Original Article

JCMCTA 2025 ; 36 (1) : 93-96

Serotype Patterns of 2022 and 2023 Dengue Outbreaks in Chattogram, Bangladesh

Rajat Sanker Roy Biswas[1*] Austin Sequeira[2] Anamul Hasan[3] Md Fahad Zamil[3]
Mohammad Shafiul Alam[3] Jean Bishop[2]

Abstract

Background: Dengue viruses have been circulating in Bangladesh, including the Chattogram region, since 2000. This study aimed to investigate the dengue virus serotype patterns in Chattogram during 2022 and 2023.

Materials and methods: The observational study was conducted at Chattagram Maa-O-Shishu Hospital between June and December 2022 and from October to December 2023. Patients who showed clinical signs of dengue and tested positive for the NS1 antigen were included. A total of 80 patients 68 in 2022 and 12 in 2023 underwent serotype testing. The 2022 samples were tested at SlieaGen L.L.C in Texas, USA, while the 2023 samples were analyzed at ICDDR'B in Bangladesh.

Results: In 2022, 68 samples were tested via qPCR, with 27 (40%) testing positive for dengue. Of those, DENV-1 was found in 25 samples (36.8%) DENV-2 in 3 samples (4.5%) DENV-3 in 16 samples (23.6%) and DENV-4 in 1 sample (1.5%). The distribution showed that DENV-1 appeared alone in 10 samples (14.7%) DENV-3 and DENV-4 each in one sample. Co-infections were also seen: 12 samples (17.6%) had both DENV-1 and 3, and 3 samples (4.1%) had DENV-1, 2 and 3.

In 2023, 12 samples were tested, with 10 (83.3%) testing positive for dengue. One sample had insufficient material and another was PCR-negative. Among the positives, DENV-2 was found in 9 samples (75%) and DENV-1 in 1 sample (8.3%). No co-infections were detected and DENV-3 and DENV-4 were not identified that year.

Conclusions: All four dengue serotypes were present in Chattogram in 2022, with DENV-1 and DENV-3 being the most common. However, in 2023, the cases were primarily DENV-2, with a few DENV-1 cases. Notably, double and triple serotype co-infections were observed during the 2022 outbreak. There appears to have been a shift in dominant serotypes from DENV-1 in 2022 to DENV-2 in 2023.

Key words: Dengue; NS1;Outbreak; Serotype.

Introduction

Dengue, a fast-spreading disease transmitted by mosquitoes, has become a major global health concern and Bangladesh has been particularly hard hit. The World Health Organization (WHO) lists dengue as one of the top ten global health threats.[1] The disease is caused by the dengue virus, a member of the Flavivirus family, which is spread by Aedes mosquitoes. Dengue viruses exist in four different varieties:

ENV-1, DENV-2, DENV-3 and DENV-4. Each has unique genetic variants. The specific serotype involved, and even cases where multiple serotypes infect the same person, can affect the symptoms and severity of the disease.[2]

The genetic diversity of the dengue virus, both in its serotypes and genotypes, complicates efforts to manage the disease and increases the risk of severe outcomes, especially in people experiencing a second or third infection. Dengue has now spread to over 125 countries, causing around 400 million infections and 40,000 deaths annually.[2]. About 70% of the global dengue burden is concentrated in tropical and subtropical regions, particularly in South and Southeast Asia.[3] The NS1 antigen is typically detectable during the first 4-5 days of the fever phase, when the viral load is highest. A person who is infected with one dengue serotype and later contracts a different one may experience a more severe second infection, making it vital to monitor the patterns of circulating serotypes over time. However, in Bangladesh particularly in Chattogram, there has been limited documentation of dengue serotypes among patients. This study aims to point out the serotypes of dengue virus in NS1-positive cases over two consecutive years, 2022 and 2023.

---

1. Associate Professor of Medicine
Chattagram Maa-O-Shishu Hospital Medical College, Chattogram.

2. Research Scientists, SleaGen LLC
Austin, Texas, USA.

3. Research Officer, Infectious Diseases Division,
International Centre for Diarrheal Disease Research,
Bangladesh (icddr,b) Dhaka.

***Correspondence:** **Dr. Rajat Sanker Roy Biswas**
Cell : 01819 80 84 33
E-mail: rajatbiswas76@yahoo.com

Submitted on : 25.02.2025
Accepted on : 30.04.2025

Materials and methods

This observational study was carried out at the Department of Medicine, Chattagram Maa-O-Shishu Hospital and the International Center for Diarrhoeal Disease Research, Bangladesh (icddr, b) from June to December 2022 and in November and December 2023. Patients showing symptoms of Dengue Fever (DF) for less than five days were included in the study and all underwent a Rapid Diagnostic Test (RDT) for the NS1 antigen.

Following strict aseptic and universal precautions, about 3 mL of venous blood was drawn from each patient and collected in a Serum-Separating Tube (SST). The serum was then separated by centrifuging the SSTs and stored in 1.5-mL Eppendorf tubes. Each sample was initially screened using the dengue NS1 RDT.

