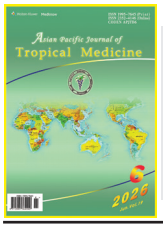

Systematic Review and Meta-Analysis
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Prevalence of dengue infection in Bangladesh: A systematic review and meta−analysis

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ABSTRACT

Objective: To estimate the pooled prevalence of dengue infection in Bangladesh.

Methods: Literature search was conducted across PubMed, Web of Science, and Hinari between December 2024 and April 2025, supplemented by references searching. The Joanna Briggs Institute checklist was used for evaluating study quality. A random effects meta-analysis of proportion, including subgroup analyses, was performed with R software (version 4.5.1).

Results: Out of 2 087 records, 28 studies were included. The pooled prevalence of confirmed dengue infection among clinically suspected patients was 49.3% (95% *CI* 36.1-62.6), with a significant high heterogeneity (I^2=99.2%, τ^2=1.81, P<0.001). Stratified analysis showed a pooled prevalence of 47.9% (95% *CI* 34.0-62.2, I^2=99.1%, τ^2=1.71, P<0.001) for acute/recent infection, and 7.9% (95% *CI* 1.3-36.8, I^2=89.3%, τ^2=2.64, P<0.001) for prior infection among clinically suspected patients. In the general population, based on a limited number of studies, the pooled prevalence of prior dengue infection was 52.8% (95% *CI* 8.5-93.1, I^2=99.9%, τ^2=3.23, P<0.001). DENV-3 was the most prevalent of 52.0% (95% *CI* 23.4-79.4, I^2=98.3%, τ^2=4.11, P<0.001) among molecularly confirmed serotype-positive patients, followed by DENV-2 of 35.8% (95% *CI* 13.7-66.2, I^2=98.4%, τ^2=4.23, P<0.001).

Conclusions: Despite significant heterogeneity among studies, the pooled estimates provide a clear picture of dengue infection burden in Bangladesh and provide a benchmark for monitoring future trends.

KEYWORDS: Bangladesh; Dengue infection; Meta-analysis; Pooled prevalence

1. Introduction

Dengue is a mosquito-borne viral illness caused by four antigenically distinct dengue virus serotypes (DENV-1 to DENV-4), transmitted primarily by infected female *Aedes* mosquitoes. Although immunologically distinct, DENV serotypes cause similar clinical syndromes and are found across the world[1,2]. Infection with one serotype does not confer long-term immunity against others[3,4], leaving individuals susceptible to multiple infections throughout their lifetime. Clinical outcomes of dengue range from asymptomatic or mild fever to life-threatening forms, such as hemorrhagic fever and shock syndrome[5,6].

Two vaccines against dengue, Dengvaxia (CYD-TDV) and

Summary

Question: What is the pooled prevalence of dengue infection in Bangladesh?
Findings: In this analysis, approximately half of the clinically suspected patients had confirmed dengue infection. Around 48% of the clinically suspected patients had evidence of acute/recent infections, while around 53% of the general population had evidence of prior infection. All four dengue virus serotypes were found, with DENV-3 being the most prevalent serotype, followed by DENV-2.
Meaning: These findings indicate ongoing transmission and high endemicity of dengue in Bangladesh and provide a clear picture of the disease burden.

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Qdenga (TAK-003), have been prequalified by the World Health Organization[7]. However, both have significant limitations, including the requirement of prior dengue infection and variable effectiveness across serotypes[8,9]. Consequently, none of them is approved for routine use in many dengue-endemic countries, including Bangladesh[10,11], and mosquito avoidance and vector control remain the cornerstone of dengue prevention.

The spread of dengue is strongly influenced by climatic factors, such as prolonged rainfall, hot and humid conditions[12,13]. Prolonged rainfall provides abundant breeding sites for mosquito vectors, and warm and humid conditions support vector survival and viral replication. Rapid and unplanned urbanization, overcrowded conditions, poor sanitation, and waste management increase human-mosquito contacts and undermine vector control efforts[12,14]. Increased human mobility further facilitates dengue spread into previously unaffected regions[15].

Since the first reported outbreak in 2000[16], Bangladesh has become dengue-endemic and has experienced recurrent seasonal outbreaks annually. In 2023, the country recorded a major outbreak, with 321 179 cases and 1 705 deaths[17], and ranked as the second most dengue-affected country after Brazil in case numbers and first in number of deaths among the major dengue-endemic countries[18]. Dengue surveillance in Bangladesh is passive, hospital-based, which mainly relies on routine reporting of dengue cases from selected public and private healthcare facilities[19]. Beyond surveillance, a limited number of small-scale epidemiological studies have attempted to estimate dengue prevalence[20–22].

Despite the high burden, the true prevalence of dengue infection in Bangladesh remains poorly quantified. Existing estimates are fragmented, often restricted to hospitalized cases or subpopulations, and may not reflect community-level transmission. Reliable pooled estimates are essential to track disease burden, evaluate control strategies, and inform public health planning. Therefore, this systematic review and meta-analysis aimed to synthesize existing studies to estimate the pooled prevalence of dengue infection in Bangladesh.

2. Methods

2.1. Study design and registration

This systematic review and meta-analysis followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines[23] and was registered in the PROSPERO (CRD42025630738).

2.2. Inclusion and exclusion criteria

We included studies that reported the prevalence or proportion of confirmed dengue infection in a defined population, published between January 2000 and April 2025 in English, and conducted in Bangladesh. We included original articles of all formats, and studies reporting dengue with coinfections (*e.g.*, malaria, Zika).

We excluded studies without dengue prevalence data (*e.g.*, those limited to confirmed cases, molecular analyses, or preventive practices), reviews, and studies without full-text. When multiple studies used the same dataset, we included the most comprehensive and recent one.

2.3. Case definitions

Confirmed dengue infection was defined as a positive result by any accepted diagnostic methods, such as detection of NS1 antigen, dengue viral RNA by RT-PCR/qPCR, virus isolation, hemagglutination inhibition assay, anti-dengue IgM and/or IgG antibodies by ELISA, threshold-based methods (*e.g.*, IgM or IgG >40 units in ELISA) or a combination of these tests. For subgroup analysis, we later classified dengue infection into two groups: (1) acute/recent dengue infection, defined as positivity for one or more of the following: NS1 antigen, RT-PCR/qPCR, virus isolation and IgM antibody (with or without IgG positivity), and (2) prior dengue infection, defined as only IgG antibody positivity.

2.4. Search strategy

A comprehensive search was conducted through PubMed, Web of Science, and Hinari by two reviewers (M.E.R. and M.S.) independently. The initial search was performed in December 2024, and the search strategy was later refined and conducted again in April 2025. The search strategy was developed using a combination of MeSH terms, and keywords, and provided in Supplementary Table 1. Additionally, references of the retrieved studies were manually screened to identify any further eligible studies.

