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Prevalence of Severe Dengue Infection in Bangladesh: A Bayesian Meta-analysis

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Abstract

Severe dengue represents a critical and potentially life-threatening stage of dengue infection, often characterizes by internal bleeding which leads to death. Several studies existed on severe dengue but a meta-analysis can provide robust understanding of the epidemiology of the disease.This study aimed to estimate the pooled prevalence of dengue cases which developed to severe dengue in Bangladesh. A systematic literature search was conducted across five databases between January 2000 and June 2025: PubMed, Google Scholar, Cochrane Central, ScienceDirect, and BanglaJOL. After title and abstract screening and full text review, this study included 41 cross-sectional studies. The quality of included studies were assessed using the STROBE checklist. Bayesian random-effects model was applied to estimate the pooled prevalence, with both non-informative and informative priors. Further, model diagnostics including trace plots and autocorrelation checks were used to assess MCMC convergence. A Bayesian random-effects model using the strongly informative prior estimated a pooled prevalence of 33.9% (95% Credible Interval: 25.4, 42.0), and a between-study heterogeneity (τ^2) of 0.074. Model diagnostics were further supported these findings by the evidence of adequate mixing and convergence, with no signs of autocorrelation in the MCMC chains. However, this study have found one-third of the dengue cases developed to severe dengue cases which indicates a serious burden for the healthcare system of the country. These findings have important implications for public health surveillance and can inform policymakers in planning and prioritizing interventions to manage severe dengue cases in Bangladesh.

Keywords: Prevalence, Severe dengue, Informative prior, Bangladesh, Bayesian meta-analysis.

I. Introduction

Dengue fever, caused by the *flavivirus*, is one of the most rapidly spreading vector-borne diseases worldwide. Severe dengue represents the life-threatening stage of this infection, characterized by plasma leakage, severe bleeding, organ impairment, and dyspnea. This condition is also classified as dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS)[1]. The Centers for Disease Control and Prevention (CDC) estimates that severe dengue occurs in approximately 1 in 20 patients and is responsible for the majority of dengue-related mortality[2]. Consequently, early diagnosis and appropriate clinical management are critical to preventing progression to severe disease.

The global burden of dengue has increased dramatically in recent decades. According to a 2024 World Health Organization (WHO) estimate, there were 7.6 million reported dengue cases globally, including 16,000 severe cases and over 3,000 deaths[3]. WHO further estimates that approximately 390 million dengue infections occur annually worldwide, of which only about 96 million are clinically diagnosed[4]. Dengue is now endemic in more than 100 countries, with the highest burden in tropical regions of Southeast Asia, the Americas, and the Western Pacific[5]. Between 1990 and 2021, the global burden of dengue nearly doubled, increasing from 26.45 million to 58.96 million cases and from 14,315 to 29,075 deaths[6]. South Asian countries, including India, Bangladesh, Sri Lanka, and Pakistan, have emerged as significant contributors to this global burden[7, 8].

Bangladesh is experiencing an alarming rise in dengue outbreaks. The country faced its most severe epidemic in 2023, with a record 321,179 reported cases and 1,705 deaths between January and December[9]. The Directorate General of Health Services (DGHS) reported that cases and deaths in 2023 increased approximately five-fold and six-fold, respectively, compared to 2022[10]. The case fatality rate (CFR) between January and August 2023 was reported by the WHO to be 0.47%[11]. Among the total deaths in 2023, about 74% involved DSS and 7% involved DHF[12]. The epidemiology is highly concentrated in urban areas, particularly the Dhaka and Chittagong divisions[13]. With all four dengue virus serotypes circulating in Bangladesh, the increasing trend of severe cases necessitates adequate management and control strategies[14].

Despite the growing burden, a significant knowledge gap exists regarding the precise prevalence of severe dengue infection in Bangladesh. While several studies have estimated the overall prevalence, seroprevalence, and mortality of dengue in Bangladesh, there remains a scarcity of robust, and pooled estimate of severe dengue in the country by incorporating studies from different regions and time periods. Traditional frequentist meta-analyses often struggle with the sparse data and high heterogeneity characteristic of observational studies. In contrast, a

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Bayesian meta-analysis can provide more consistent and reliable estimates by incorporating prior knowledge, thereby offering a more nuanced understanding of the country's severe dengue situation.

