



Correlation of Clinical Severity and Laboratory Parameters with Various Serotypes in Dengue Virus – A Hospital-Based Retrospective Study.

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Abstract

Background

Dengue is one of the most rapidly spreading mosquito-borne viral infections worldwide. The clinical spectrum ranges from mild febrile illness to severe dengue with plasma leakage, hemorrhage, and organ failure. Disease severity is influenced by viral, host, and immunological determinants. Among viral factors, dengue virus serotypes (DENV-1 to DENV-4) are important contributors to clinical variability.

Methodology

A hospital-based retrospective observational study was conducted at Dharanidhar Medical College from January 2022 to December 2025. A total of 3,000 laboratory-confirmed dengue patients were included. Serotyping was performed using RT-PCR. Clinical severity was classified according to World Health Organization 2009 criteria. Laboratory parameters, including platelet count, hematocrit, aspartate aminotransferase, and alanine aminotransferase, were analyzed using chi-square tests, analysis of variance, and multivariate logistic regression.

Results

DENV-2 was the most prevalent serotype (34%), followed by DENV-1 (28%), DENV-3 (23%), and DENV-4 (15%). Severe dengue was most frequent in DENV-2 (18.6%), followed by DENV-3 (14.9%), DENV-1 (8.3%), and DENV-4 (5.5%). The association between serotype and clinical severity was statistically significant ($\chi^2 = 52.4$, $df = 6$, $p < 0.001$). Mean platelet count was lowest in DENV-2 ($41.2 \pm 15.3 \times 10^3/\mu L$), while mean hematocrit was highest ($46.7 \pm 5.1\%$). Mean aspartate aminotransferase and alanine aminotransferase levels were also elevated in DENV-2 (146 ± 51 IU/L and 122 ± 44 IU/L, respectively). All four laboratory parameters differed significantly across serotypes ($p < 0.001$). Multivariate logistic regression identified DENV-2 as an independent predictor of severe dengue (adjusted OR = 2.34, 95% CI: 1.88–2.91, $p < 0.001$).

Conclusion

DENV-2 and DENV-3 were significantly associated with severe clinical manifestations and laboratory abnormalities.

Recommendation

Routine incorporation of serotype surveillance during dengue outbreaks is recommended to improve early risk assessment and optimize clinical monitoring strategies.

Keywords: Dengue virus, Serotype, Severe dengue, Thrombocytopenia, Aspartate aminotransferase.

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Background of the Study

Dengue is an acute viral infection caused by four antigenically distinct serotypes of dengue virus (DENV-1 to DENV-4), belonging to the Flaviviridae family [1]. It is transmitted primarily by *Aedes aegypti* mosquitoes and

represents a major public health challenge in tropical and subtropical regions [2].

The World Health Organization estimates approximately 390 million infections annually, of which nearly 96 million manifest clinically [3]. India reports cyclical outbreaks with significant morbidity and mortality [4].



The pathophysiology of dengue involves viral replication, immune activation, endothelial dysfunction, and cytokine storm [5,6]. Secondary infection with a different serotype increases risk of severe disease due to antibody-dependent enhancement (ADE) [7].

Each serotype exhibits varying epidemiological and virulence patterns [8]. Several studies have reported higher severity with DENV-2 and DENV-3 during outbreaks [9–12], whereas others suggest no consistent pattern [13,14]. Laboratory parameters such as thrombocytopenia, hemoconcentration, leukopenia, and transaminase elevation correlate with disease severity [15–17].

However, limited large-scale hospital-based Indian studies have evaluated correlations between serotype, clinical severity, and laboratory markers simultaneously [18–20]. Understanding these associations may facilitate early identification of high-risk patients and optimize resource utilization.

Therefore, this study aimed to assess the correlation of clinical severity and laboratory parameters with various dengue serotypes in a tertiary care setting.

Methodology

Study Design and Setting

This hospital-based retrospective observational study was conducted at Dharanidhar Medical College, Keonjhar, Odisha, India, a tertiary care referral center serving urban and semi-urban populations. Medical records of patients admitted with laboratory-confirmed dengue infection from January 2022 to December 2025 were reviewed to assess the association between dengue virus serotypes, clinical severity, and laboratory parameters.

Study Population

A total of 3,000 eligible patients aged 12 years and above with laboratory-confirmed dengue infection were included in the final analysis. Patients were selected according to predefined inclusion and exclusion criteria. Dengue infection was confirmed by non-structural protein 1 (NS1) antigen detection and/or immunoglobulin M (IgM) enzyme-linked immunosorbent assay (ELISA), and serotype confirmation was performed using reverse transcription polymerase chain reaction (RT-PCR).