2.5. Study screening and selection

Search results were exported to Rayyan for screening. Duplicates were removed using this software, and later during title and abstract screening. Two reviewers independently screened titles and abstracts, and subsequently full-texts based on the inclusion and exclusion criteria. Potentially relevant articles after title and abstract screening were retrieved for full-text review, which both reviewers assessed

independently for final inclusion. Any disagreement during the selection process was resolved through consultation with a third reviewer (A.A.T.).

2.6. Quality assessment

Two reviewers independently assessed the study quality using the Joanna Briggs Institute (JBI) Critical Appraisal checklist for studies reporting prevalence data, which includes nine items for assessing methodological quality and potential bias[24]. Each item was rated as "yes," "no," "unclear," or "not applicable," with one point assigned for each "yes" response to generate a total score. The "response rate" item was considered as "yes" for studies using stored samples or medical records. Based on this score, studies were classified as high (score: 0-3), moderate (score: 4-6), and low (score: 7-9) risk of bias, consistent with a previous study[25]. Quality assessment was not conducted for short communications, dispatches, or letters due to lack of methodological details.

2.7. Data extraction and prevalence estimation

Data were extracted from each study, including author and year, study design, study setting, geographical location of study setting, study population, sample size and collection period, diagnostic methods, confirmed cases, and serotype-specific cases. Unless specified by the original study, we defined studies as retrospective cross-sectional if they tested previously collected clinical samples (*e.g.*, from hospitals or diagnostic centers) or used de-identified medical record data, and as prospective cross-sectional if they actively collected samples or data from participants during the study period. Again, unless specified by the original study, febrile patients or those clinically suspected of dengue attending hospitals or diagnostic centers were considered as clinically suspected patients. If a study used multiple diagnostic methods and reported the total number of positive cases regardless of the method, we used that total for prevalence estimate (*e.g.*, Sultana *et al.*, 2019[26]). Furthermore, if a study reported positive cases separately by diagnostic methods without a combined total, we considered the results from the most widely accepted diagnostic method. For Banu *et al*., 2025[27], we used RT-PCR positive cases (n=775) rather than the rapid test positive cases (n=300). However, for Aziz *et al*., 2002[28], we used IgG and/or IgM ELISA positive cases rather than RT-PCR positive cases, since samples were collected >7 days of fever onset. Extracted data were cross-checked by both reviewers for accuracy.

2.8. Statistical analysis

We conducted meta-analysis of proportions to estimate pooled prevalences. Subgroup meta-analyses were further conducted by stage of dengue infection (acute/recent *vs*. prior) and DENV serotypes. Studies with distinct population groups were excluded from meta-analysis but described separately.

Due to wide variability of prevalence estimates across the included studies, a logit transformation was applied to stabilize variance. Pooled prevalence was estimated using random-effects model with Restricted Maximum Likelihood to account for high heterogeneity, then back-transformed and presented as percentages. Heterogeneity was assessed using the I^2 statistic and τ^2. Forest plots were generated to visually display individual study estimates, their 95% confidence intervals (*CI*s), and subgroup-level pooled estimates. Subgroup differences were assessed using χ^2 test for subgroup differences. A P-value of < 0.05 was used to assess the statistical significance. Analyses were conducted in R software (version 4.5.1) using the meta package (version 8.3.0).

We further conducted sensitivity analyses by (1) excluding data from studies that were not full-length, (2) excluding coinfections data (*i.e*., excluding the coinfected cases from the numerator), and (3) including data from the abstract-only study, to check whether such exclusions or inclusions had a significant impact on the pooled estimates.

3. Results

3.1. Search results

The literature search identified 2087 records (PubMed=1693; Web of Science=290; Hinari=87, and reference lists=17). After removing 149 duplicates, 1938 articles were screened by title and abstract. Of these, 1835 articles were excluded with reasons, and the remaining 103 articles were selected for full-text screening.

For inaccessible full-texts, we reached out to the corresponding authors *via* email. Most authors provided their articles, but one full-text could not be obtained and was excluded[29]. After full-text screening, 75 articles were excluded for predefined reasons, and a total of 28 articles were included. Among these excluded articles, one study was excluded for reporting inconsistent prevalence data[30], and another for an unusually high prevalence[31]. The latter study mentioned that 360 samples from suspected dengue patients were tested, but results showed 300 dengue cases and 60 dengue hemorrhagic fever cases confirmed by serological tests[31]. We excluded this study, assuming the samples were likely from confirmed cases rather than suspected cases (Figure 1).

3.2. Study characteristics

Of the 28 included studies, the majority (n=12) were hospital-based prospective cross-sectional studies[27,28,32–41]. Twenty-three

