



Diagnostic Utility of RT LAMP Compared to Real Time RT PCR in Dengue Virus Serotype Identification at a Tertiary Care Hospital of Chattogram District of Bangladesh

Tabassuma Rahman¹, Pompy Dey², Ayesha Ahmed Khan³, Nishad Sultana⁴, Masuma Jannat⁵,
Tazrina Rahman⁶, Nusrat Fatema⁷

¹Medical Officer, Seba Hospital, Chattogram, Bangladesh; ²Lecturer, Department of Microbiology, Rangamati Medical College, Rangamati, Bangladesh; ³Assistant Professor, Department of Microbiology, Institute of Applied Health Sciences, Chattogram, Bangladesh; ⁴Lecturer, Department of Dental Public Health, Chittagong Medical College, Dental Unit, Chattogram, Bangladesh; ⁵Lecturer, Department of Forensic Medicine, Noakhali Medical College, Noakhali, Bangladesh; ⁶M. Phil. Student, Department of Microbiology, Department of Microbiology, Chittagong Medical College, Chattogram, Bangladesh; ⁷Associate Professor, Department of Virology, Chittagong Medical College, Chattogram, Bangladesh

Abstract

Background: Dengue virus (DENV) remains the most prevalent arbovirus globally, with rising incidence in tropical and subtropical regions. Its expanding geographical distribution and increasing disease severity highlight the need for early and accurate diagnosis. Rapid detection during the febrile phase is crucial to guide clinical management and prevent complications. While real-time reverse transcription polymerase chain reaction (RT-qPCR) is the gold standard for molecular detection, its limited availability in resource-constrained settings necessitates alternative methods. **Objective:** This study was evaluated the diagnostic performance of reverse transcription loop-mediated isothermal amplification (RT-LAMP) for DENV serotyping, compared with RT-qPCR. **Methodology:** This cross-sectional study was conducted in the Department of Microbiology at Chittagong Medical College, Bangladesh, from July 2023 to June 2024. Two hundred patients with clinically suspected dengue were recruited. Initial screening used an immunochromatographic test (ICT) for NS1 antigen; NS1-negative cases were further tested for anti-dengue IgM and IgG antibodies. Samples positive by NS1, IgM, or both were subjected to RT-qPCR and RT-LAMP for DENV serotyping. RT-qPCR served as the reference standard. **Results:** Of 200 suspected cases, 142 were ICT-positive. RT-qPCR confirmed DENV in 138 samples, while RT-LAMP detected 136 of these. Two RT-qPCR-positive samples were missed by RT-LAMP, and four were negative by both methods. RT-LAMP showed a sensitivity of 98.55%, specificity of 100%, positive predictive value of 100%, negative predictive value of 66.67%, and diagnostic accuracy of 98.59%. Receiver operating characteristic analysis showed an area under the curve (AUC) of 0.993 (95% CI: 0.980–1.000; $p = 0.001$), indicating excellent diagnostic capability. **Conclusion:** RT-LAMP offers a rapid, affordable, and reliable alternative to RT-qPCR for early DENV detection and serotyping. Its simplicity and minimal equipment requirements make it especially valuable in dengue-endemic and resource-limited settings, as well as during outbreaks.

Keywords: DENV, Dengue Serotyping, RT-LAMP, RT-qPCR

Bangladesh Journal of Medical Microbiology, July 2025; 19 (2): 100-106

Introduction

Dengue virus (DENV), a mosquito-borne RNA virus of the Flavivirus genus, is a growing global health

concern. It comprises four well-established serotypes (DENV-1 to DENV-4), with a potential fifth (DENV-5) reported in Malaysia in 2013^{1,2}. Each serotype contains multiple genotypes, contributing to complex regional transmission patterns¹. Dengue incidence has risen sharply over the past two decades, now affecting over 100 countries across multiple continents³. Due to underreporting and mild or asymptomatic cases, the true disease burden remains

Correspondence: Dr. Tabassuma Rahman, Medical Officer, Seba Hospital, Chattogram, Bangladesh; Email: bushrarahman222@gmail.com; Cell no: +8801919-809999
ORCID: <https://orcid.org/0009-0008-8507-459X>;
©Authors 2025. CC-BY-NC
DOI: <https://doi.org/10.3329/bjmm.v19i2.85447>

underestimated⁴. Reported cases increased tenfold from 2000 to 2019, with 5.2 million cases in 2019 and continued surges in 2023, resulting in approximately 5,000 deaths across 80 countries⁴.

