

Clinical, virological and epidemiological characterization of dengue outbreak in Myanmar, 2015

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Hospital-based surveillance was conducted at two widely separated regions in Myanmar during the 2015 dengue epidemic. Acute phase serum samples were collected from 332 clinically diagnosed dengue patients during the peak season of dengue cases. Viremia levels were measured by quantitative real-time PCR and plaque assays using FcγRIIA-expressing and non-FcγRIIA-expressing BHK cells to specifically determine the infectious virus particles. By serology and molecular techniques, 280/332 (84.3%) were confirmed as dengue patients. All four serotypes of dengue virus (DENV) were isolated from among 104 laboratory-confirmed patients including two cases infected with two DENV serotypes. High percentage of primary infection was noted among the severe dengue patients. Patients with primary infection or DENV IgM negative demonstrated significantly higher viral loads but there was no significant difference among the severity groups. Viremia levels among dengue patients were notably high for a long period which was assumed to support the spread of the virus by the mosquito vector during epidemic. Phylogenetic analyses of the envelope gene of the epidemic strains revealed close similarity with the strains previously isolated in Myanmar and neighboring countries. DENV-1 dominated the epidemic in 2015 and the serotype (except DENV-3) and genotype distributions were similar in both study sites.