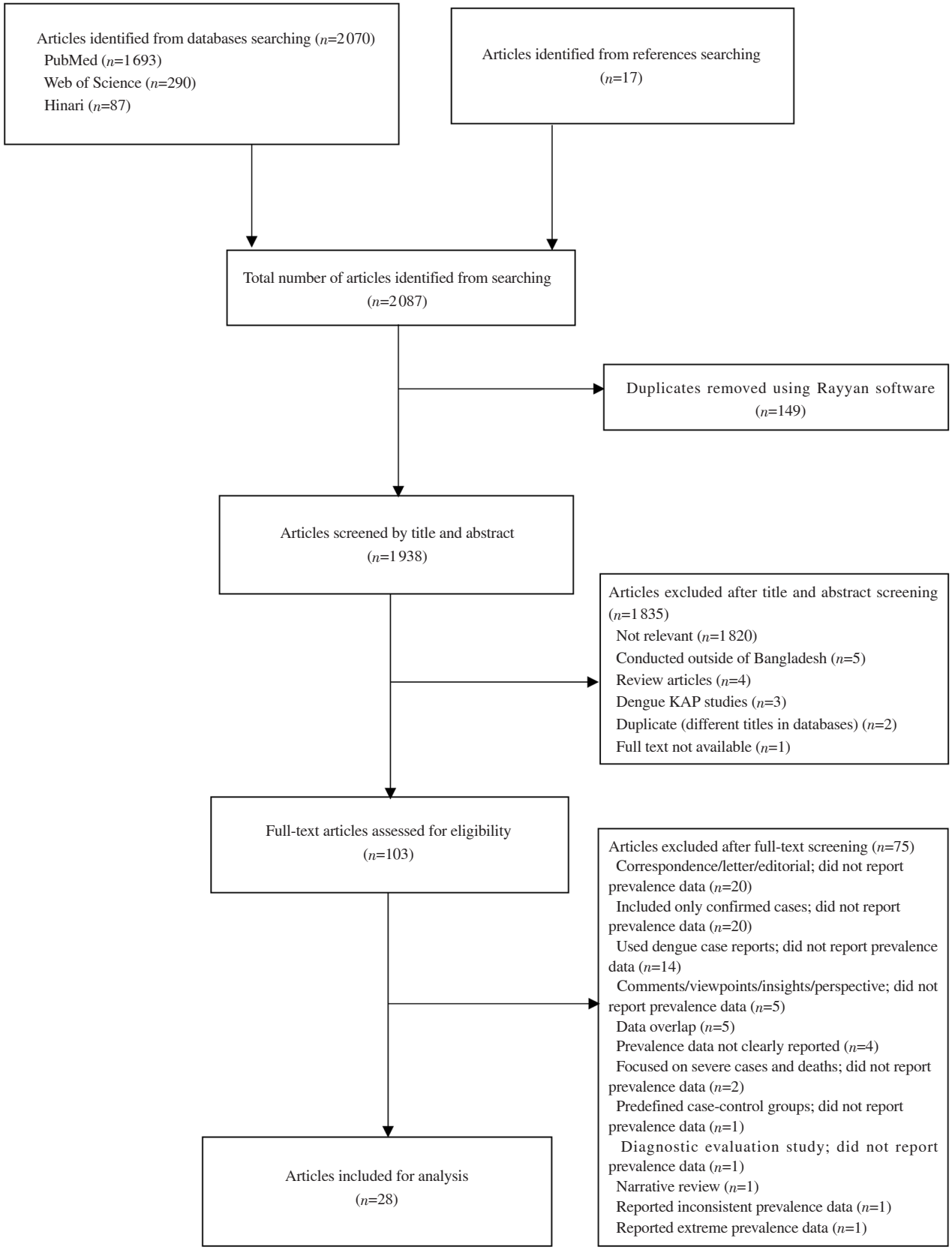

Figure 1. PRISMA flowchart of study selection.

were full-length articles, while three were dispatches[16,42,43], one communication[41], and one letter[39]. Most studies (*n*=24) tested samples from clinically suspected patients regardless of their age. Diagnostic methods varied across studies, including NS1 antigen ICT, RT-PCR/qPCR, virus isolation, and anti-dengue IgM/IgG ELISA or ICT. Thirteen studies reported DENV serotype-

specific infections[27,28,33–35,39,41,42,44–48], four of which identified coinfections[28,33,45,48]. Another study also reported DENV serotype, but data could not be reliably extracted from this study[16]. Three studies reported other infections or cross-reactivity along with dengue, such as Japanese encephalitis virus, malaria, and Zika[36,49,50] (Supplementary Table 2).

3.3. Study quality assessment

Quality assessment was not conducted for five non-full-length articles[16,39,41–43]. Among the rest 23 articles, 12 studies were rated as low[20,22,26,27,35,36,44–47,49,51] and 11 studies as moderate risk of bias[21,28,32–34,37,38,40,48,50,52] (Supplementary Table 2).

3.4. Prevalence of dengue infection in clinically suspected patients

Out of these 28 studies, 24 included clinically suspected patients. Meta-analysis found that among the clinically suspected patients (24 studies, n=22 387), the pooled prevalence of confirmed dengue infection was 49.3% (95% *CI* 36.1-62.6), with a significant high heterogeneity among studies (I^2=99.2%, τ^2=1.81, P<0.001) (Figure 2).

The sensitivity analysis by excluding non-full-length articles lowered the pooled prevalence of confirmed dengue infection at 42.1% (95% *CI* 29.3-56.0) (Supplementary Figure 1). However, the sensitivity analysis excluding coinfected cases, and including the abstract-only data from the inaccessible full-text showed no substantial change in the pooled estimates (Supplementary Figures 2 and 3).

Subgroup meta-analysis by stage of dengue infection found that among the clinically suspected patients, the pooled prevalence of acute/recent infection was 47.9% (95% *CI* 34.0-62.2, I^2=99.1%, τ^2=1.71, P<0.001), while prior dengue infection (IgG seropositivity) was 7.9% (95% *CI* 1.3-36.8, I^2=89.3%, τ^2=2.64, P<0.001). The difference between subgroups was statistically significant (χ^2=5.41, df=1, P=0.02) (Figure 3). This analysis included 20 studies, because we could not reliably differentiate acute/recent infection from prior infection of the rest four studies due to insufficient information, which were therefore excluded.

3.5. Prevalence of dengue infection in the general population

Of these 28 studies, two included the general population. Meta-analysis showed that in the general population (2 studies, n=6 691), the pooled prevalence of prior dengue infection (IgG seropositivity) was 52.8% (95% *CI* 8.5-93.1), with a significant high heterogeneity among studies (I^2=99.9%, τ^2=3.23, P<0.001) (Figure 4). One of them further showed that the prevalence of acute/recent dengue infection (IgM seropositivity) in the general population was