Bangladesh remains highly endemic, with seasonal outbreaks intensified by rapid urbanization, climate change, and poor vector control⁵⁻⁷. Major cities such as Dhaka and Chattogram are particularly affected⁸. Since the first major outbreak in 2000, the country has faced recurring epidemics, with over 308,000 cases and nearly 1,600 deaths reported in 2023 alone³. DENV-3 dominated the 2000 outbreak, followed by shifts toward DENV-1 and DENV-2, with the latter re-emerging as the predominant strain in 2023, linked to increased disease severity^{9,10}. While primary infection confers lifelong immunity to the same serotype, secondary infection with a different serotype may lead to severe disease due to antibody-dependent enhancement^{11,12}, highlighting the need for timely and accurate serotype-specific diagnostics.

Diagnostic approaches include NS1 antigen detection, serology (IgM/IgG), and molecular methods. Although RT-qPCR is the gold standard for early detection and serotyping¹³, its reliance on costly equipment and skilled personnel limits accessibility in low-resource settings. Virus isolation is impractical, and NS1/serology tests have limitations in sensitivity and timing¹⁴. Loop-mediated isothermal amplification (LAMP) offers a rapid, sensitive, and low-cost molecular alternative. RT-LAMP enables detection of viral RNA under isothermal conditions with minimal instrumentation, yielding results within an hour¹⁵. Its utility for point-of-care diagnosis has been demonstrated for various pathogens, including DENV¹³.

Given Bangladesh's recurrent dengue outbreaks and limited molecular diagnostic capacity, this study aimed to evaluate the performance of RT-LAMP in comparison to RT-qPCR for DENV serotyping during the 2023 outbreak in Chattogram.

Methodology

Study Settings and Population: This was a cross-sectional study done among clinically suspected dengue patients in the Department of Microbiology at Chittagong Medical College (CMC), Chattogram, Bangladesh from July 2023 to June 2024 for a period of one year. Suspected dengue patients attending the outpatient department and those admitted to the in-patient departments (Medicine, Paediatrics, and Dengue wards) of Chittagong Medical College

Hospital (CMCH). A purposive sampling technique was used to recruit study participants and a total of 200 clinically suspected dengue patients were enrolled in the study. Patients with clinically suspected dengue, as per WHO 2009 dengue case classification, were included and diagnosed cases of febrile illness other than dengue were excluded. As per WHO 2009 modified dengue case classification¹⁶ individuals with a recent travel/residency in dengue-endemic areas, fever of 2–7 days, and at least two of the following: nausea, vomiting, rash, aches, positive tourniquet test, leucopenia, or any warning signs.

Study Procedure: After proper counseling and informed written consent, 3 mL of venous blood was collected aseptically using a red-top vacutainer tube. Intravenous blood was taken following standard venipuncture protocol¹⁷. Each sample was anonymized with a unique ID. Blood samples were allowed to clot, then centrifuged at 3,000–5,000 rpm for 10–15 minutes to separate serum. Serum was aliquoted into two RNase-free 1.5 mL Micro-centrifuge tubes. One tube of the processed serum was used for NS1 and IgM/IgG testing, another tube was used for RT-qPCR and RT-LAMP assays. Following NS1 and IgM/IgG testing, serum samples were stored at -80°C until RNA extraction, RT-qPCR, and RT-LAMP procedures were performed.

Laboratory Procedure: Dengue NS1 antigen was detected using an immunochromatographic test (ICT) with a commercially available Bioline™ Dengue NS1 Ag kit (Korea), following manufacturer's instructions. Detection of dengue-specific IgM and IgG antibodies was performed using Bioline Dengue Duo (Korea) ICT kits.

RNA Extraction: Viral RNA was extracted from 142 serum samples positive for either NS1 or IgM/IgG, using the PureLink™ Viral RNA/DNA Mini Kit (Invitrogen, Thermo Fisher Scientific) as per manufacturer protocol. Serum samples were thawed and centrifuged at 4,000 rpm for 10 minutes to remove debris.

RT-qPCR for Dengue Virus Detection: Dengue viral RNA was amplified using a commercial Bosphore dengue virus real Time RT-PCR Detection Kit (Anatolia geneworks, Turkey). Amplification was performed in a QuantStudio 5 Real-Time PCR system. Each reaction included extracted RNA template, master mix, and specific primers/probes. Thermal cycling conditions followed manufacturer guidelines. **RT-LAMP Assay for Dengue Virus Detection:** RT-LAMP was performed on RNA extracted from the