For further testing, the 2022 samples were sent to SlieaGen L.L.C in the USA, while the 2023 samples were analyzed at the Emerging Infections & Parasitology Laboratory (EIPL) at icddr,b in Bangladesh to determine the dengue serotypes. Informed written consent was obtained from all participants, and ethical approval was granted by the respective Ethical Review Boards (ERBs).

Results

27 (39.7%) of the 68 samples examined in 2022 shown positive for dengue viruses using PCR. The most common serotype identified was DENV-1, which was present in 25 cases (36.8%) followed by DENV-3, which was present in 16 cases (23.6%) (Table Ia).

Table Ia Distribution of serotypes in 2022 samples (n=68)

Serotypes	Number	Percent
DENV-1	25	36.8
DENV-2	3	4.5
DENV-3	16	23.6
DENV-4	1	1.5
Virus detected	27	39.71
Virus not detected	41	60.29

Table Ib Serotype distribution in individual test samples of 2022 (n=27)

Serotypes	Number	Percent
DENV-1	10	37.03
DENV-2	0	00
DENV-3	1	3.70
DENV-4	1	3.70
DENV-1+ DENV-3	12	44.44
DENV-1+ DENV-2+ DENV-3	3	11.11

In 2022, among the 27 PCR-positive samples, 10 cases (37.03%) were DENV-1 only, and 12 cases (44.44%) were double positive for DENV-1 and DENV-3. Single cases of DENV-3 and DENV-4 were also identified. Additionally, 3 cases (11.11%) were triple positive for DENV-1, 2 and 3 (Table Ib).

Table II Serotype distribution in individual samples of 2023 (n= 12)

Serotypes	Number	Percent
DENV-1	1	8.3
DENV-2	9	75.00
DENV-3	0	00
DENV-4	0	00
PCR negative	1	8.3
Inadequate samples	1	8.3

In 2023, out of the 12 samples tested, 10 (83.3%) were PCR-positive for dengue. The predominant serotype was DENV-2, found in 9 cases (75%), with only one case (8.3%) testing positive for DENV-1. No cases of DENV-3 or DENV-4 were detected (Table II).

Discussion

In the current study, DENV-2 emerged as the most common serotype in 2023, whereas DENV-1 and DENV-3 were more prevalent in 2022 in Chattogram, Bangladesh. These shifting trends in serotype distribution could influence the severity and outcomes of dengue cases. It's noteworthy that all four serotypes were detected during the 2022 outbreak, which is both rare and concerning for the potential severity of future outbreaks.[2] A shift in the dominant serotype and the re-emergence of DENV-2 was observed across many districts in Bangladesh, including Chattogram, in 2023.[4] This is in contrast to previous years, where DENV-3 had been the most prevalent serotype in these areas.[5-7]

There is very little information available about the variety and evolution of the dengue virus in Bangladesh, particularly in Chattogram. Previous studies have examined dengue genotypes but often relied on very small sample sizes.[8] While all four serotypes were present during the 2000–2002 dengue outbreaks in Bangladesh, DENV-3 was the most common. Serotype data become scarce after that until 2012. DENV-1 and DENV-2 were later found to be the predominant serotypes circulating from 2013 to 2016 by research conducted by Muraduzzaman et al.[9] According to the current analysis, the most prevalent serotypes during the Chattogram dengue outbreak in 2022 were DENV-1 and DENV-3. Remarkably, DENV-3 and DENV-2 were the most common serotypes in 2017 after a lapse. DENV-3 has been the predominant serotype since the significant epidemic in 2019.[10] 450 confirmed dengue cases were included in a 2023 observational research that was carried out at Dhaka Medical College Hospital and Chittagong Medical College Hospital between July and September.[11] Of these, 89% of patients with non-severe cases showed at least one warning sign, but 17% of patients experienced severe dengue. Severe cases showed signs of plasma leakage, such as ascites, pleural effusion and edema. The study suggested that the resurgence of different serotypes, particularly DENV-2 in 2023, may have contributed to the higher number of severe cases during that year's outbreak, highlighting the need for further research into these changing trends.

The genetic diversity of the Dengue Virus (DENV) in Bangladesh is not well documented. Three DENV-3 genotypes (I, II, and III) and the cosmopolitan DENV-2 genotype are now in circulation in the nation.[12] The reappearance of the DENV-4 serotype, which was detected in 2022 after being absent for more than 20 years, raises serious public health concerns, especially regarding the risk of severe secondary infections.[11] The emergence of new serotypes is often linked to factors such as rapid population growth, mass migration, increased travel from dengue-endemic areas, changing weather patterns, unplanned urbanization and a lack of effective control strategies.[5]

In 2019, there was a resurgence of DENV-3, which coincided with DENV-2 losing its status as the dominant serotype. That year saw an unprecedented dengue outbreak, with approximately 100,000 cases officially reported more than double the number of all cases reported since 2000.[13] A high death toll was also noted in 2022 and a similar pattern emerged in the dengue surge of 2023, which saw record-breaking numbers of cases and fatalities. This surge was marked by another shift in dominant serotypes, with DENV-2 becoming more prevalent again as DENV-3 receded.[4]

Limitations

However, the small sample size and the limited timeframe of the study may not fully represent the overall serotype distribution in the region. Despite some limitations, the study underscores the urgent need for robust dengue surveillance and public health interventions to mitigate the impact of future outbreaks in Bangladesh and the global community.