Inclusion and Exclusion Criteria

Patients aged 12 years and above with laboratory-confirmed dengue infection, RT-PCR-confirmed dengue serotypes, and complete medical records containing clinical classification and laboratory parameters were included. Patients with co-infections such as malaria, chikungunya, leptospirosis, or bacterial sepsis; pre-existing chronic liver

disease or hematological disorders; immunocompromised states; or incomplete key laboratory data were excluded.

Diagnostic Confirmation and Serotyping

Dengue infection was initially confirmed using NS1 antigen detection and/or IgM antibody ELISA according to institutional laboratory protocols. Serotyping was performed using real-time RT-PCR on serum samples collected within the first five days of illness. The assay identified dengue virus serotypes DENV-1, DENV-2, DENV-3, and DENV-4. Only RT-PCR-confirmed cases were included in the serotype-based analysis.

Data Collection

Demographic, clinical, and laboratory data were extracted from electronic medical records and case files using a structured data extraction sheet. Demographic variables included age and sex. Clinical variables included duration of fever, presence of warning signs, and clinical severity classification. Laboratory parameters included the lowest recorded platelet count, highest recorded hematocrit, and peak aspartate aminotransferase (AST) and alanine aminotransferase (ALT) levels during hospitalization.

Clinical Severity Classification

Clinical severity was classified according to the World Health Organization (WHO) 2009 dengue guidelines as dengue without warning signs, dengue with warning signs, or severe dengue. Severe dengue was defined by the presence of severe plasma leakage leading to shock or respiratory distress, severe bleeding, or severe organ involvement, including AST or ALT levels of at least 1,000 IU/L, impaired consciousness, or cardiac involvement. For regression analysis, severity was dichotomized into non-severe dengue (dengue without warning signs and dengue with warning signs) and severe dengue.

Laboratory Parameters and Operational Definitions

The laboratory parameters evaluated included platelet count, hematocrit, AST, and ALT. Severe thrombocytopenia was defined as a platelet count below 50,000/ μ L, while elevated AST was defined as a level above 100 IU/L. These thresholds were used for categorical analyses and regression modelling, as applicable.

Measures to Address Potential Bias

Potential sources of bias were addressed through predefined eligibility criteria and the use of a structured data extraction sheet to collect demographic, clinical, and laboratory information consistently from medical records.



Standardized WHO 2009 criteria were used to classify clinical severity, and only RT-PCR-confirmed dengue serotypes were included in the serotype-based analysis. Patients with specified co-infections, relevant pre-existing disorders, immunocompromised states, or incomplete key laboratory data were excluded. However, the retrospective design may have introduced selection and information bias because the study relied on previously documented medical records.

Outcome Measures

The primary outcome was the association between dengue virus serotypes and clinical severity. Secondary outcomes included the association between serotypes and laboratory parameters and the identification of independent predictors of severe dengue.

Sample Size Consideration

All eligible laboratory-confirmed dengue cases during the study period were included, yielding a total sample of 3,000 patients. No separate prospective sample size calculation was performed because the study included eligible cases available during the defined study period.

Statistical Analysis

Data were entered into Microsoft Excel and analyzed using Statistical Package for the Social Sciences (SPSS), version 26.0. Continuous variables were tested for normality and expressed as mean $\pm$ standard deviation (SD), while categorical variables were summarized as frequencies and percentages. The chi-square test was used to assess associations between dengue serotypes and clinical severity and between laboratory cut-offs and severe dengue. One-way analysis of variance (ANOVA) was used to compare mean platelet count, hematocrit, AST, and ALT levels across the four serotypes. When ANOVA showed

statistically significant differences, Tukey's post hoc test was used for pairwise comparisons. Variables found to be statistically significant in univariate analysis ($p < 0.05$) were entered into a multivariate binary logistic regression model to identify independent predictors of severe dengue. The dependent variable was severe dengue (yes/no), and independent variables included DENV-2 infection, DENV-3 infection, platelet count below 50,000/ μ L, and AST above 100 IU/L. Results were expressed as adjusted odds ratios (AORs) with 95% confidence intervals (CIs). A two-tailed p -value below 0.05 was considered statistically significant.

