The 3rd International Conference on Japan–Bangladesh Research and Practice (JBRP2024)
November 29–30, 2024
Online, Coordinated from The University of the Ryukyus, Okinawa, Japan
Organized by the Network of Bangladeshi Researchers in Japan (NBRJ)
Submission Number: 38

Serotype and Genotype Changes of Dengue Virus in Bangladesh during 2018–2023 and Its Association with Disease Severity

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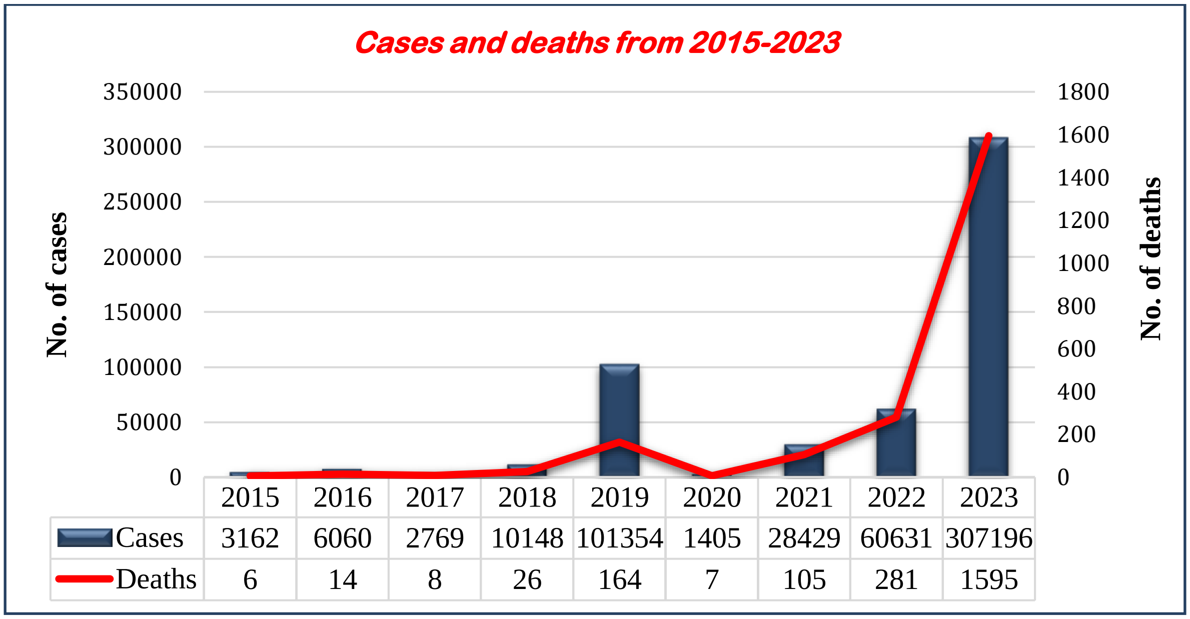
Track: Medicine, Pharmaceuticals, and Public Health

Keywords: DENV, Bangladesh, Serotypes, Phylogenetic Tree, Clades.

Extended Abstract



	2015	2016	2017	2018	2019	2020	2021	2022	2023
▬ Cases	3162	6060	2769	10148	101354	1405	28429	60631	307196
▬ Deaths	6	14	8	26	164	7	105	281	1595

Figure 1: Number of dengue cases and death in Bangladesh from 2015 to 2023.

Dengue virus (DENV) infections have unpredictable clinical outcomes, ranging from asymptomatic or minor febrile illness to severe and fatal disease. The severity of dengue infection is at least partly related to the replacement of circulating DENV serotypes and/or genotypes [1-2]. To describe clinical profiles of patients and the viral sequence diversity corresponding to non-severe and severe cases, we collected patient samples from 2018 to 2022 at Evercare Hospital Dhaka, Bangladesh. Serotyping of 495 cases and sequencing of 179 cases showed that the dominant serotype of DENV shifted from DENV2 in 2017 [3] and 2018 to DENV3 in 2019. DENV3 persisted as the only representative serotype until 2022. Cocirculation of clades B and C of the DENV2 cosmopolitan genotype in 2017 was replaced by circulation of clade C alone in 2018 with all clones disappearing thereafter. DENV3 genotype I was first detected in 2017 [4] and was the only genotype in circulation until 2022. We observed a high incidence of severe cases in 2019 when the DENV3 genotype I became the only virus in circulation. Phylogenetic analysis revealed clusters of severe cases in several different subclades of DENV3 genotype I. Again, huge case outbreak and fatality in 2023 (Fig. 1) was found associated with shift of serotype dominance from DENV3 to DENV2. Thus, these serotype and genotype changes in DENV may explain the large dengue outbreaks and increased severity of the disease in 2019 and 2023.

References

[1].Nunes, P.C.G., Sampaio, S.A.F., da Costa, N.R., de Mendonça, M.C.L., Lima, M.D.R.Q., Araujo, S.E.M., dos Santos, F.B., Simões et al., Dengue severity associated with age and a new lineage of dengue virus-type 2 during an outbreak in Rio De Janeiro, Brazil. J. Med. Virol., 88, 1130–1136, 2016.
[2].Hang, V.T.T., Holmes, E., Veasna, D., Quy, N.T., Hien, T.T., Quail, M., Churcher, C., Parkhill, J., Cardosa, J., Farrar, J. et al., Emergence of the Asian 1 Genotype of Dengue Virus Serotype 2 in Viet Nam: In Vivo Fitness Advantage and Lineage Replacement in South-East Asia, PLoS Negl. Trop. Dis., 4, e757, 2010.
[3].Rahim, R., Hasan, A., Hasan, N., Nakayama, E.E., Shioda, T., Rahman, M., Diversity of Dengue Virus Serotypes in Dhaka City: From 2017 to 2021, Bangladesh J. Med. Microbiol, 15, 23–29, 2021.
[4].Suzuki, K., Phadungsombat, J., Nakayama, E.E., Saito, A., Egawa, A., Sato, T., Rahim, R., Hasan, A., Lin, M.Y.-C., Takasaki, T. et al., Genotype replacement of dengue virus type 3 and clade replacement of dengue virus type 2 genotype Cosmopolitan in Dhaka, Bangladesh in 2017, Infect. Genet. Evol., 75, 103977, 2019.