Conclusion

This study provides a snapshot of the dengue situation in Chattogram, Bangladesh, during the 2022 and 2023 outbreaks. In 2022, all four dengue serotypes were present, with the unique finding of multiple serotype infections in some patients. In contrast, DENV-2 emerged as the dominant serotype in 2023.

Recommendations

The study's findings also highlight the need for ongoing surveillance and further research into the serotype distribution and genetic diversity of the dengue virus in Bangladesh, particularly given the limited data available from regions like Chattogram.

Acknowledgements

The authors express gratitude to the authorities of CMOSH and icddr, b.

Funding

Sliea Gen L.L.C, Texas, USA.

Contribution of authors

RSRB-Conception, acquisition of data, drafting and final approval.

AS-Design, interpretation of data, critical revision and final approval.

AH-Acquisition of data data analysis, critical revision and final approval.

MFZ-Acquisition of data data analysis, critical revision and final approval.

MSA-Interpretation of data, drafting and final approval.

JB-Data analysis, critical revision and final approval.

Disclosure

All the authors declared no conflict of interest.

References

1. Hossain MS , Noman AA, Mamun SMAA, Mosabbir AA. Twenty two years of dengue outbreaks in Bangladesh: epidemiology, clinical spectrum, serotypes, and future disease risks. Tropical Medicine and Health. 2023; 51:37.

2. Biswas RSR, Sequeira A, Nafisa S, Alam KMT, Bishop J. Serotype Variations and Distributions of Dengue Virus During the 2022 Outbreak in Chattogram, Bangladesh Bangladesh Coll Phys Surg. 2023; 41: 39-43.

3. Hasan MJ, Tabassum T, Sharif M, Khan MAS, Bipasha AR, Basher A et al. Clinico-epidemiologic characteristics of the 2019 dengue outbreak in Bangladesh. Trans R Soc Trop Med Hyg. 2021;115:733–740.

4. Hasan A, Zamil MF, Trina AT, Biswas RSR, Kumkum A, Ahmed D, Alam MS. Resurgence of Dengue Virus Serotype 2: Findings from the 2023 Bangladesh Outbreak AJTMH. 2024

5. Aziz M, Hasan K, Hasanat M, Siddiqui M, Salimullah M, Chowdhury A, Ahmed M, Alam M, Hassan M, 2002. Predominance of DEN-3 genotype during the recent dengue outbreak in Bangladesh. Southeast asian journal of tropical medicine and public health. 2002;33: 42-48.

6. Rahim R, Hasan A, Phadungsombat J, Hasan N, Ara N, Biswas SM, Nakayama E E, Rahman M, Shioda T, 2023. Genetic analysis of Dengue virus in severe and non-severecases in Dhaka, Bangladesh, in 2018–2022. Viruses. 2023; 15: 1144.

7. Haider N, Hasan MN, Khalil I, Tonge D, Hegde S, Chowdhury MAB, Rahman M, Khan MH, Ansumana R, Zumla A, 2023. The 2022 dengue outbreak in Bangladesh: Hypotheses for the late resurgence of cases and fatalities. Journal of Medical Entomology. 2023; 60: 847- 852.

8. Rahim R, Hasan A, Hasan N, Nakayama EE, Shioda T, Rahman M. Diversity of dengue virus serotypes in Dhaka City: From 2017 to 2021. Bangladesh J MedMicrobiol. 2021;15:23–29.

9. Muraduzzaman AKM, Alam AN, Sultana S, SiddiquaM,Khan MH, Akram A, et al. Circulating dengue virus serotypes in Bangladesh from 2013 to 2016. Virusdisease. 2018;29:303–307.

10. Rafi A, Mousumi AN, Ahmed R, Chowdhury RH, Wadood A, Hossain G. Dengue epidemic in a non-endemic zone of Bangladesh: Clinical and laboratory profiles of patients. PLoSNegl Trop Dis. 2020;14:1–14.

11. Anika US, Islam M, Mou FEN et al. The 2023 Dengue Outbreak in Bangladesh: Exploring the Epidemiology in Hospitalized Patients. The American Journal of Tropical Medicine and Hygiene. 2024;110(6):1165-1171.

12. Islam MA, Ahmed MU, Begum N, Chowdhury NA, Khan AH, del Parquet M et al. Molecular characterization and clinical evaluation of dengue outbreak in 2002 in Bangladesh. Jpn J Infect Dis. 2006;59:85–91.

13. Riad MH, Cohnstaedt LW, Scoglio CM. Risk Assessment of dengue transmission in Bangladesh using a spatiotemporal network model and climate data. The American journal of tropical medicine and hygiene. 2021; 104: 1444.