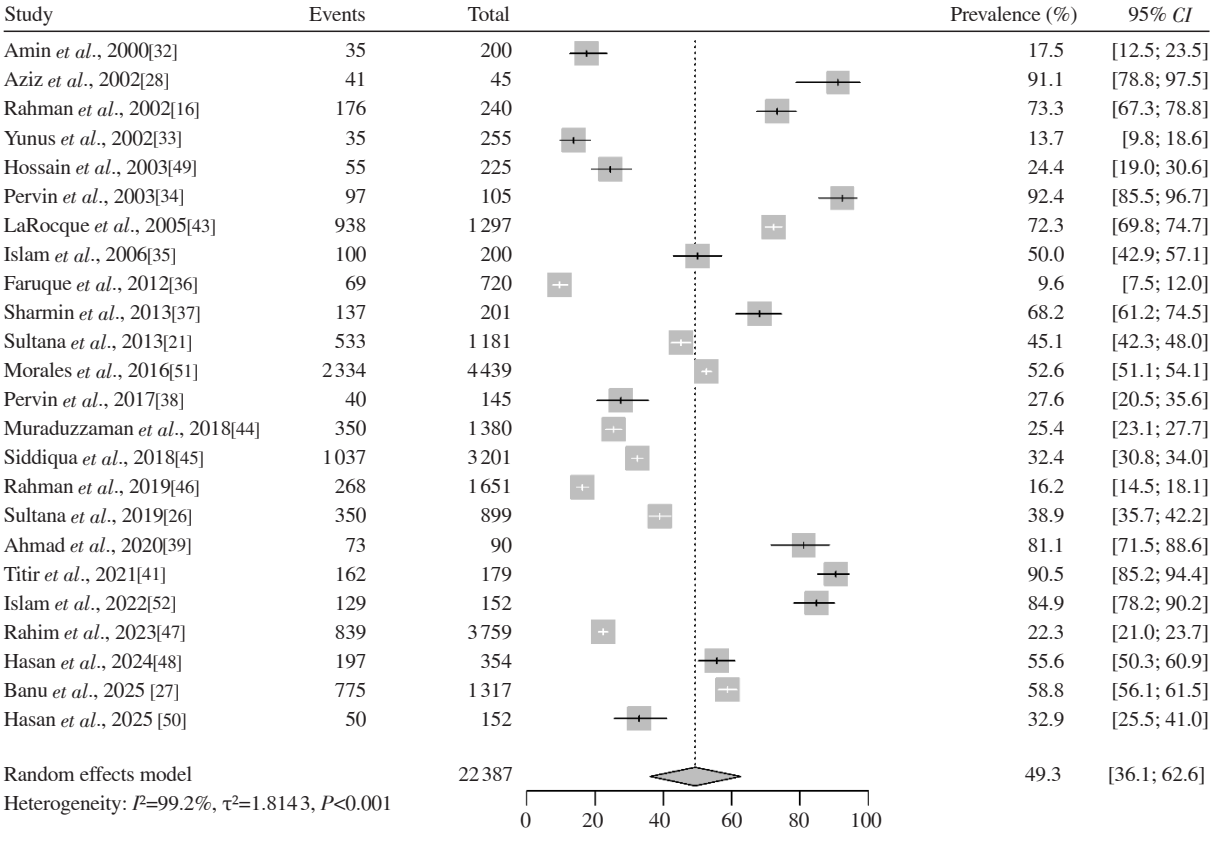

Figure 2. Pooled prevalence of confirmed dengue infection among clinically suspected patients.

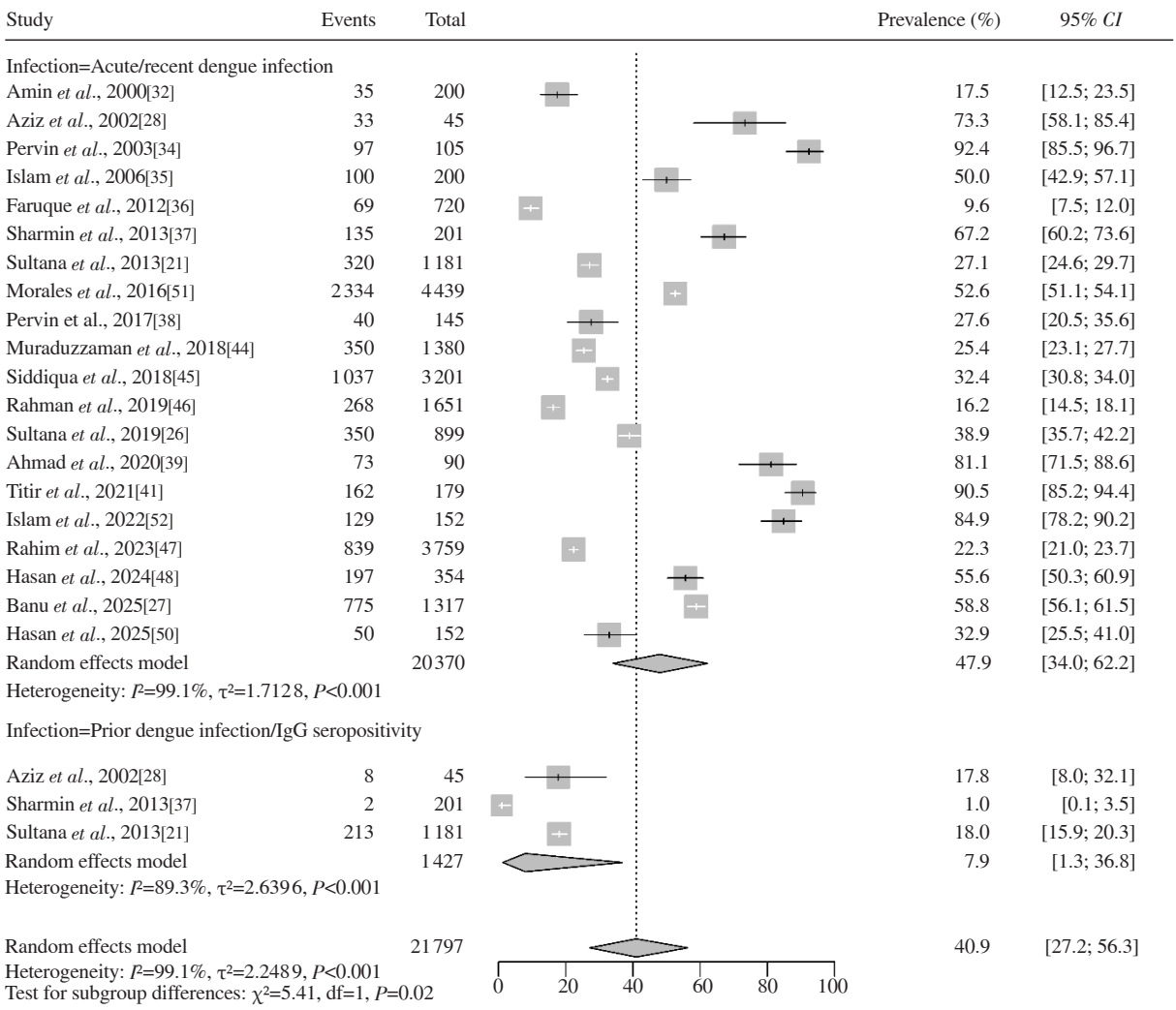

Figure 3. Pooled prevalence of acute/recent and prior dengue infection among clinically suspected patients.

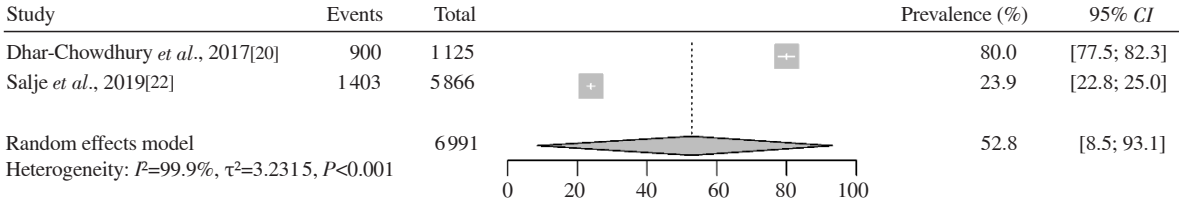

Figure 4. Pooled prevalence of prior dengue infection among the general population.

approximately 2.0% (23 of 1 125), and within the longitudinal cohort, around 57.7% (56 of 97) of initially seronegative individuals seroconverted during monsoon[20].

3.6. Prevalence of dengue infection in distinct populations

Of these 28 studies, two studies were excluded from the meta-analysis due to single distinct population groups. One of them reported the prevalence of prior dengue infection (IgG seropositivity) among general afebrile patients of 51.2% (349 out of 681)[40]. The latter study reported the prevalence (either recent or prior) of 12.1% (13 out of 107) among a recreational club staff[42].