Table 1: Sequences of RT-LAMP Primers Used in this Study

Virus serotype	Target (genome position)	Primer	Sequence (5'→ 3')
DEN-1	10469–10667 (199 bp)	F3	GAGGCTGCAAACCATGGAA
		B3	CAGCAGGATCTCTGGTCTCT
		FIP	GCTGCGTTGTGTCTTGGGAGGTTTTCTGTACGCATGGGGTAGC
		BIP	CCCAACACCAGGGGAAGCTGTTTTTTTTGTTGTTGTGCGGGGG
		FLP	CTCCTCTAACCCTAGTC
		BLP	GGTGGTAAGGACTAGAGG
DEN-2	10449–10659 (211 bp)	F3	TGGAAGCTGTACGCATGG
		B3	GTGCCTGGAATGATGCTG
		FIP	TTGGGCCCCATTGTTGCTGTTTTAGTGGACTAGCGGTTAGAGG
		BIP	GGTTAGAGGAGACCCCCCAATTTGGAGACAGCAGGATCTCTGG
		FLP	GATCTGTAAGGGAGGGG
		BLP	GCATATTGACGCTGGGA
DEN-3	10289–10506 (218 bp)	F3	GCCACCTTAAGCCACAGTA
		B3	GTTGTGTCATGGGAGGG
		FIP	TGGCTTTTGGGCTGACTTCTTTTTTTGAAGAAGCTGTGCAGCCTG
		BIP	CTGTAGCTCCGTCGTGGGGATTTCTAGTCTGCTACACCGTGC
		FLP	CCTTGGACGGGGCT
		BLP	GGAGGCTGCAAACCGTG
DEN-4	10289–10517 (229 bp)	F3	CTATTGAAGTCAGGCCAC
		B3	ACCTCTAGTCCTTCCACC
		FIP	TGGGAATTATAACGCCTCCCGTTTTTTCCACGGCTTGAGCAAACC
		BIP	GGTTAGAGGAGACCCCTCCCTTTTAGCTTCCTCCTGGCTTCG
		FLP	GGCGGAGCTACAGGCAG
		BLP	TCACCAACAAAACGCAG

same 142 samples using serotype-specific primers(Macrogen, Korea) designed based on 3' untranslated region (UTR)13 of the DENV genome. targeting the DENV genome. 25µl reaction mix was prepared by adding 12.5µL of master mix (WarmStart Colorimetric RT-LAMP 2X Master Mix with UDG, New England Biolab), 1 µL of extracted RNA, 2.5 µL of RT-LAMP primer mix (Macrogen, Korea), 9 µL of nuclease free water. Reactions were incubated at 63°C for 60 minutes and visualized by color change or turbidity.

Statistical Analysis: Data were analyzed using SPSS version 25. Descriptive statistics (mean, standard deviation, frequency, and percentage) were calculated. Chi square test and ROC analysis was done to detect the Sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) of RT-LAMP by using RT-qPCR as the gold standard.

Ethical Consideration: Ethical approval was obtained from the Ethical Review Committee of Chittagong Medical College (Memo no: 59.27.0000.013.19. PG.009.2023/1005, dated 02.10.2023). Written informed consent was obtained from all participants or guardians of minors, following the Declaration of

Helsinki, Good Clinical Practice guidelines, and national regulations. Study aims and procedures were explained in Bengali or the local language.

Results

Among 200 suspected dengue patients, 106(53.0%) were positive for dengue NS1. Of 94 patients tested further, 32(34.0%) were IgM positive, and 4(4.2%) were positive for both IgM and IgG. Additionally, 23 (24.0%) showed IgG positivity alone. A total of 165 patients had at least one positive test. Based on CDC guidelines, 142 cases were identified as recent dengue infections (positive for NS1 and/or IgM). (Table 2)

Table 2: ICT Test Result for Dengue NS1 and Dengue IgM, IgG (N=200)

Number of patients, n	Dengue NS1	Dengue IgM	Dengue IgG
106	Positive	Not done	Not done
4	Negative	Positive	Positive
32	Negative	Positive	Negative
23	Negative	Negative	Positive
35	Negative	Negative	Negative
200	Total		

Of the 142 confirmed dengue cases, RT-qPCR detected 138 (97.2%) while RT-LAMP detected 136 (95.8%). Two samples were positive by RT-qPCR but negative by RT-LAMP. Four samples were negative by both assays. The difference was statistically significant ($p < 0.0001$) (Table 3).

Table 3: Type Specific RT-qPCR and RT-LAMP Assay for Dengue Serotyping (n=142)

Test name	RT-qPCR positive	RT-qPCR negative	Total	P value
RT-LAMP positive	136 (95.77%)	0 (0.0%)	136 (95.77%)	
RT-LAMP negative	2 (1.40%)	4 (2.81%)	6 (4.23%)	<0.0001
Total	138 (97.18%)	4 (2.81%)	142 (100.0%)	

Note: 142 serum samples, that were classified as recent dengue virus infection, were tested by both RT-qPCR, and RT-LAMP assay; Positive = detected; Negative =undetected; p-value <0.0001 which is statistically significant [Chi-square test done (level of significance ≤ 0.05)

ROC curve analysis revealed that RT-LAMP had a sensitivity of 98.5%, specificity of 100%, PPV of 100.0%, and NPV of 66.7%, with an overall accuracy of 98.59%. The AUC was 0.993 (95% CI: 0.980–1.000; $p = 0.001$), indicating excellent diagnostic performance compared to RT-qPCR (Figure I, Table 4).

