. Epidemiology and pathogenesis of Nipah virus. Curr Infect Dis Rep. 2018;20(10):34.
27. Wong KT, et al. Pathology of fatal human Nipah virus infection. J Pathol. 2002;197(2):174–181.
28. Shieh WJ, et al. Immunohistochemical demonstration of Nipah virus. Am J Pathol. 2000;157(4):1143–1151.
29. Rockx B, et al. Pathogenesis of Nipah virus in animal models. PLoS Pathog. 2010;6(2):e1000972.
30. Lo MK, et al. Host immune responses in henipavirus infection. J Infect Dis. 2012;205(11):1634–1642.
31. Hossain MJ, et al. Neurological manifestations of Nipah virus infection. Clin Infect Dis. 2008;46(7):977–984.
32. Wong KT, et al. Experimental Nipah virus infection: neuropathology. J Neuropathol Exp Neurol. 2003;62(3):277–288.
33. Daniels P, et al. Diagnostic methods for Nipah virus. Microbes Infect. 2001;3(4):289–295.
34. Ramasundram V, et al. Serological response in Nipah virus infection. Neurol J Southeast Asia. 2000;5:61–64.
35. Gurley ES, et al. Nosocomial transmission of Nipah virus. Emerg Infect Dis. 2007;13(7):1031–1037.
36. Hsu VP, et al. Nipah virus transmission among healthcare workers. Emerg Infect Dis. 2004;10(2):254–257.
37. World Health Organization. Nipah virus fact sheet. Geneva: WHO; 2023.
38. Chong HT, et al. Ribavirin treatment in Nipah virus infection. Ann Neurol. 2001;49(6):810–813.
39. Georges-Courbot MC, et al. Experimental therapy in Nipah virus. Antiviral Res. 2006;69(1):39–47.
40. Tan CT, et al. Clinical management of Nipah virus infection. Neurol J Southeast Asia. 2000;5:61–64.
41. Clayton BA, et al. Epidemiological variability in Nipah outbreaks. Antiviral Res. 2017;142:84–88.
42. Sazzad HM, et al. Differences in outbreak patterns in Bangladesh. Epidemiol Infect. 2013;141(6):1208–1218.
43. Arunkumar G, et al. Comparative outbreak analysis India vs Bangladesh. Emerg Infect Dis. 2019;25(5):1003–1006.
44. Mire CE, et al. Compassionate use of monoclonal antibody m102.4. Sci Transl Med. 2014;6(242):242ra82.
45. WHO R&D Blueprint. Prioritizing diseases for research and development in emergency contexts. Geneva: WHO; 2018.