3.7. Distribution of DENV serotypes

Subgroup meta-analysis by DENV-serotypes showed that among the molecularly confirmed serotype-positive patients, DENV-3 accounted the most pooled prevalence of 52.0% (95% *CI* 23.4-79.4), followed by DENV-2 of 35.8% (95% *CI* 13.7-66.2), while DENV-4 was least prevalent of 4.2% (95% *CI* 0.2-51.8). A significant high heterogeneity was observed among studies (I^2 ≥93%, P<0.001). For coinfections by different DENV-serotypes, DENV-3 and DENV-4 coinfection (7.6%), and DENV-2 and DENV-3 coinfection (6.5%) were more prevalent than DENV-1 and DENV-2 (2.1%), with low heterogeneity among studies (I^2 ≤17.4%) (Figure 5).

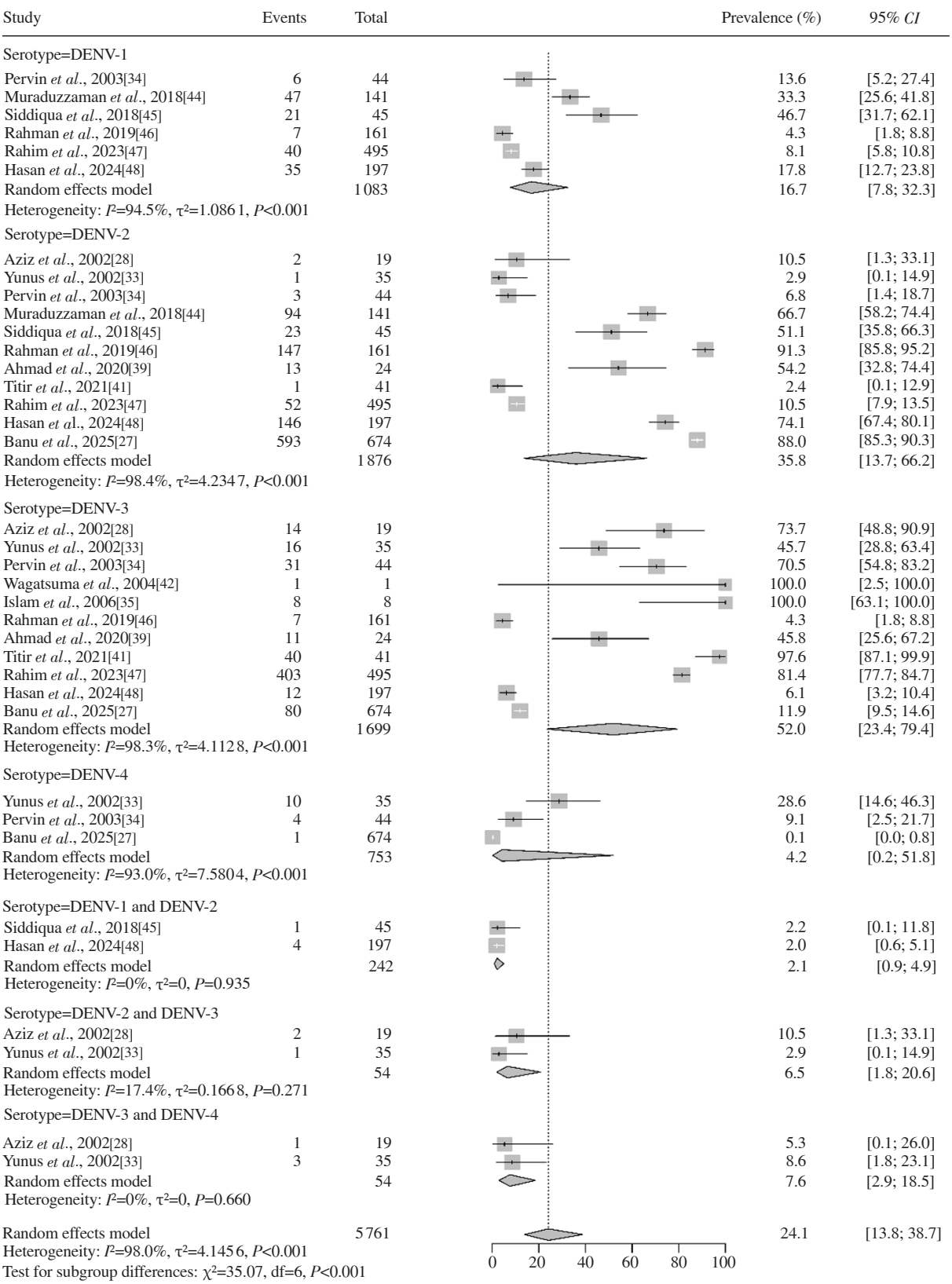

Figure 5. Pooled prevalence of dengue infection by DENV serotypes among molecularly confirmed serotype-positive patients.

This subgroup analysis was conducted with 13 studies[27,28,33-35,39,41,42,44-48], in which serotyping was conducted on a subset of samples from confirmed cases, mostly PCR-positive samples with PCR cycle threshold (Ct) cutoffs (*e.g.*, Ct value <34) (Supplementary Table 3). One study reported a single subgroup of four patients coinfected by DENV-2 and DENV-4[33], which data was also excluded.

4. Discussion

This systematic review and meta-analysis aimed to synthesize existing studies to estimate the pooled prevalence of dengue infection in Bangladesh. The findings provide a clear picture of the national burden of dengue infection and establish a benchmark for monitoring future trends.

Our analysis found that the pooled prevalence of confirmed dengue infection was 49.3% among clinically suspected patients in Bangladesh, and around half of them had acute/recent infection. In the general population, the pooled prevalence of prior infection (IgG seropositivity) was 52.8%, while about half of general afebrile patients (*i.e*., patients presenting at hospitals for any cause) had prior dengue infections (based on a single study by Hoque *et al*., 2021[40]) and the prevalence of confirmed dengue infection (recent or prior) was 12.1% among a recreational club staff (based on the previous study by Wagatsuma *et al*., 2004[42]).

Differences in case definitions limited the comparability of our findings with previous studies from dengue-endemic countries. A previous meta-analysis from India found a pooled prevalence of laboratory-confirmed dengue infection of 38.3% among clinically suspected patients, which defined confirmed infection primarily based on markers of acute infection[53], while our definition was based on the positive results of any accepted method. This meta-analysis from India further showed the pooled estimate of dengue seroprevalence (IgG or neutralizing antibodies) of 56.9% in the general population[53]. Another meta-analysis from Peru showed that the pooled prevalence of laboratory-confirmed dengue or dengue antibodies among febrile patients ranged from 16% to 21% depending on the diagnostic methods[54]. Despite the differences in case definitions, these comparisons highlight the widespread exposure of dengue in clinically suspected and febrile patients in endemic countries.