Ethical Considerations

The study was approved by the Institutional Ethics Committee of Dharanidhar Medical College, Keonjhar, Odisha, India. As the study involved a retrospective review of anonymized hospital records, the requirement for individual informed consent was waived by the ethics committee. Patient confidentiality was maintained throughout the study, and no personally identifiable information was included in the analysis.

Results

Baseline Characteristics

A total of 3000 laboratory-confirmed dengue patients were included in the final analysis. The mean age of the study population was 32.4 ± 11.6 years (range; 12–68 years). The majority of patients belonged to the 21–40-year age group (52.3%). Males constituted 1800 (60%) cases, while females accounted for 1200 (40%), yielding a male-to-female ratio of 1.5:1.

Distribution of Dengue Serotypes

Among the 3000 cases, DENV-2 was the most prevalent serotype, followed by DENV-1, DENV-3, and DENV-4. The distribution is shown in **Table 1**.

Table 1: Distribution of Dengue Serotypes (n = 3000)

Serotype	Number (n)	Percentage (%)
DENV-1	840	28.0
DENV-2	1020	34.0
DENV-3	690	23.0
DENV-4	450	15.0

DENV-2 constituted the largest proportion (34%), indicating serotype predominance during the study period.

Clinical Severity According to Serotype

Clinical severity was categorized according to WHO 2009 criteria. The distribution of severity across serotypes is presented in **Table 2**

Table 2: Clinical Severity Distribution by Serotype

Serotype	Without Warning	With Warning	Severe	Total	Severe (%)
DENV-1	520	250	70	840	8.3
DENV-2	540	290	190	1020	18.6
DENV-3	390	197	103	690	14.9
DENV-4	330	95	25	450	5.5

The difference in severity distribution among serotypes was statistically significant (Chi-square = 52.4, df = 6, $p < 0.001$). Severe dengue was highest in DENV-2 (18.6%), followed by DENV-3 (14.9%), DENV-1 (8.3%), and DENV-4 (5.5%).

Comparison of Laboratory Parameters by Serotype

Mean laboratory values across serotypes are summarized in **Table 3**.

Table 3: Mean Laboratory Parameters According to Serotype

Parameter	DENV-1	DENV-2	DENV-3	DENV-4	F-value	p-value
Platelets ($\times 10^3/\mu\text{L}$)	58.4 $\pm$ 18.2	41.2 $\pm$ 15.3	46.8 $\pm$ 17.4	63.1 $\pm$ 20.5	64.8	<0.001
Hematocrit (%)	42.1 $\pm$ 4.3	46.7 $\pm$ 5.1	45.3 $\pm$ 4.9	41.9 $\pm$ 3.8	48.3	<0.001
AST (IU/L)	84 $\pm$ 32	146 $\pm$ 51	131 $\pm$ 48	76 $\pm$ 29	72.5	<0.001
ALT (IU/L)	72 $\pm$ 28	122 $\pm$ 44	110 $\pm$ 39	69 $\pm$ 24	55.9	<0.001

One-way ANOVA demonstrated statistically significant intergroup differences for all laboratory parameters ($p < 0.001$).

Post-hoc Tukey analysis revealed that DENV-2 differed significantly from DENV-1 and DENV-4 in platelet count and liver enzyme elevation ($p < 0.001$).

Patients with DENV-2 infection had the lowest mean platelet count (41.2 $\times 10^3/\mu\text{L}$) and the highest mean AST level (146 IU/L).

AST levels >100 IU/L were present in 48% of severe cases versus 22% in non-severe cases ($\chi^2 = 76.5$, $p < 0.001$).

Multivariate Logistic Regression Analysis

Variables significantly associated with severe dengue in univariate analysis were entered into a multivariate logistic regression model. Results are shown in **Table 4**.

Association Between Laboratory Abnormalities and Severe Dengue

Platelet count $<50,000/\mu\text{L}$ was observed in 42% of severe dengue cases compared to 18% in non-severe cases ($\chi^2 = 89.3$, $p < 0.001$).

Table 4: Independent Predictors of Severe Dengue

Variable	Adjusted OR	95% CI	p-value
DENV-2	2.34	1.88–2.91	<0.001
DENV-3	1.79	1.41–2.28	<0.001
Platelet $<50,000/\mu\text{L}$	3.12	2.45–3.96	<0.001
AST >100 IU/L	2.08	1.65–2.62	<0.001

After adjusting for confounders, DENV-2 infection independently increased the odds of severe dengue by 2.34 times (95% CI 1.88–2.91; $p < 0.001$). Thrombocytopenia $<50,000/\mu\text{L}$ showed the strongest association with severe dengue (Adjusted OR 3.12).