This study aims to estimate the pooled prevalence of severe dengue in Bangladesh using a Bayesian random-effects model. By synthesizing existing data and incorporating appropriate prior distributions, this approach will yield a robust posterior prevalence estimate. The findings are expected to inform national dengue surveillance strategies, healthcare capacity planning, clinical management protocols, and resource allocation decisions.

II. Methodology

Search Strategy

A systematic literature search was conducted across five electronic databases from January 2000 to June 2025: PubMed, ScienceDirect, Cochrane Central, Google Scholar, and BanglaJOL. The search strategy employed the following Boolean query:

(("Severe Dengue" OR "dengue hemorrhagic fever" OR "dengue shock syndrome") AND ("dengue fever" OR "dengue") AND ("prevalence" OR "seroprevalence") AND ("NS1" OR "IgM" OR "IgG" OR "DENV-1" OR "DENV-2" OR "DENV-3" OR "DENV-4") AND ("Bangladesh*")).

This initial search strategy yielded 3,049 records. After removing 832 duplicates, the titles and abstracts of the remaining 2,217 articles were screened using the Rayyan software. Following this screening, 401 articles were selected for full-text review. Ultimately, 41 articles met the eligibility criteria and were included in the meta-analysis. The study selection process followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines[15], as illustrated in Figure 1. This meta-analysis was not registered under any protocol.

Inclusion and Exclusion Criteria

Studies were included if they were cross-sectional, conducted on human populations in Bangladesh, and clearly defined severe dengue cases according to WHO or DGHS guidelines. Only studies published in English in peer-reviewed journals were considered.

Exclusion criteria encompassed case reports, case series, review articles, letters, editorials, and conference abstracts. Studies focusing on animals or dengue patients co-infected with other infectious diseases were also excluded. If multiple publications used the same dataset, only the study with the highest quality assessment score was included to avoid duplication.

Risk of Bias Assessment

The risk of bias for the included cross-sectional studies was assessed using a modified version of the Joanna Briggs Institute (JBI) critical appraisal checklist[16] for prevalence studies (Table A1), which incorporates items from the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) guidelines[17]. The quality assessment scores are provided in Appendix (Table A2).

Prior Selection

To estimate the posterior prevalence of severe dengue, three distinct prior distributions were specified for the model parameters:

1. Non-informative Prior: A Jeffrey's prior was used to represent a state of minimal prior knowledge about the prevalence parameter. While robust against prior misspecification, this approach can result in wider credible intervals and less precise estimates[18].

2. Weakly Informative Prior: A weakly informative prior was employed when we do not have enough evidence regarding the prior distribution of the parameter. For the prevalence parameter, a standard normal distribution, i.e., N(0, 1), was used. For the heterogeneity parameter (τ^2), an inverse-gamma distribution, i.e., igamma (0.5, 0.125), was specified. This approach offers a computational efficiency, though the posterior may remain somewhat sensitive to the prior choice[18].

3. Strongly Informative Prior: A strongly informative prior was constructed in this study from the meta-analysis of the included studies. The prevalence parameter was assigned a normal distribution with a mean of 0.337 and a variance of 0.0664, i.e., N(0.337, 0.0664). The heterogeneity (τ^2) parameter was again assigned an inverse-gamma distribution, i.e., igamma (0.5, 0.125). The use of a strongly informative prior is expected to yield the most precise and stable estimates with narrower credible intervals, provided the prior information is accurate[19].