Although the pooled prevalence of confirmed infection was estimated among clinically suspected patients and included all positive cases, including recent and prior infections, this finding suggests a substantial burden of dengue in Bangladesh. The stratified analysis by stage of infection further found that around half of the clinically suspected patients had acute/recent infection, which was comparable to our pooled estimate of confirmed infection and indicates an ongoing transmission. This finding further underscores the importance of early diagnosis, as it can significantly impact patient management, such as providing timely supportive treatment and reducing the risk of severe complications. Clinicians should consider dengue infection at the top of their differential diagnoses list for patients attending hospitals with fever-like illnesses.

More than 50% of individuals in the general population had evidence of prior infection (IgG seropositivity). Although this estimate was based on a limited number of studies, the high prevalence of IgG seropositivity indicates a high endemicity of dengue in Bangladesh. The IgG antibodies can persist for months or years[55,56], and therefore, positive results may reflect inactive or resolved infections. The evidence of prior infection is also of clinical importance and cannot be overlooked. Individuals can be infected multiple times by DENV serotypes, and secondary infections, particularly with different serotypes, often leads to severe and fetal outcomes[57]. Consequently, individuals with prior infection, particularly in the context of ongoing transmission, are at higher risk of severe complications during subsequent infections[58,59]. We also found that around 57.7% of initially seronegative individuals seroconverted during monsoon (based on the findings of Dhar-Chowdhury *et al*., 2017[20]), indicating substantial seasonal transmission. These findings also highlight the critical need for continuous monitoring and efforts to reduce dengue transmission.

Our analysis also found that all four DENV serotypes and coinfections by different serotypes were prevalent among molecularly confirmed serotype-positive dengue cases, with DENV-3 accounting for almost half of the infections and DENV-2 for about one-third. Understanding the distribution and co-circulation of DENV serotypes offer valuable insights about dengue virus spread and outbreak potential. Although the pooled DENV serotype-specific prevalence was estimated only among serotype-positive patients, not all individuals tested in each study, this finding was important, as certain serotypes are linked with major outbreaks. Previous studies reported that DENV-2 and DENV-3 serotypes are associated with severe dengue outbreaks, such as the severe dengue outbreak in the Loreto region of Peru during 2010 and 2011[60], and in Indonesia in 2019[61]. The predominance of DENV-3 and DENV-2 might also contribute to the recurring annual dengue outbreaks observed in Bangladesh.

To our knowledge, this is the first systematic review and meta-analysis to estimate the pooled prevalence of dengue infection in Bangladesh. The study had several limitations, which emerged from the primary studies included in the analysis. Most of the studies were hospital-based and relied on retrospective samples or collected specimens from inpatients and outpatients. Additionally, many studies did not clearly describe the sampling procedures or report response rates. The pooled estimate of prevalence in the general population was based on a limited number of studies, which might limit the generalizability of the findings. Methodological heterogeneity, despite using the random effects models, remained a major concern in our analysis. We did not report funnel plot because, in meta-analysis of proportion, funnel plot asymmetry may reflect true between-study heterogeneity rather than publication bias, which can mislead the interpretations[62]. We included studies reporting original data on dengue prevalence, regardless of their

publication format, but excluded a potentially relevant study due to the unavailability of its full text[29].

In conclusion, our findings indicate ongoing transmission and a high level of endemicity of dengue in Bangladesh. The DENV-2 and DENV-3 serotypes were found to be most prevalent among the serotype-positive patients. Although we observed significant heterogeneity among studies, this review provides a clear picture of dengue infection burden in Bangladesh and provides a benchmark for monitoring future trends. Future efforts should focus on strengthening surveillance systems to detect changes in the endemicity of dengue and predict outbreaks. Community-level transmission should be evaluated by repeated well-conducted cross-sectional studies that include carefully selected representative samples.

Conflict of interest statement

The authors declare that there is no conflict of interest.

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Previous presentation

Preliminary findings of this systematic review and meta-analysis were presented as a poster at Research Day 2025, Macon & Joan Brock Virginia Health Sciences, Old Dominion University, Norfolk, VA, USA, on November 21, 2025.

Authors' contributions

M.E.R contributed to conceptualization, methodology, investigation, analysis, and drafting the manuscript. A.A.T contributed to methodology, investigation, analysis, and editing the manuscript. M.S. contributed to methodology, investigation and editing the manuscript. M.A.K., and A.N.A. contributed to reviewing and editing the manuscript. All authors read and approved the final manuscript.

References

[1] Bell SM, Katzelnick L, Bedford T. Dengue genetic divergence generates within-serotype antigenic variation, but serotypes dominate evolutionary dynamics. *eLife* 2019; **8**: e42496.

[2] Hannemann H, Sung PY, Chiu HC, Yousuf A, Bird J, Lim SP, et al. Serotype-specific differences in dengue virus non-structural protein 5 nuclear localization. *J Biol Chem* 2013; **288**(31): 22621-22635.

[3] Reich NG, Shrestha S, King AA, Rohani P, Lessler J, Kalayanarooj S, et al. Interactions between serotypes of dengue highlight epidemiological impact of cross-immunity. *J R Soc Interface* 2013; **10**(86): 20130414.

[4] Rothman AL. Immunity to dengue virus: A tale of original antigenic sin and tropical cytokine storms. *Nat Rev Immunol* 2011; **11**(8): 532-543.

[5] Thomas L, Moravie V, Besnier F, Valentino R, Kaidomar S, Coquet LV, et al. Clinical presentation of dengue among patients admitted to the adult emergency department of a tertiary care hospital in Martinique: Implications for triage, management, and reporting. *Ann Emerg Med* 2012; **59**(1): 42-50.

[6] Chatchen S, Sabchareon A, Sirivichayakul C. Serodiagnosis of asymptomatic dengue infection. *Asian Pac J Trop Med* 2017; **10**(1): 11-14.

[7] World Health Organization. *WHO prequalifies new dengue vaccine. 2024.* [Online]. Available from: https://www.who.int/news/item/15-05-2024-who-prequalifies-new-dengue-vaccine. [Accessed on 12 December 2025].

[8] Sridhar S, Luedtke A, Langevin E, Zhu M, Bonaparte M, Machabert T, et al. Effect of dengue serostatus on dengue vaccine safety and efficacy. *N Engl J Med* 2018; **379**(4): 327-340.

[9] Tricou V, Yu D, Reynales H, Biswal S, Saez-Llorens X, Sirivichayakul C, et al. Long-term efficacy and safety of a tetravalent dengue vaccine (TAK-003): 4·5-year results from a phase 3, randomised, double-blind, placebo-controlled trial. *Lancet Glob Health* 2024; **12**(2): e257-e270.

[10]Kayesh MEH, Nazneen H, Kohara M, Tsukiyama-Kohara K. An effective pan-serotype dengue vaccine and enhanced control strategies could help in reducing the severe dengue burden in Bangladesh-a perspective. *Front Microbiol* 2024; **15**: 1423044.

[11]World Health Organization. *Dengue–Bangladesh. 2023.* [Online]. Available from: https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON481. [Accessed on 12 December 2025].

