WEB FIG. 1 *Phylogenetic trees of partial 5'-NCR (396 nt) sequences of CV-A16 showing the genetic relatedness between isolates of Andaman (GenBank accession numbers of partial 5'NCR: KU523388 – KU523399) and intra-serotype reference sequences. Neighbor-Joining tree was constructed using MEGA 6 software with the bootstrap testing of 1000 replicates. The evolutionary distances of the nucleotides were computed using the Kimura 2-parameter (K2P) model as a method for nucleotide substitution.*