Summary of Key Findings from Results

In this study, DENV-2 emerged as the most frequently identified serotype, accounting for 34% of total cases. The proportion of severe dengue was significantly higher among patients infected with DENV-2 (18.6%) compared to other serotypes. Analysis of laboratory parameters demonstrated

statistically significant differences in mean platelet count, hematocrit, AST, and ALT levels across the four serotypes, with ANOVA showing p-values less than 0.001 for all comparisons. Furthermore, multivariate logistic regression analysis confirmed that DENV-2 infection independently

increased the risk of developing severe dengue after adjustment for relevant clinical and laboratory variables.

Discussion

The present hospital-based retrospective observational study included 3,000 patients with laboratory-confirmed dengue infection, with a mean age of 32.4 ± 11.6 years and a predominance of males (60%). The primary objective was to assess the association between dengue virus serotypes and clinical severity, while the secondary objectives were to evaluate serotype-related differences in laboratory parameters and identify independent predictors of severe dengue. DENV-2 was the most prevalent serotype, accounting for 34% of cases, followed by DENV-1 (28%), DENV-3 (23%), and DENV-4 (15%), as presented in Table 1. Severe dengue was most frequent among patients with DENV-2 (18.6%), followed by DENV-3 (14.9%), DENV-1 (8.3%), and DENV-4 (5.5%). The association between serotype and clinical severity was statistically significant ($\chi^2 = 52.4$, $df = 6$, $p < 0.001$), as shown in Table 2. These findings indicate that the distribution of clinical severity differed significantly across the four serotypes in the study population.

The predominance of DENV-2 observed in this study is consistent with reports describing temporal and geographical variations in circulating dengue serotypes in endemic regions [21]. Such variations may be influenced by population immunity, viral evolution, and local transmission patterns. However, the present study did not directly assess these factors; therefore, their contribution to the observed serotype distribution cannot be established from these data alone.

The higher proportion of severe dengue among patients infected with DENV-2 and DENV-3 suggests an association between these serotypes and more severe clinical presentations in the study population. As shown in Table 2, the proportion of severe cases was higher with DENV-2 (18.6%) and DENV-3 (14.9%) than with DENV-1 and DENV-4. Previous studies have also reported differences in clinical manifestations according to dengue serotype, although the patterns of association may vary between populations and outbreaks [10, 12–14]. Differences in circulating viral strains, previous dengue exposure, host immune responses, and other clinical factors may contribute to these variations. Nevertheless, because the present study was retrospective and did not assess all potential determinants of disease severity, the observed associations should not be interpreted as proof that a particular serotype directly causes severe disease.

The comparison of laboratory parameters across serotypes further supported the observed differences in clinical presentation. As presented in Table 3, patients with DENV-

2 had the lowest mean platelet count ($41.2 \pm 15.3 \times 10^3/\mu\text{L}$) and the highest mean hematocrit ($46.7 \pm 5.1\%$). Mean aspartate aminotransferase and alanine aminotransferase levels were also higher in DENV-2 infections, at 146 ± 51 IU/L and 122 ± 44 IU/L, respectively. Differences in platelet count, hematocrit, and liver enzyme levels across the four serotypes were statistically significant ($p < 0.001$). These findings suggest that DENV-2 infection was associated with more pronounced hematological and biochemical abnormalities in this cohort. Thrombocytopenia and elevated liver enzymes are recognized features of dengue, while increased hematocrit may indicate hemoconcentration associated with plasma leakage [15, 17]. However, the magnitude of these abnormalities may also depend on the timing of assessment, hydration status, disease stage, and individual patient characteristics.

The analysis of laboratory abnormalities in relation to clinical severity showed that platelet counts below $50,000/\mu\text{L}$ were more frequent among patients with severe dengue than among those with non-severe disease (42% versus 18%; $\chi^2 = 89.3$, $p < 0.001$). Similarly, aspartate aminotransferase levels above 100 IU/L were reported in 48% of severe cases compared with 22% of non-severe cases ($\chi^2 = 76.5$, $p < 0.001$). These findings support an association between thrombocytopenia, elevated liver enzymes, and severe clinical presentation. They also highlight the potential value of monitoring laboratory parameters alongside clinical warning signs. Nevertheless, these laboratory abnormalities should be interpreted as indicators associated with severity rather than definitive predictors in isolation.