[12]Ogieuhi IJ, Ahmed MM, Jamil S, Okesanya OJ, Ukoaka BM, Eshun G, et al. Dengue fever in Bangladesh: Rising trends, contributing factors, and public health implications. *Trop Dis Travel Med Vaccines* 2025; **11**(1): 26.

[13]Xu C, Xu J, Wang L. Long-term effects of climate factors on dengue fever over a 40-year period. *BMC Public Health* 2024; **24**(1): 1451.

[14]Kolimenakis A, Heinz S, Wilson ML, Winkler V, Yakob L, Michaelakis A, et al. The role of urbanisation in the spread of *Aedes* mosquitoes and the diseases they transmit-A systematic review. *PLoS Negl Trop Dis* 2021; **15**(9): e0009631.

[15]Wesolowski A, Qureshi T, Boni MF, Sundsøy PR, Johansson MA, Rasheed SB, et al. Impact of human mobility on the emergence of dengue epidemics in Pakistan. *Proc Natl Acad Sci U S A* 2015; **112**(38): 11887-11892.

[16]Rahman M, Rahman K, Siddque A, Shoma S, Kamal A, Ali K, et al. First outbreak of dengue hemorrhagic fever, Bangladesh. *Emerg Infect Dis* 2002; **8**(7): 738-740.

[17]Directorate General of Health Services (DGHS), Government of Bangladesh. *Dengue press release–31 December 2023*. [Online]. Available from: https://old.dghs.gov.bd/images/docs/vpr/20231231_dengue_all.pdf. [Accessed on 4 November 2025].

[18]Khan S, Akbar SMF, Mahtab MA, Yahiro T, Hashimoto T, Kimitsuki K, et al. Bangladesh records persistently increased number of dengue deaths in recent years: Dissecting the shortcomings and means to resolve. *IJID Reg* 2024; **12**: 100395.

[19]Directorate General of Health Services (DGHS), Government of Bangladesh. *Mapping of the infectious disease surveillance system in Bangladesh. 2025*. [Online]. Available from: https://dghs.gov.bd/pages/notices/mapping-of-the-infectious-disease-surveillance-system-in-bangladesh-dfx8et-698975c215676b17b1e61d41. [Accessed on 4 November 2025].

[20]Dhar-Chowdhury P, Paul KK, Haque CE, Hossain S, Lindsay LR, Dibernardo A, et al. Dengue seroprevalence, seroconversion and risk factors in Dhaka, Bangladesh. *PLoS Negl Trop Dis* 2017; **11**(3): e0005475.

[21]Sultana N, Biswas SK, Sultan T, Ahmed S, Hossain Z, Chowdhury R. Seroprevalence of dengue fever in Chittagong, Bangladesh. *Chatt Maa Shi Hosp Med Coll J* 2013; **12**(1): 38-40.

[22]Salje H, Paul KK, Paul R, Rodriguez-Barraquer I, Rahman Z, Alam MS, et al. Nationally-representative serostudy of dengue in Bangladesh allows generalizable disease burden estimates. *eLife* 2019; **8**: e42869.

[23]Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: An updated guideline for reporting systematic reviews. *BMJ* 2021; **372**: n71.

[24]Munn Z, Moola S, Lisy K, Riitano D, Tufanaru C. Methodological guidance for systematic reviews of observational epidemiological studies reporting prevalence and cumulative incidence data. *Int J Evid Based Healthc* 2015; **13**(3): 147-153.

[25]Nigussie E, Atlaw D, Negash G, Gezahegn H, Baressa G, Tasew A, et al. A dengue virus infection in Ethiopia: A systematic review and meta-analysis. BMC Infect Dis 2024; **24**(1): 297.

[26]Sultana N, Fatema N, Hossain MZ, Rahman MA, Nehar N, Yeasmin MM, et al. Frequency of dengue infection in febrile pateints attended Dhaka Medical College Hospital during January to December 2018. *J Dhaka Med Coll* 2019; **28**(1): 105-111.

[27]Banu SS, Nahar K, Sultana N, Tony SR, Alam S, Rashed A, et al. Molecular epidemiology of circulating dengue serotypes in Dhaka, Bangladesh: 2023 outbreak. *IJID Reg* 2025; **14**: 100597.

[28]Aziz M, Hasan K, Hasanat M, Siddiqui M, Salimullah M, Chowdhury A, et al. Predominance of DEN-3 genotype during the recent dengue outbreak in Bangladesh. *Southeast Asian J Trop Med Public Health* 2002; **33**(1): 42-48.

[29]Rahman M, Tahmin H, Mannan T, Sultana R. Seropositivity and pattern of dengue infection in Dhaka city. *Mymensingh Med J* 2007; **16**(2): 204-208.

[30]Hoque MS, Sarkar PK, Ahmed ANU. Clinical characteristics & observation of hospitalized cases of dengue fever: A study in tertiary care hospital, Dhaka, Bangladesh. *Saudi J Med Pharm Sci* 2020; **6**(12): 740-749.

[31]Farhana R, Awatef KF, Khanum H, Akter T. Prevalence of dengue fevers among the patients of different economic status attended at local hospital in Dhaka. *Bangladesh J Zool* 2014; **42**(2): 161-168.

[32]Amin M, Hussain A, Nahar K, Chowdhury I, Murshed M, Chowdhury S. Sero-diagnosis of dengue infections in four metropolitan cities of Bangladesh. *Dengue Bull* 2000; **24**: 29-33.

[33]Yunus IB, Banu D, Talukder KR, Chowdhury M, Bangali AM, Montanari R. Sero-epidemiological study of dengue/dengue haemorrhagic fever in a metropolitan hospital in Bangladesh. *Dengue Bull* 2002; **26**: 1-6.

[34]Pervin M, Tabassum S, Kumar Sil B, Islam MN. Isolation and serotyping of dengue viruses by mosquito inoculation and cell culture technique: An experience in Bangladesh. *Dengue Bull* 2003; **27**: 81-90.

[35]Islam MA, Ahmed MU, Begum N, Chowdhury NA, Khan AH, del Carmen Parquet M, et al. Molecular characterization and clinical evaluation of dengue outbreak in 2002 in Bangladesh. *Jpn J Infect Dis* 2006; **59**(2): 85-91.

[36]Faruque LI, Zaman RU, Alamgir A, Gurley ES, Haque R, Rahman M, et al. Hospital-based prevalence of malaria and dengue in febrile patients in Bangladesh. *Am J Trop Med Hyg* 2012; **86**(1): 58-64.

[37]Sharmin R, Tabassum S, Mamun K, Nessa A, Jahan M. Dengue infection in Dhaka City, Bangladesh. *Mymensingh Med J* 2013; **22**(4): 781-786.

