

Complete Genome Sequencing and Phylogenetic Analysis of Dengue Type 1 Isolated from Sri Lanka from 1983-2014

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Sri Lanka faces regular outbreaks of dengue and from 1989 onwards dengue became endemic to the country. All four serotypes of dengue have been recorded, and the outbreak of dengue virus 1 (DENV 1) in 2009 resulted in the largest epidemic recorded up to that point. This raised the question of whether a significant genetic mutation had increased the transmissibility and virulence of DENV1. Hence, this research focused on studying the genetic/phylogenetic differences of DENV1 found in Sri Lanka from 1983 to 2014. To determine the genetic diversity of DENV 1 circulating in Sri Lanka within this period we conducted a genome-wide analysis using sanger sequencing and next-generation sequencing, followed by phylogenetic and amino acid analyses. The results showed a single dominant strain of DENV1 circulating in Sri Lanka after 2009 and almost all strains isolated after 2009 were of this genotype. The pre-2009 strains were different from the post-2009 strains and coincided with the largest epidemic in Sri Lanka. Our analysis of the phylogenetic tree and the amino acid substitutions generated by these two groups shows a clear difference. We conclude that these differences may contribute to the severe epidemic that was seen in 2009.

Keywords: DENV1, 2009, phylogenetic analysis, amino acid substitutions