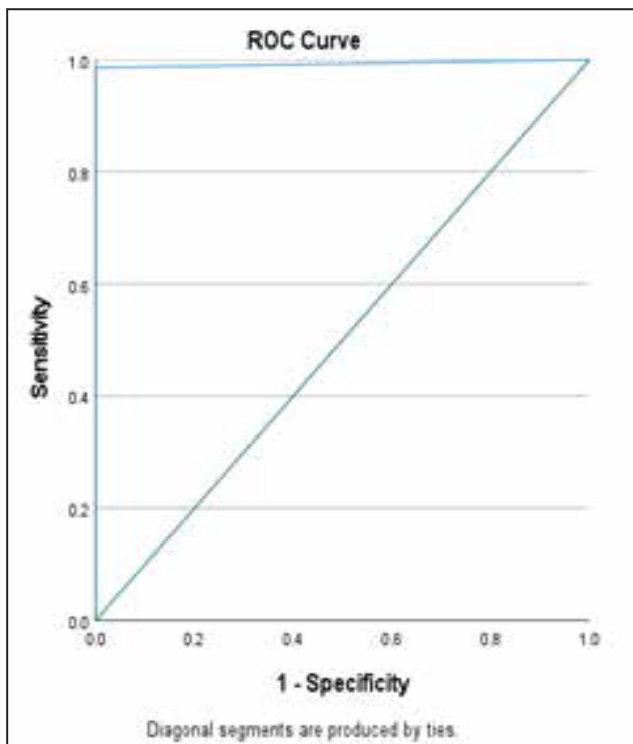


Figure I: ROC Curve Analysis to Evaluate the RT-LAMP Assay in Comparison to RT-qPCR for Serotyping of Dengue

Table 4: Results of ROC curves of RT-LAMP

Parameters	Percentage	AUC	P value	Cut off value
Sensitivity	98.55	0.993		
Specificity	100.00	(95% CI:		
Positive predictive value	100.00	0.980–1.000)	0.001	≥ 0.5
Negative predictive value	66.67			
Accuracy	98.59			

Note: p-value ≤ 0.05 was considered significant.

RT-qPCR identified DENV-1 in 11 (8%), DENV-2 in 99 (70%), and DENV-3 in 17 (12%) cases. RT-LAMP showed similar distribution: DENV-1 (8%), DENV-2 (69%), and DENV-3 (12%). No DENV-4 was detected. Both assays identified 3 cases (2%) of triple serotype infection (DENV-1,2,3), and mixed DENV-2,3 infection in 8 (RT-qPCR) and 7 (RT-LAMP) cases. Four (3%) samples were undetected by RT-qPCR, and six (4%) by RT-LAMP (Table 5).

Table 5: Distribution of Dengue virus serotypes detected by RT-qPCR and RT-LAMP

Serotypes	Category	RT-qPCR	RT-LAMP
Undetected		4(3.0%)	6(4.0%)
Detected	DEN-1	11(8.0%)	11(8.0%)
	DEN-2	99(70.0%)	98(69.0%)
	DEN-3	17(12.0%)	17(12.0%)
	DEN-4	0	0
	DEN-1,2,3	3(2.0%)	3 (2.0%)
	DEN-2,3	8(5.0%)	7 (5.0%)
Total		138	136

Note: Dengue ICT detected positive patients= 142; Dengue serotype detected patients=138; 4 (3%) were undetected by RT-qPCR and 6(4%) were undetected by RT-LAMP

Among NS1-positive patients (n=106), both RT-qPCR and RT-LAMP detected all cases. In IgM-positive cases (n=32), 28 (87.5%) were detected by both methods. For patients positive for both IgM and IgG (n=4), RT-qPCR detected all, while RT-LAMP detected 2 (50%). The mean CT values (RT-qPCR) for detected cases were: NS1-positive (24.61), IgM-positive (25.70), and IgM plus IgG-positive (27.13) (Table 6).

Among 142 recent dengue cases, RT-LAMP detected all NS1-positive samples (106/106; 100%). Among IgM-positive cases, 28/32 (87.5%) were detectable. In patients positive for both IgM and IgG, 2/4 (50%) were detected (Table 7).

