

Tracing the phylogeography of the recent dengue strain (DENV1) found in Sri Lanka

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In 2009, a severe dengue epidemic occurred in Sri Lanka that caused a high level of mortality and morbidity than any other dengue epidemic in the country. In each subsequent year, dengue has continued to reach epidemic proportions, posing a major clinical burden to the population. The 2009 epidemic correlated with a shift in the predominant disease-causing dengue virus serotypes in Sri Lanka: prior to the epidemic, two serotypes, DENV2 and 3, were isolated from the majority of patients presenting with serious dengue disease, however, in 2009, a previously undetected DENV1 strain dominated as the major causative agent of dengue disease, and DENV1 has since then persisted as the dominant serotype in Sri Lanka. We amplified dengue virus from sera of patients who presented with severe disease to Colombo North Teaching Hospital in Sri Lanka during the early months of 2012, and sequenced the full genomes of four DENV1 isolates. In this work the phylogenetic analysis reveals that the 2009 epidemic DENV1 strain has continued to circulate within the population and was present in Colombo, Sri Lanka during the 2012 epidemic. We applied bayesian phylogeographic methods to infer the historic spatial dispersion of this virus, using the sequences of our Sri Lankan virus isolates and other reported sequences in the literature. These analyses suggest that the 2009 Sri Lankan epidemic DENV1 strain may have traveled directly or indirectly from Thailand, through China, to Sri Lanka, and, caused this epidemic. Our findings delineate the dissemination route of a virulent DENV1 strain in Asia and will be helpful in global monitoring efforts.