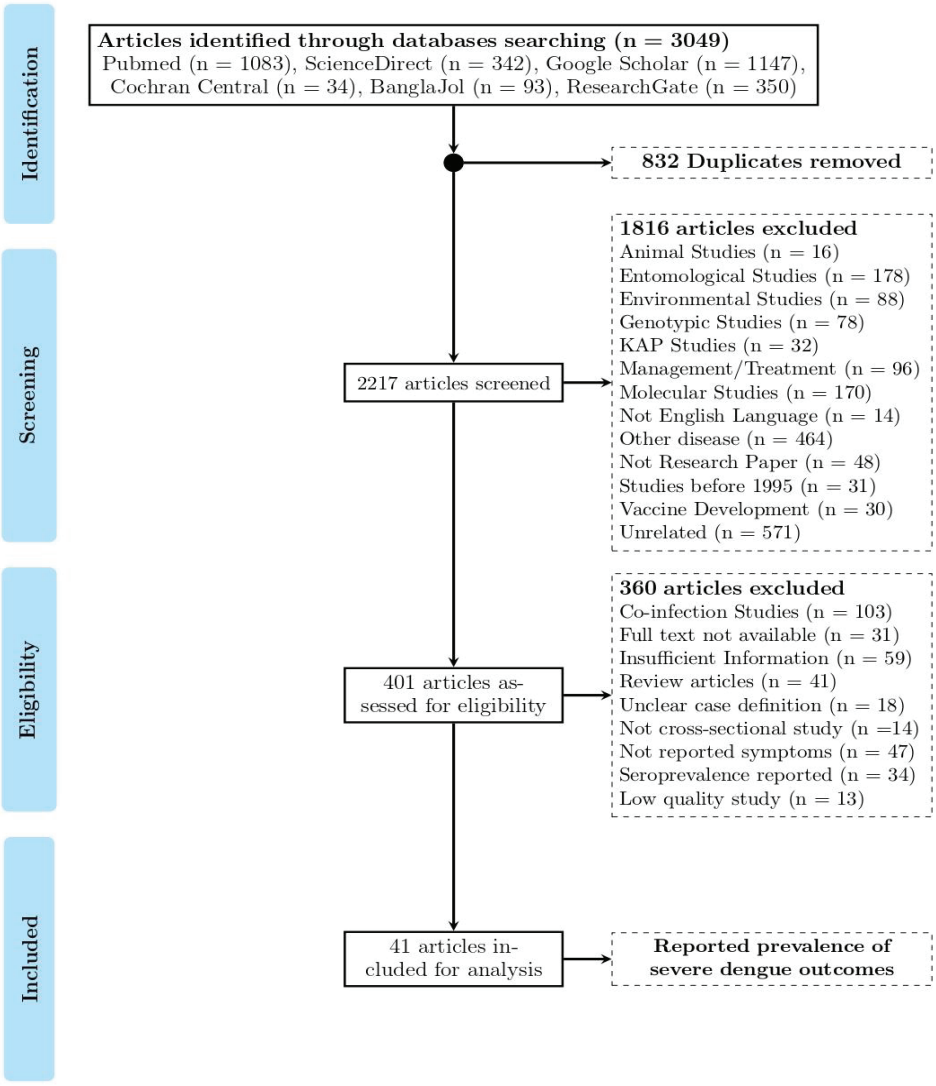

Fig. 1. PRISMA flowchart for article selection process in this study.

Statistical Analysis

The pooled prevalence of severe dengue was estimated using a Bayesian random-effects model. The model was implemented using the Metropolis-Hastings algorithm. For each prior specification (non-informative, weakly informative, and strongly informative), the model was run with four Markov chains.

Each chain consisted of 50,000 iterations, with a burn-in period of 2,500 iterations discarded to ensure convergence. A thinning interval of 50 was applied to reduce autocorrelation, resulting in 1,000 posterior samples per chain for analysis.

Model convergence was assessed using trace plots and the Gelman-Rubin convergence statistic (R-hat), with a value of less than 1.10 indicating satisfactory convergence. The best-performing prior was selected based on the lowest standard error (SE) and Monte Carlo standard error (MCSE), as well as the narrowest 95% credible interval (CrI), indicating higher precision and stability. All analyses were performed using the bayesmh module in STATA.

III. Results

A Bayesian random-effects model was performed to estimate the pooled prevalence of severe dengue in Bangladesh using three distinct priors: non-informative, weakly informative, and strongly informative. The results are summarized in Table 1[31-71]. The pooled prevalence estimates were highly consistent across all three approaches, ranging from 33.6% to 33.9%. A similar pattern was observed for the heterogeneity statistic (τ^2), which varied narrowly between 0.074 and 0.075. The low Monte Carlo Standard Errors (MCSE) for all estimates indicated adequate computational precision. Furthermore, all models achieved satisfactory convergence, which was evident by Gelman-Rubin diagnostic statistics (R-hat < 1.10).

Table 1. Summary results and convergence of the Bayesian random-effects model for three priors.