Table 6: Frequency of Dengue Detection among Different Positive Serological Tests by RT-qPCR (n=142)

Serology	RT-qPCR with mean CT-value		
	Positive	Negative	(mean CT-value)
NS1 positive (n=106)	106(100.0%)	0	24.61
IgM positive (n=32)	28(87.5%)	4(12.5%)	25.70
IgM, IgG positive (n=4)	4(100.0%)	0	27.13
Total	138(97.2%)	4 (2.8%)	

Note: Dengue ICT detected positive patients= 142; Dengue serotype detected patients=138; 4 (3%) were undetected by RT-qPCR and 6(4%) were undetected by RT-LAMP

Table 7: Frequency of Dengue Detection among Different Positive Serological Tests by RT-LAMP (n=142)

Serology	RT-LAMP		Total
	Positive	Negative	
NS1 Positive	106(100.0%)	0(0.0%)	106(100.0%)
IgM Positive	28(87.5%)	4(12.5%)	32(100.0%)
IgM, IgG both Positive	2(50.0%)	2(50.0%)	4(100.0%)
Total	136 (95.8%)	6(4.2%)	

Discussion

Dengue remains a significant public health challenge in endemic regions like Bangladesh, where limited diagnostic infrastructure, financial constraints, and inadequate public awareness hinder early and accurate diagnosis. The circulation of multiple dengue virus (DENV) serotypes, including cases of co-infection, can exacerbate disease severity depending on host immune status¹⁸. Early detection and serotype identification are therefore essential for both clinical management and outbreak control.

Among 200 clinically suspected dengue cases in this study, 142(71.0%) were confirmed as recent infections. Of these, 106 (53%) were NS1-positive, aligning with findings, reported 85.1% NS1 positivity in the acute phase¹⁹, underscoring the utility of NS1 antigen detection in early diagnosis. To assess RT-LAMP's diagnostic performance, these 142 confirmed cases were tested using both RT-qPCR and RT-LAMP assays. RT-qPCR identified 138 (97.18%) positive cases, while RT-LAMP detected 136 (95.77%). Four IgM-positive samples with symptom onset beyond six days were negative in both molecular assays, likely due to declining viral load or cross-reactivity with other flaviviruses, consistent with WHO guidelines²⁰. The negative results may also be attributed to RNA degradation, primer-probe mismatches, or low viral copy numbers below the RT-qPCR detection threshold. Notably, RNA viruses like DENV have high mutation rates due to the lack of

proofreading activity in their RNA-dependent RNA polymerase, which can compromise primer binding¹⁶.

Two samples positive by RT-qPCR were missed by RT-LAMP. These cases also tested positive for both IgM and IgG, indicating a later stage of infection with likely reduced viremia. RT-qPCR, known for its high sensitivity, can detect low viral loads, whereas RT-LAMP may fail to amplify RNA near its detection limit. Teoh et al. observed a similar trend, where low viral loads resulted in false negatives in RT-LAMP despite RT-qPCR positivity²¹. The diagnostic accuracy of RT-LAMP was evaluated using ROC analysis, which yielded an AUC of 0.993, with sensitivity and specificity of 98.55% and 100%, respectively, when compared to RT-qPCR. These findings are consistent with earlier reports where RT-LAMP closely matched RT-qPCR performance²¹. Although RT-LAMP did not surpass RT-qPCR in sensitivity, it offered a significant time advantage, requiring only 30 minutes versus 150 minutes for RT-qPCR. Similar time and performance benefits have been reported in several studies^{21,22}. Interestingly, a study found RT-LAMP to be even more sensitive than RT-qPCR²³, achieving 100% sensitivity and specificity compared to RT-qPCR's 85.2% sensitivity.

Serotype analysis revealed DENV-2 as the predominant circulating strain (70.0%), followed by DENV-3 (12%), DENV-1 (8.0%), mixed DENV-2 and 3(5.0%), and triple serotype infections (2.0%). These findings are consistent with studies from Chattogram and nationwide surveillance data, where DENV-2 accounted for the majority of cases²⁴⁻²⁷. The absence of DENV-4 in this study may reflect its lower replication efficiency in Aedes mosquitoes or underdiagnosis due to mild or asymptomatic presentations^{5,28}.

All NS1-positive samples were successfully serotyped by both RT-qPCR and RT-LAMP, while among IgM-positive samples, 87.5% were detected by RT-qPCR and RT-LAMP. However, among samples positive for both IgM and IgG, only 50.0% were detected by RT-LAMP, compared to 100.0% by RT-qPCR. These results suggest that NS1-positive samples, typically collected during early infection, are optimal for molecular detection due to high viral load. Some studies reported similar patterns, where NS1-positive samples showed significantly higher RT-qPCR detection rates^{29,30}. A study also found maximal sensitivity of NS1 and RT-qPCR assays within the first three days of illness³¹. In contrast, antibody-positive samples often yield lower molecular detection due to reduced viremia as immune responses

clear circulating virus³².

