

Emergence of non-classical genotype constellations of G9P [8] rotavirus strains in diarrheic children in Sabah, Malaysia

ABSTRACT

G9P [8] has been the predominant rotavirus A (RVA) genotype in Malaysia since the 2000s. However, the overall genetic makeup and evolution of Malaysian G9P[8] strains are still unknown. Therefore, this study aimed to evaluate and characterize the complete genomes of three G9P[8] RVA strains isolated from diarrheic children under five years old in Sabah. Contrary to the classical Wa-like constellation, these strains contained a DS-1-like genotype. Two strains, namely L202 and L234, were genotype G9-P [8]-I1-R1-C1-M1-A1-N1-T1-E2-H1, while one (KN102) was genotype G9-P[8]-I1-R1-C1-M1-A2-N1-T1-E1-H1. Phylogenetic analysis revealed that the NSP4 genes of L202 and L234 strains were closer to that of G9P[8]-E2 strains from Japan, suggesting they might share a common ancestor. The findings from this study provide new insights into the genetic characteristics of circulating G9P[8] strains in Sabah, which are important for rotavirus surveillance and potential vaccine development in the region.