Method	Parameter	Estimate	SE	MCSE	95% Credible Interval		R-hat
					Lower	Upper	
Non-informative	Prevalence	0.336	0.042	0.00067	0.250	0.419	1.0009
	τ^2	0.074	0.018	0.00028	0.047	0.116	1.0005
Weakly informative prior	Prevalence	0.337	0.042	0.00069	0.253	0.420	1.0002
	τ^2	0.075	0.018	0.00030	0.047	0.116	1.0001
Strongly informative prior	Prevalence	0.339	0.042	0.00067	0.254	0.420	1.0003
	τ^2	0.074	0.017	0.00028	0.048	0.115	1.0013

Firstly, the model utilizing a non-informative prior yielded a prevalence of 33.6% (95% CrI: 25.0-41.9) with a heterogeneity (τ^2) of 0.074 (95% CrI: 0.047-0.116). Nearly identical results were obtained with the weakly informative prior, which produced a prevalence of 33.7% (95% CrI: 25.3-42.0) and heterogeneity (τ^2) of 0.075 (95% CrI: 0.047-0.116). In comparison, the model with the strongly informative prior estimated a slightly higher prevalence of 33.9% (95% CrI: 25.4-42.0) and a heterogeneity (τ^2) of 0.074 (95% CrI: 0.048-0.115).

The strongly informative prior was selected as the preferred model for producing the most precise and consistent results. This choice was based on three key criteria: standard error (SE), Monte Carlo standard error (MCSE), and the width of the credible interval (CrI). Firstly, all models exhibited the same SE for the prevalence estimate (0.042). Secondly, the MCSE was lowest for both the non-informative and strongly informative priors (MCSE = 0.00067), which outperforming compared to the weakly informative prior (MCSE = 0.00069). Thirdly, the strongly informative prior produced the narrowest CrI. The CrI width for the strongly informative prior was 0.166 (0.420 - 0.254), whereas 0.169 (0.419 - 0.250) for the non-informative prior. Consequently, the combination of a low SE, minimal MCSE, and the narrowest CrI indicates that the strongly informative prior provided the most precise and reliable estimate.

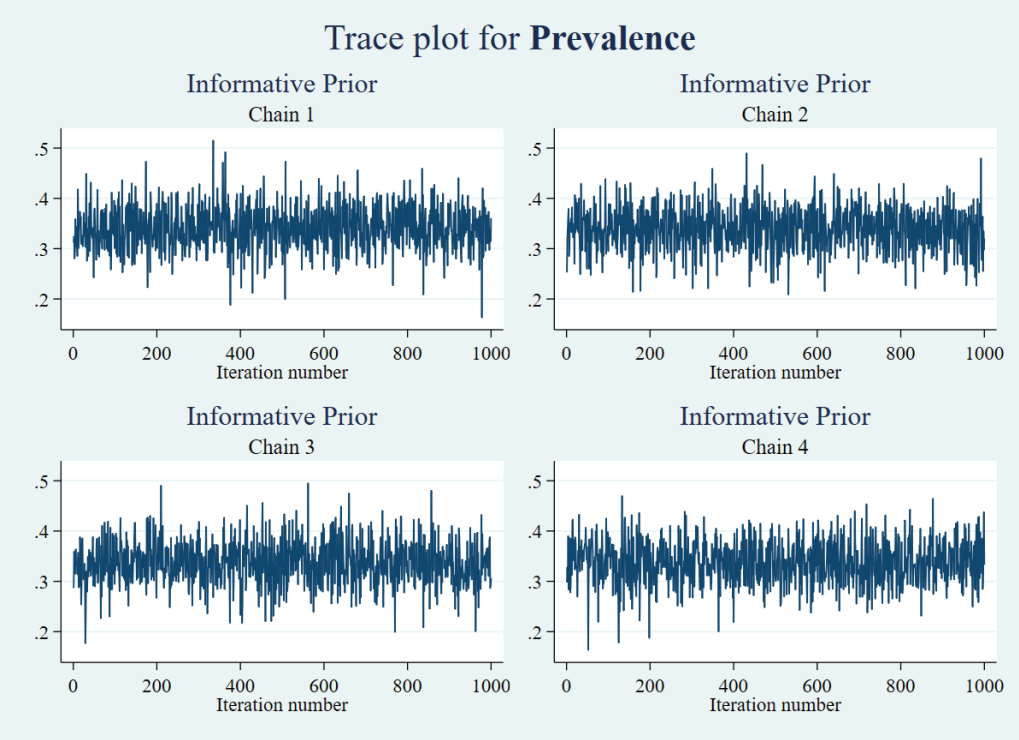

Fig. 2. Trace plots of the prevalence estimate of severe dengue in Bangladesh.