[38]Pervin M, Sweety AA, Hossain MZ, Sharmin R, Fatema N, Rahman MA, et al. Sera-epidemiology of dengue virus infection in clinically suspected patients attended in Dhaka Medical College Hospital during January to December 2016. *J Dhaka Med Coll* 2017; **26**(2): 111-116.

[39]Ahmad F, Paul S, Aung M, Mazid R, Alam M, Ahmed S, et al. Co-circulation of dengue virus type 3-genotype Ⅰ and type 2-Cosmopolitan genotype in 2018 outbreak in Dhaka, Bangladesh. *New Microbes New Infect* 2020; **33**: 100629.

[40]Hoque MM, Amin MR, Biswas S, Islam MR. Hospital seroprevalence of dengue virus infection among adults of urban Dhaka. *Bangladesh Med*

Res Counc Bull 2021; **47**: 17-22.

[41]Titir SR, Paul SK, Ahmed S, Haque N, Nasreen SA, Hossain KS, et al. Nationwide distribution of dengue virus type 3 (Denv-3) genotype Ⅰ and emergence of DENV-3 genotype Ⅲ during the 2019 outbreak in Bangladesh. *Trop Med Infect Dis* 2021; **6**(2): 58.

[42]Wagatsuma Y, Breiman RF, Hossain A, Rahman M. Dengue fever outbreak in a recreation club, Dhaka, Bangladesh. *Emerg Infect Dis* 2004; **10**(4): 747-750.

[43]LaRocque RC, Breiman RF, Ari MD, Morey RE, Janan FA, Hayes JM, et al. Leptospirosis during dengue outbreak, Bangladesh. *Emerg Infect Dis* 2005; **11**(5): 766-769.

[44]Muraduzzaman AKM, Alam AN, Sultana S, Siddiqua M, Khan MH, Akram A, et al. Circulating dengue virus serotypes in Bangladesh from 2013 to 2016. *Virusdisease* 2018; **29**(3): 303-307.

[45]Siddiqua M, Alam AN, Muraduzzaman A, Shirin T. NS-1 antigen positive dengue infection and molecular characterization of dengue viruses in a private medical college hospital in Dhaka, Bangladesh. *Bangladesh J Med Sci* 2018; **17**(4): 669-673.

[46]Rahman M, Rahim R, Hasan A, Murad AS, Biswas M. Co-circulation of three dengue virus serotypes in 2017 in Dhaka city: First report from Bangladesh. *Biores Commun* 2019; **5**(1): 637-641.

[47]Rahim R, Hasan A, Phadungsombat J, Hasan N, Ara N, Biswas SM, et al. Genetic analysis of Dengue virus in severe and non-severe cases in Dhaka, Bangladesh, in 2018-2022. *Viruses* 2023; **15**(5): 1144.

[48]Hasan A, Zamil MF, Trina AT, Biswas RSR, Kumkum A, Ahmed D, et al. Resurgence of dengue virus serotype 2: Findings from the 2023 Bangladesh outbreak. *Am J Trop Med Hyg* 2024; **111**(3): 617-621.

[49]Hossain MA, Khatun M, Arjumand F, Nisaluk A, Breiman RF. Serologic evidence of dengue infection before onset of epidemic, Bangladesh. *Emerg Infect Dis* 2003; **9**(11): 1411-1414.

[50]Hasan A, Hossain MM, Zamil MF, Trina AT, Hossain MS, Kumkum A, et al. Concurrent transmission of Zika virus during the 2023 dengue outbreak in Dhaka, Bangladesh. *PLoS Negl Trop Dis* 2025; **19**(1): e0012866.

[51]Morales I, Salje H, Saha S, Gurley ES. Seasonal distribution and climatic correlates of dengue disease in Dhaka, Bangladesh. *Am J Trop Med Hyg* 2016; **94**(6): 1359-1361.

[52]Islam S, Khan MAS, Badal MFA, Khan MZI, Gozal D, Hasan MJ. Clinical and hematological profiles of children with dengue residing in a non-endemic zone of Bangladesh. *PLoS Negl Trop Dis* 2022; **16**(10): e0010847.

[53]Ganeshkumar P, Murhekar MV, Poornima V, Saravanakumar V, Sukumaran K, Anandaselvasankar A, et al. Dengue infection in India: A systematic review and meta-analysis. *PLoS Negl Trop Dis* 2018; **12**(7): e0006618.

[54]León-Figueroa DA, Garcia-Vasquez EA, Diaz-Torres M, Aguirre-Milachay E, Villanueva-De La Cruz JP, Saldaña-Cumpa HM, et al. Prevalence of dengue in febrile patients in Peru: A systematic review and meta-analysis. *PLoS One* 2025; **20**(6): e0310163.

[55]Luo S, Cui W, Li C, Ling F, Fu T, Liu Q, et al. Seroprevalence of dengue IgG antibodies in symptomatic and asymptomatic individuals three years after an outbreak in Zhejiang Province, China. *BMC Infect Dis* 2018; **18**(1): 92.

[56]Wu Q, Jing Q, Wang X, Yang L, Li Y, Chen Z, et al. Kinetics of IgG antibodies in previous cases of dengue fever-A longitudinal serological survey. *Int J Environ Res Public Health* 2020; **17**(18): 6580.

[57]Sinha S, Singh K, Ravi Kumar YS, Roy R, Phadnis S, Meena V, et al. Dengue virus pathogenesis and host molecular machineries. *J Biomed Sci* 2024; **31**(1): 43.

[58]Fried JR, Gibbons RV, Kalayanarooj S, Thomas SJ, Srikiatkhachorn A, Yoon IK, et al. Serotype-specific differences in the risk of dengue hemorrhagic fever: An analysis of data collected in Bangkok, Thailand from 1994 to 2006. *PLoS Negl Trop Dis* 2010; **4**(3): e617.

[59]Shih HI, Wang YC, Wang YP, Chi CY, Chien YW. Risk of severe dengue during secondary infection: A population-based cohort study in Taiwan. *J Microbiol Immunol Infect* 2024; **57**(5): 730-738.

[60]Williams M, Mayer SV, Johnson WL, Chen R, Volkova E, Vilcarromero S, et al. Lineage Ⅱ of Southeast Asian/American DENV-2 is associated with a severe dengue outbreak in the Peruvian Amazon. *Am J Trop Med Hyg* 2014; **91**(3): 611-620.

[61]Tatura SN, Denis D, Santoso MS, Hayati RF, Kepel BJ, Yohan B, et al. Outbreak of severe dengue associated with DENV-3 in the city of Manado, North Sulawesi, Indonesia. *Int J Infect Dis* 2021; **106**: 185-196.

[62]Hunter JP, Saratzis A, Sutton AJ, Boucher RH, Sayers RD, Bown MJ. In meta-analyses of proportion studies, funnel plots were found to be an inaccurate method of assessing publication bias. *J Clin Epidemiol* 2014; **67**(8): 897-903.

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