

PHYLOGENETIC ANALYSIS OF HUMAN ROTAVIRUS IN MYANMAR : DETECTION OF INDIAN-BANGLADESHI G1/G2 LINEAGES, CHINESE G3 LINEAGE AND OP354-LIKE P[8] LINEAGE (P[8]B SUBTYPE)

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Abstract. As a first phylogenetic study of human rotavirus in Myanmar, VP7 and VP8* gene sequences of 5 group A human rotaviruses detected in children in Yangon City were determined and analyzed for their relatedness to rotavirus strains reported in other countries. VP7 genes of the two G1P[8] strains and the two G2P[4] strains clustered phylogenetically with those of Indian-Bangladeshi lineages with extremely high sequence identities. In contrast, a G3P[8] strain exhibited a close relatedness of VP7 gene to G3 rotaviruses currently prevailing in China, which had been referred to as a new variant G3 rotavirus. While VP8* genes of P[4] and P[8] strains clustered with those of Indian and Bangladeshi strains, only the G1 strain was grouped into a rare P[8] subtype, *ie*, P[8]b (OP354-like P[8]) with close relatedness to the P[8]b strains in eastern India and Thailand. The coexistence in Myanmar of G1/G2 and G3 rotaviruses, which are virtually identical to those predominating in India/Bangladesh and China, respectively, suggests the spread of these predominant rotaviruses from the two regions into Myanmar.

Key word: rotavirus, phylogenetic study, gene sequence, Myanmar

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