Model convergence for the strongly informative prior was assessed using trace plots for both prevalence (Figure 2) and heterogeneity (Figure 3). The plots demonstrated excellent convergence across all four Markov Chain Monte Carlo (MCMC) chains. For the prevalence parameter, all chains achieved stable oscillation around the posterior mean with

adequate mixing and no evidence of autocorrelation over 1,000 iterations. The chains showed rapid convergence from the initial iteration and remained stationary throughout the sampling process. Similarly, the trace plots for heterogeneity indicated well-mixed chains with no signs of autocorrelation. The absence of any discernible patterns in the trace plots confirmed that an adequate burn-in period was used and reinforced the reliability of the posterior estimates. These visual diagnostics were further supported by the Gelman-Rubin statistics for both prevalence (R-hat = 1.0003) and heterogeneity (R-hat = 1.0013).

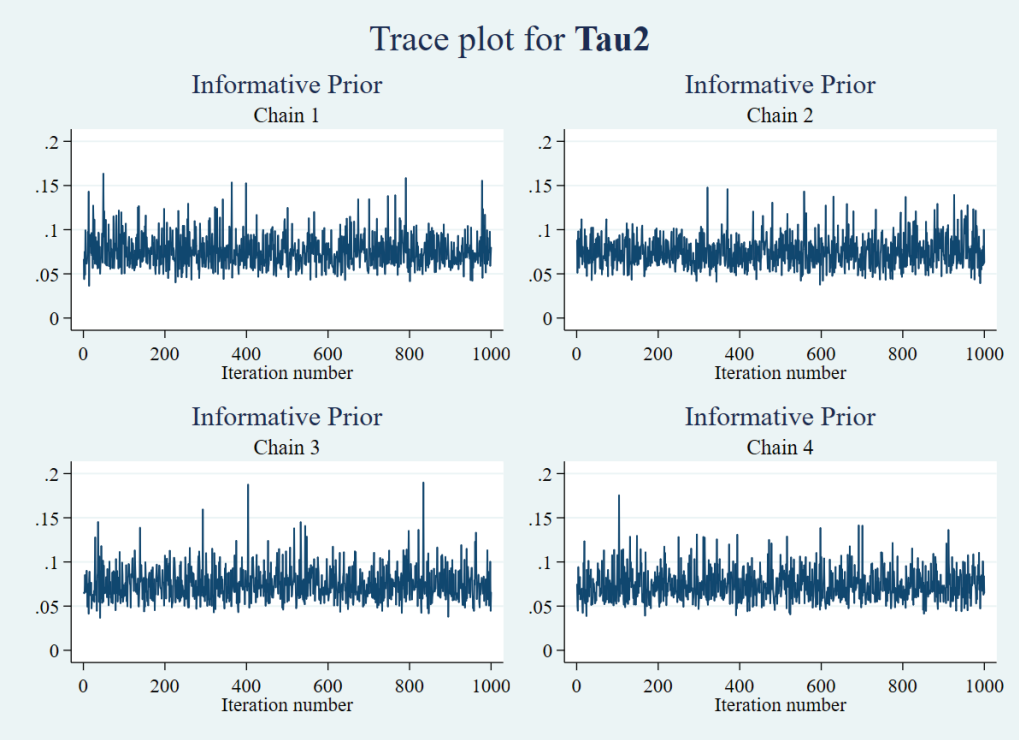

Fig. 3. Trace plots of the heterogeneity estimate of severe dengue in Bangladesh.

A frequentist random-effects model was also applied to compare the posterior pooled prevalence, which yielded a pooled prevalence of 33.7% and a heterogeneity estimate (τ^2) of 0.0664. This method underestimated both prevalence and heterogeneity compared to the Bayesian approach. However, given the strong justification for the prior information and the superior performance metrics (lowest MCSE and narrowest CrI), we conclude that the parameter estimates obtained using the strongly informative prior are the most reliable, consistent, and accurate for estimating the prevalence of severe dengue in Bangladesh.

IV. Discussion

This study represented the first comprehensive estimate of the pooled prevalence of severe dengue in Bangladesh using a Bayesian meta-analysis technique. The primary finding indicated that approximately one-third of dengue cases in Bangladesh develop to severe dengue. The estimate provided a strong evidence for understanding the significant burden of severe dengue in the country.