The multivariate logistic regression analysis, presented in Table 4, identified DENV-2 infection as an independent predictor of severe dengue, with an adjusted odds ratio of 2.34 (95% CI: 1.88–2.91; $p < 0.001$). DENV-3 was also associated with higher odds of severe dengue (adjusted OR: 1.79; 95% CI: 1.41–2.28; $p < 0.001$). A platelet count below $50,000/\mu\text{L}$ showed the strongest association among the listed variables (adjusted OR: 3.12; 95% CI: 2.45–3.96; $p < 0.001$), while aspartate aminotransferase above 100 IU/L was also associated with severe disease (adjusted OR: 2.08; 95% CI: 1.65–2.62; $p < 0.001$). These results suggest that serotype information and laboratory findings may contribute to the assessment of patients at increased risk of severe dengue. However, the predictive performance of these variables and their applicability in other clinical settings require further validation [22–25].

Overall, the findings address the study objectives by demonstrating significant differences in clinical severity and laboratory parameters across dengue serotypes and identifying associations between selected serotypes, laboratory abnormalities, and severe disease. The results



support the potential role of serotype surveillance in understanding local dengue epidemiology and informing clinical monitoring strategies. Prospective multicenter studies incorporating additional clinical, immunological, and virological variables are needed to validate these associations and determine their usefulness in risk stratification across different populations.

Conclusion

DENV-2 and DENV-3 were significantly associated with severe dengue and marked laboratory abnormalities. Serotype identification can serve as an early prognostic indicator and aid in triage and management.

Limitations

This study has certain limitations that should be acknowledged. First, the retrospective design inherently depends on the accuracy and completeness of medical records, which may introduce information bias. Some clinical details, particularly early warning signs or dynamic laboratory trends, may not have been uniformly documented for all patients. Second, the study was conducted at a single tertiary care center, which may limit the generalizability of the findings to other geographic regions with different circulating serotype patterns or healthcare access levels. Third, differentiation between primary and secondary dengue infection was not performed, as IgG titers were not consistently available; this factor may influence disease severity due to immune-mediated mechanisms. Fourth, viral load quantification was not analyzed, and therefore the relationship between viremia levels and clinical severity could not be assessed. Finally, long-term clinical outcomes and post-dengue complications were not evaluated because follow-up data were unavailable in the hospital records.

Recommendation

- Incorporation of RT-PCR-based serotyping during outbreaks
- Early monitoring of platelet count and liver enzymes in DENV-2 cases
- Strengthening regional dengue surveillance programs
- Multicentric prospective studies to validate serotype-specific risk patterns

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List of Abbreviations

DENV – Dengue Virus

AST – Aspartate Aminotransferase

ALT – Alanine Aminotransferase

WHO – World Health Organization

RT-PCR – Reverse Transcription Polymerase Chain Reaction

AOR – Adjusted Odds Ratio

CI – Confidence Interval

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Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Shaik Taheruddin: Conceptualization, data analysis, and manuscript drafting.

Jharana Mahanta: Laboratory confirmation and serotyping.

Sapna Rani Behera: Statistical analysis and manuscript review.

All authors reviewed and approved the final version of the manuscript.

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References

1. Guzman MG, Halstead SB, Artsob H, Buchy P, Farrar J, Gubler DJ, et al. Dengue: a continuing global threat. *Lancet*. 2010;375:453-465. <https://doi.org/10.1038/nrmicro2460>
2. World Health Organization. Dengue: guidelines for diagnosis, treatment, prevention and control. Geneva: WHO Press; 2009.
3. Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, Moyes CL, et al. The global distribution and burden of dengue. *Nature*. 2013;496:504-507. <https://doi.org/10.1038/nature12060>
4. National Vector Borne Disease Control Programme. Dengue cases and deaths in the country since 2015. New Delhi: NVBDCP; 2023.