Although RT-qPCR remains the reference standard for DENV detection and serotyping, this study demonstrates that RT-LAMP offers comparable diagnostic performance. Its ease of use, rapid turnaround, and lower resource requirements make it a valuable tool for dengue surveillance and clinical application, especially in resource-limited settings. This study was limited by its single-center design and relatively small sample size, which may not reflect the broader dengue patient population in Chittagong. The cross-sectional nature and time constraints prevented follow-up sampling, particularly for IgG-positive cases, limiting confirmation of secondary infections. Due to budget limitations and the high cost of reagents, serotyping was restricted to ICT-positive samples only. Consequently, the study could not assess RT-LAMP's performance in ICT-negative suspected cases, which may have affected the overall evaluation of the assay's diagnostic utility.

Conclusion

This study demonstrates that the RT-LAMP assay offers diagnostic performance comparable to RT-qPCR for dengue virus (DENV) serotyping, with high sensitivity and specificity. Its ability to amplify nucleic acids under isothermal conditions using only a simple heat block eliminates the need for complex instrumentation, making it a practical tool for resource-limited settings. The assay is rapid, user-friendly, and requires minimal technical expertise, making it suitable for both centralized laboratories and decentralized rural healthcare facilities. Given its performance and operational advantages, RT-LAMP represents a promising alternative for molecular dengue diagnostics, particularly in endemic regions such as Bangladesh. The RT-LAMP assay is recommended for use in point-of-care settings during dengue outbreaks to facilitate rapid detection and serotype differentiation. Its adoption could significantly strengthen epidemiological surveillance and outbreak response efforts. Training programs should be implemented for healthcare and laboratory personnel to ensure proper technique, quality control, and accurate interpretation of results.

Acknowledgements

We thank all patients who participated and acknowledge Mr. Suzan Chowdhury, Lab technologist (Virology), and Miss Nadia Islam Tumpa, Lab Consultant, Advanced Microbiology Lab, Chittagong Medical College, for their valuable assistance in laboratory procedures.

Conflict of Interest

The authors declare that there is no conflict of interest

Financial Disclosure

No external funding was received.

Authors' contributions

Marium Sukanya: conceptualized and designed the study, analyzed the data, interpreted the results, and wrote up the draft manuscript. Lovely Barai, Mili Rani Saha, and Tanjila Rahman contributed to the data analysis, interpretation of the results, and critical review of the manuscript. Minhaj Rashidur Rahman and Md. Rokibul Hasan contributed to the analysis of the data. All authors read and approved the final manuscript.

Data Availability

Any inquiries regarding supporting data availability of this study should be directed to the corresponding author and are available from the corresponding author on reasonable request.

Ethics Approval and Consent to Participate

Ethical approval for the study was obtained from the Institutional Review Board. As this was a prospective study the written informed consent was obtained from all study participants. All methods were performed in accordance with the relevant guidelines and regulations.

Copyright: © Rahman et al. 2025. Published by Bangladesh Journal of Medical Microbiology. This is an open-access article and is licensed under the Creative Commons Attribution Non-Commercial 4.0 International License (CC BY-NC 4.0). This license permits others to distribute, remix, adapt and reproduce or changes in any medium or format as long as it will give appropriate credit to the original author(s) with the proper citation of the original work as well as the source and this is used for noncommercial purposes only. To view a copy of this license, please See: <https://creativecommons.org/licenses/by-nc/4.0/>

How to cite this article: Rahman T, Dey P, Khan AA, Sultana N, Jannat M, Rahman T, Fatema N. Diagnostic Utility of RT LAMP Compared to Real Time RT PCR in Dengue Virus Serotype Identification at a Tertiary Care Hospital of Chattogram District of Bangladesh. *Bangladesh J Med Microbiol*, 2025;19(2):100-106

ORCID

Tabassuma Rahman: <https://orcid.org/0009-0008-8507-459X>
 Pompy Dey: <https://orcid.org/0009-0002-3145-9626>
 Ayesha Ahmed Khan: <https://orcid.org/0000-0003-4101-2035>
 Nishad Sultana: <https://orcid.org/0009-0004-6071-9911>
 Masuma Jannat: <https://orcid.org/0009-0001-8867-1655>
 Tazrina Rahman: <https://orcid.org/0000-0002-2544-6725>
 Nusrat Fatema: <https://orcid.org/0009-0008-9754-0906>