Comparison with Regional and Global Estimates

Our finding of a severe dengue prevalence (33.9%) into a global context is challenging due to the scarcity of similar pooled estimates. The WHO and CDC often cite a figure of around 5% of dengue cases develop to severe cases[2]. Our estimate is substantially higher, which likely reflects both the specific epidemiological context of Bangladesh and the methodological approach. The 5% figure is a global average, whereas hyperendemic regions like Bangladesh, with co-circulation of all four dengue serotypes, may experience higher rates of severe disease due to the increased risk of secondary infections[20]. Studies from other South Asian countries report varying rates[21, 22]. For instance, research from India has reported severe dengue proportions ranging from 15% to 40% in hospital-based studies[21, 22], indicating a wide spectrum that aligns with our pooled estimate. The high prevalence underscores the intense transmission dynamics and the significant public health threat posed by dengue in Bangladesh, necessitating a heightened focus on severe disease management.

Methodological Advantages of the Bayesian Approach

A key contribution of this study is the demonstration of the advantages offered by Bayesian meta-analysis over traditional frequentist methods in this context. While the frequentist meta-analysis produced prevalence of 33.7%, and heterogeneity of 0.0664, which is lower compared to our Bayesian technique. The frequentist approach is known to

underestimate both prevalence and heterogeneity with limited number of studies, as it does not fully account for the uncertainty in the estimation of between-study heterogeneity[23-24]. On the other hand, Bayesian methods treat heterogeneity as a random variable with its own prior distribution, provide a more accurate and reliable estimate of the true variation across studies[25-26]. This is critical problem for prevalence estimates, as underestimating heterogeneity can lead to overly precise (narrow) confidence intervals that may not capture the true range of possible values[27]. Our findings align with simulations and methodological reviews that encourage the use of Bayesian models for pooling proportions, especially when dealing with sparse data or substantial clinical diversity among studies[28-30].

The choice of prior is a primary consideration in Bayesian analysis. We implemented a tiered approach for selecting an appropriate prior from non-informative to strongly informative priors, to assess the sensitivity of our results. The high consistency across models suggested that the data were reliable. However, the strongly informative prior was derived from the meta-analysis of the data, which yielded the most precise estimate. This approach was similar to the methodological work from Reis et al. (2022), who also highlighted that while Bayesian models were sensitive to prior choice, using data-driven informative priors could enhance the stability and precision of the estimates without introducing significant bias[28, 30]. Our study operationalized this recommendation, demonstrating its practical utility in an epidemiological context.

Public Health Implications

This study estimated the high prevalence of severe dengue, which has profound implications for public health planning in Bangladesh. A prevalence of 33.9% suggeststhat a substantial number of patients requiring advanced clinical care, including careful treatment on fluid leakage, bleeding signs, monitoring for warning signs, and access to intensive care units. This finding strongly suggests that the current healthcare infrastructure of the country, which must be strengthened to manage this volume of severe cases during outbreaks[13].

Strengths and Limitations

The study has some notable strengths such as the comprehensive meta-analysis followed PRISMA guidelines, which minimized the risk of missing relevant studies. The use of a Bayesian random-effects model is a methodological strength, providing a more realistic estimate of both prevalence and heterogeneity, and allows for the incorporation of uncertainty in a way that frequentist methods cannot. However, this study was restricted to thecross-sectional studies, which might be subject to selection bias, particularly if they were hospital-based and mightoverrepresent severe cases. To address this limitation, we used standardized WHO/DGHS case definitions to improve consistency of the included studies.

V. Conclusion

Application of Bayesian method on estimating pooled prevalence of severe dengue is not only a unique study in Bangladesh but also worldwide. Due to limited number of studies and small sample size, the frequentist approach can provide misleading information. In such situations, Bayesian approach can provide more reliable and consistent estimates by incorporating prior knowledge. Bayesian approach is a powerful method for estimating posterior parameters by taking information from the prior distribution of the parameter, which is the main advantage over the frequentist approach. This study found that the frequentist meta-analysis underestimated the true pooled prevalence and heterogeneity estimate of severe dengue infection in Bangladesh, and further an accurate estimate was obtained from the Bayesian meta-analysis approach. These findings are crucial for national dengue surveillance strategies, enabling evidence-based resource allocation and capacity planning to address the growing burden of severe dengue manifestations.

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Conflict of interest

Authors do not have any conflict of interest.