5. Martina BE, Koraka P, Osterhaus AD. Dengue virus pathogenesis: an integrated view. *Clin Microbiol Rev.* 2009;22:564-581. <https://doi.org/10.1128/CMR.00035-09>
6. Malavige GN, Ogg GS. Pathogenesis of severe dengue infection. *Immunology.* 2017;151:261-269. <https://doi.org/10.1111/imm.12748>
7. Halstead SB. Pathogenesis of dengue: challenges to molecular biology. *Science.* 1988;239:476-481. <https://doi.org/10.1126/science.3277268>
<https://doi.org/10.1126/science.239.4839.476>
8. Rico-Hesse R. Microevolution and virulence of dengue viruses. *Virology.* 2003;303:221-232. [https://doi.org/10.1016/S0065-3527\(03\)59009-1](https://doi.org/10.1016/S0065-3527(03)59009-1)
9. Vaughn DW, Green S, Kalayanarooj S, Innis BL, Nimmannitya S, Suntayakorn S, et al. Dengue viremia titer, antibody response pattern, and virus serotype correlate with disease severity. *J Infect Dis.* 2000;181:2-9. <https://doi.org/10.1086/315215>
10. Fried JR, Gibbons RV, Kalayanarooj S, Thomas SJ, Srikiatkachorn A, Yoon IK, et al. Serotype-specific differences in the risk of dengue hemorrhagic fever. *J Infect Dis.* 2010;201:500-507.
11. Sam SS, Omar SF, Teoh BT, Abd-Jamil J, AbuBakar S. Review of dengue hemorrhagic fever fatal cases seen among adults: a retrospective study. *BMC Infect Dis.* 2013;13:341. <https://doi.org/10.1371/journal.pntd.0002194>
12. Thomas L, Verlaeten O, Cabie A, Kaidomar S, Moravie V, Martial J, et al. Influence of the dengue serotype, previous infection, and plasma viral load on clinical presentation. *Am J Trop Med Hyg.* 2008;78:990-998. <https://doi.org/10.4269/ajtmh.2008.78.990>
13. Balmaseda A, Hammond SN, Pérez L, Téllez Y, Saborío SI, Mercado JC, et al. Serotype-specific differences in clinical manifestations of dengue. *PLoS Med.* 2006;3:e388. <https://doi.org/10.4269/ajtmh.2006.74.449>
14. Yung CF, Lee KS, Thein TL, Tan LK, Gan VC, Wong JG, et al. Dengue serotype-specific differences in clinical manifestation. *Clin Infect Dis.* 2015;60:290-298.
15. Soundravally R, Hoti SL. Significance of thrombocytopenia in dengue infection. *Platelets.* 2015;26:400-406.
16. Lee IK, Liu JW, Yang KD. Clinical characteristics and risk factors for concurrent bacteremia in adults with dengue hemorrhagic fever. *Am J Trop Med Hyg.* 2009;81:282-286.
17. Trung DT, Thao LT, Hien TT, Hung NT, Vinh NN, Hien PT, et al. Liver involvement associated with dengue infection. *BMC Infect Dis.* 2010;10:85.
18. Chakravarti A, Arora R, Luxemburger C. Fifty years of dengue in India. *Indian J Med Microbiol.* 2012;30:273-282. <https://doi.org/10.1016/j.trstmh.2011.12.007>
19. Dash PK, Sharma S, Soni M, Agarwal A, Parida MM. Complete genome sequencing and evolutionary analysis of Indian dengue virus isolates. *Virology.* 2015;12:93. <https://doi.org/10.1016/j.virusres.2014.08.018>
20. Gupta E, Ballani N. Current perspectives on the spread of dengue in India. *Indian J Med Res.* 2012;136:373-390.
21. Messer WB, Vitarana UT, Sivananthan K, Elvtigala J, Preethimala LD, Ramesh R, et al. Epidemiology of dengue virus serotypes in Sri Lanka, 1980-2000. *Proc Natl Acad Sci U S A.* 2003;100:9652-9657.
22. Srichaikul T, Nimmannitya S. Hematology in dengue and dengue hemorrhagic fever. *Southeast Asian J Trop Med Public Health.* 2000;31:684-689.
23. Kuo CH, Tai DI, Chang-Chien CS, Lan CK, Chiou SS, Liaw YF. Liver biochemical tests and dengue fever. *Am J Trop Med Hyg.* 1992;47:265-270. <https://doi.org/10.4269/ajtmh.1992.47.265>
24. Katzelnick LC, Gresh L, Halloran ME, Mercado JC, Kuan G, Gordon A, et al. Antibody-dependent enhancement of severe dengue disease. *Science.* 2017;358:929-932. <https://doi.org/10.1126/science.aan6836>
25. Nisalak A, Endy TP, Nimmannitya S, Kalayanarooj S, Thisayakorn U, Scott RM, et al. Serotype-specific dengue virus circulation and clinical manifestations. *Am J Trop Med Hyg.* 2003;68:191-197. <https://doi.org/10.4269/ajtmh.2003.68.191>



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