Article Info

Received: 7 April 2025

Accepted: 24 May 2025

Published: 1 July 2025

References

- Suzuki K, Phadungsombat J, Nakayama EE, Saito A, Egawa A, Sato T, Rahim R, Hasan A, Lin MY, Takasaki T, Rahman M. Genotype replacement of dengue virus type 3 and clade replacement of dengue virus type 2 genotype Cosmopolitan in Dhaka, Bangladesh in 2017. *Infection, Genetics and Evolution*. 2019 Nov 1;75:103977.
- Obi JO, Gutierrez-Barbosa H, Chua JV, Deredge DJ. Current trends and limitations in dengue antiviral research. *Tropical Medicine and Infectious Disease*. 2021 Sep 30;6(4):180.
- World Health Organization. Dengue-global situation. *Disease Outbreak News*. 2023 Dec;21. Available at: <https://www.who.int/emergencies/disease-outbreak-news/item/2023->

- DON498 (last accessed 06 August, 2025).
4. World Health Organization. Dengue and severe dengue. 2024 Dec;17. Available at: <https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue> (last accessed 06 August, 2025).
 5. Noor R. Reemergence of dengue virus in Bangladesh: Current fatality and the required knowledge. *Tzu Chi Medical Journal*. 2020 Jul 1;32(3):227-33.
 6. Islam MT, Sultana S, Hasan KA, Khaled S, Hasan MN, Masum AA, Khan AH, Khan MM. Clinical and laboratory profile of dengue cases in a tertiary care hospital of Bangladesh: an archival research. *Vietnam J Public Health*. 2022 Dec;8:30.
 7. Bonna AS, Pavel SR, Mehjabin T, Ali M. Dengue in Bangladesh. *International Journal of Infectious Diseases One Health*. 2023; 1(10):1-3.
 8. Asaduzzaman M, Khan EA, Hasan MN, Rahman M, Ashrafi SA, Haque F, Haider N. The 2023 dengue fatality in Bangladesh: Spatial and demographic insights. *IJID regions*. 2025 Apr 22:100654.
 9. Kayesh ME, Khalil I, Kohara M, Tsukiyama-Kohara K. Increasing dengue burden and severe dengue risk in Bangladesh: an overview. *Tropical Medicine and Infectious Disease*. 2023 Jan 3;8(1):32.
 10. Rahim R, Hasan A, Phadungsombath J, Hasan N, Ara N, Biswas SM, Nakayama EE, Rahman M, Shioda T. Genetic analysis of dengue virus in severe and non-severe cases in Dhaka, Bangladesh, in 2018–2022. *Viruses*. 2023 May 10;15(5):1144.
 11. Halstead S, Wilder-Smith A. Severe dengue in travellers: pathogenesis, risk and clinical management. *Journal of travel medicine*. 2019;26(7):taz062.
 12. Suppiah J, Ching SM, Amin-Nordin S, Mat-Nor LA, Ahmad-Najimudin NA, Low GK, Abdul-Wahid MZ, Thayan R, Chee HY. Clinical manifestations of dengue in relation to dengue serotype and genotype in Malaysia: A retrospective observational study. *PLoS neglected tropical diseases*. 2018 Sep 18;12(9):e0006817.
 13. Parida M, Horioko K, Ishida H, Dash PK, Saxena P, Jana AM, Islam MA, Inoue S, Hosaka N, Morita K. Rapid detection and differentiation of dengue virus serotypes by a real-time reverse transcription-loop-mediated isothermal amplification assay. *Journal of clinical microbiology*. 2005 Jun;43(6):2895-903.
 14. Azad DA, Ferdousic DS, Islam QT. National guideline for clinical management of dengue syndrome. Dhaka: Government of the People's Republic of Bangladesh. 2018.
 15. Notomi T, Okayama H, Masubuchi H, Yonekawa T, Watanabe K, Amino N, Hase T. Loop-mediated isothermal amplification of DNA. *Nucleic acids research*. 2000 Jun 15;28(12):e63-.
 16. World Health Organization. Dengue guidelines for diagnosis, treatment, prevention and control: New edition. 2009. Available at: <https://iris.who.int/handle/10665/44188> (last accessed 06 August, 2025)
 17. World Health Organization. Guidelines on drawing blood : Best practices in phlebotomy. Safe Injection Global Network.;World Health Organization.;National Center for HIV, Viral Hepatitis, STD, and TB Prevention (U.S.). Global AIDS Program. 2010. Available at: <https://stacks.cdc.gov/view/cdc/41566> (last accessed 6 August, 2025).