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Appendix

Table A1. Critical Appraisal Checklist for Quality Assessment of Studies

S.N.	Studies to address	Criteria item and adopted score
Major criteria		
1	Inclusion of study participants – Whether case definition of severe dengue is mentioned?	1. DGHS/WHO case definition = 1 2. Fever case definition = 0.5 3. No case definition / Unclear = 0
2	Whether any sampling method for inclusion of patients is adopted in the study?	1. Included all/Systematically/Randomly = 1 2. Unknown / Unclear = 0
3	Measurement of disease condition	1. NS1/ IgM/RT-PCR = 1 2. IgG = 0.5 3. Unclear = 0
4	Whether total number of tested is mentioned in the paper?	1. Yes = 1 2. Unclear/No = 0
Minor criteria		
5	Whether age distribution of cases is given?	1. Both in tested and positive = 1 2. Only in tested or positive = 0.5 3. Not given / Unclear = 0
6	Whether study is not limited any specific setting?	1. Yes = 1 2. No = 0
7	Whether bleeding signs are reported?	1. Yes = 1 2. No = 1
Overall risk of bias assessment		
Quality	**Risk of bias**	**Criteria**
High	Low	All Major = 1 + (All Minor = 1 or Only One Minor = 0)
Moderate	Moderate	2 Major = 1 + At least One Minor = 1
Low	High	2 Major = 0 + Two Minor = 0
Very low	Very high	No Major = 1 + No Minor = 1

Table A2. Quality of the included cross-sectional studies for severe dengue infection in Bangladesh.

Study	Time period	Score	Quality
Ahsan et al., 2020[31]	July-October, 2018	6.5	High
Rahman et al., 2021[32]	May-September, 2019	6.5	High
Hoque et al., 2020[33]	July-October, 2018	6.5	High
Ismail et al., 2023[34]	April-October, 2022	6.5	High
Basak et al., 2014[35]	2005	6	High
Yesmin et al., 2023[36]	June-September, 2019	6.5	High
Rafi et al., 2020[37]	July-September, 2019	6.5	High
Akram et al., 2023[38]	June-November, 2019	6.5	High
Khan et al., 2021[39]	August-September, 2019	6.5	High
Islam et al., 2022[40]	June-September, 2019	6	High
Sami et al., 2022[41]	June-November, 2022	6.5	High
Mosleh et al., 2023[42]	July-December, 2021	6.5	High
Mobarak et al., 2017[43]	June-December, 2016	6.5	High
Azad et al., 2006[44]	July, 2000-March, 2001	6.5	High
Anika et al., 2024[45]	July-September, 2023	6.5	High
Khanduker et al., 2025[46]	June, 2019-October, 2020	6	High
Khan et al., 2025a[47]	August–December, 2023	6	High
Rahman et al., 2002[48]	July-October, 2000	5.5	Moderate
Rouf et al., 2020[49]	July, 2018-April, 2019	6.5	High
Sharmin et al., 2013[50]	January-December 2008	6.5	High
Rahman et al., 2019[51]	2017	5	Moderate
Ahmed et al., 2020[52]	July-December, 2019	6.5	High
Prattay et al., 2021[53]	July-August, 2019	6.5	High
Datta et al., 2021[54]	July-December, 2019	6.5	High
Islam et al., 2019[55]	January-November, 2018	6.5	High
Yang et al., 2022[56]	August-September, 2019	6.5	High
Islam et al., 2021[57]	July-December, 2019	6.5	High
Yasmin et al., 2020[58]	June-July, 2019	6	High
Parvin et al., 2021[59]	July-October, 2019	6.5	High
Rahim et al., 2021[60]	2017-2021	6.5	Moderate
Akter et al., 2021[61]	August, 2019-July, 2020	6	High
Tony et al., 2025[62]	2023	6.5	High
Wahiduzzaman et al., 2024[63]	January-August, 2023	6.5	High
Afroz et al., 2024[64]	July-September, 2023	6.5	High
Khan et al., 2025b[65]	July-December, 2024	6.5	High
Banu et al., 2025[66]	July-August, 2023	6.5	High
Uddin et al., 2014[67]	January, 2008-December, 2010	6.5	High
Chowdhury et al., 2024[68]	July-December, 2019	6.5	High
Pulock et al., 2025[69]	August-December, 2023	6.5	High
Hassan et al., 2025[70]	June-September, 2024	6.5	High
Mutanabbi et al., 2022[71]	April-September, 2019	7	High