 18. Senaratne UT, Murugananthan K, Sirisena PD, Carr JM, Noordeen F. Dengue virus co-infections with multiple serotypes do not result in a different clinical outcome compared to mono-infections. *Epidemiology & Infection*. 2020 Jan;148:e119.
 19. Sami CA, Tasnim R, Hassan SS, Khan AH, Yasmin R, Monir-uz-Zaman M, Sarker MA, Arafat SM. Clinical profile and early severity predictors of dengue fever: Current trends for the deadliest dengue infection in Bangladesh in 2022. *IJID regions*. 2023 Dec 1;9:42-8.
 20. Koo C, Kaur S, Teh ZY, Xu H, Nasir A, Lai YL, Khan E, Ng LC, Hapuarachchi HC. Genetic variability in probe binding regions explains false negative results of a molecular assay for the detection of dengue virus. *Vector-Borne and Zoonotic Diseases*. 2016 Jul 1;16(7):489-95.
 21. Teoh BT, Sam SS, Tan KK, Johari J, Danlami MB, Hooi PS, Md-Esa R, AbuBakar S. Detection of dengue viruses using reverse transcription-loop-mediated isothermal amplification. *BMC infectious diseases*. 2013 Aug 21;13(1):387.
 22. Escorcía-Lindo K, Hurtado-Gómez L, Rosero JS, Llanos NS, Sánchez CB, Pérez AD, Díaz-Olmos Y, García J, Bello-Lemus Y, Pacheco-Londoño LC, Acosta-Hoyos AJ. Development and Validation of a Combined RT-LAMP Assay for the Rapid and Sensitive Detection of Dengue Virus in Clinical Samples from Colombia.
 23. Lau YL, Lai MY, Teoh BT, Abd-Jamil J, Johari J, Sam SS, Tan KK, AbuBakar S. Colorimetric detection of dengue by single tube reverse-transcription-loop-mediated isothermal amplification. *PloS one*. 2015 Sep 18;10(9):e0138694.
 24. Hasan MJ, Tabassum T, Sharif M, Khan MA, Bipasha AR, Basher A, Islam MR, Amin MR, Gozal D. Clinico-epidemiologic characteristics of the 2019 dengue outbreak in Bangladesh. *Transactions of the Royal Society of Tropical Medicine and Hygiene*. 2021 Jul;115(7):733-40.
 25. Biswas RS, Sequeira A, Nafisa S, Alam KM, Bishop J. Serotype variations and distributions of dengue virus during the 2022 outbreak in Chattogram, Bangladesh. *Journal of Bangladesh College of Physicians and Surgeons*. 2023 Nov 28:39-43.
 26. IEDCR.. Institute of Epidemiology, Disease Control and Research (IEDCR). Available at: <http://iedcr.portal.gov.bd/site/page/45aea1fa-5756-4feb-8d09-f0da895a3baa/> (last accessed 06 August 2025).
 27. Rob MA, Hossain M, Sattar MA, Ahmed IU, Chowdhury AF, Mehedi HH, Mohammed N, Maruf ul Quader M, Hossain MZ, Rahman M, Chakma K. Circulating dengue virus serotypes, demographics, and epidemiology in the 2023 dengue outbreak in Chittagong, Bangladesh. *European Journal of Microbiology and Immunology*. 2024 Sep 11;14(3):272-9.
 28. Nguyen NM, Thi Hue Kien D, Tuan TV, Quyen NT, Tran CN, Vo Thi L, Thi DL, Nguyen HL, Farrar JJ, Holmes EC, Rabaa MA. Host and viral features of human dengue cases shape the population of infected and infectious *Aedes aegypti* mosquitoes. *Proceedings of the National Academy of Sciences*. 2013 May 28;110(22):9072-7.
 29. Tandel K, Kumar M, Bhalla GS, Shergill SP, Swarnim V, Sahai K, Gupta RM. Detection of dengue virus serotypes by single-tube multiplex RT-PCR and multiplex real-time PCR assay. *medical journal armed forces india*. 2022 Jul 1;78(3):333-8.
 30. Tsai HP, Tsai YY, Lin IT, Kuo PH, Chang KC, Chen JC, Ko WC, Wang JR. Validation and application of a commercial quantitative real-time reverse transcriptase-PCR assay in investigation of a large dengue virus outbreak in southern Taiwan. *PLoS neglected tropical diseases*. 2016 Oct 12;10(10):e0005036.
 31. Ahmed NH, Broor S. Comparison of NS1 antigen detection ELISA, real time RT-PCR and virus isolation for rapid diagnosis of dengue infection in acute phase. *Journal of vector borne diseases*. 2014 Jul 1;51(3):194-9.
 32. Titir SR, Paul SK, Ahmed S, Haque N, Nasreen SA, Hossain KS, Ahmad FU, Nila SS, Khanam J, Nowsher N, Al Amin AM. Nationwide distribution of dengue virus type 3 (Denv-3) genotype I and emergence of denv-3 genotype III during the 2019 outbreak in Bangladesh. *Tropical medicine and infectious disease*. 2021 Apr 21;6(2):58