

Emergence of equine-like G3 strains as the dominant rotavirus among children under five with diarrhea in Sabah, Malaysia during 2018 - 2019

ABSTRACT

Rotavirus infection is a dilemma for developing countries, including Malaysia. Although commercial rotavirus vaccines are available, these are not included in Malaysia's national immunization program. A scarcity of data about rotavirus genotype distribution could be partially to blame for this policy decision, because there are no data for rotavirus genotype distribution in Malaysia over the past 20 years. From January 2018 to March 2019, we conducted a study to elucidate the rotavirus burden and genotype distribution in the Kota Kinabalu and Kunak districts of the state of Sabah. Stool specimens were collected from children under 5 years of age, and rotavirus antigen in these samples was detected using commercially available kit. Electropherotypes were determined by polyacrylamide gel electrophoresis of genomic RNA. G and P genotypes were determined by RT-PCR using type specific primers. The nucleotide sequence of the amplicons was determined by Sanger sequencing and phylogenetic analysis was performed by neighbor-joining method. Rotavirus was identified in 43 (15.1%) children with watery diarrhea. The male:female ratio (1.9:1) of the rotavirus-infected children clearly showed that it affected predominantly boys, and children 12–23 months of age. The genotypes identified were G3P[8] (74% n = 31), followed by G1P[8] (14% n = 6), G12P[6](7% n = 3), G8P[8](3% n = 1), and GxP[8] (3% n = 1). The predominant rotavirus circulating among the children was the equine-like G3P[8] (59.5% n = 25) with a short electropherotype. Eleven electropherotypes were identified among 34 strains, indicating substantial diversity among the circulating strains. The circulating genotypes were also phylogenetically diverse and related to strains from several different countries. The antigenic epitopes present on VP7 and VP4 of Sabahan G3 and equine-like G3 differed considerably from that of the RotaTeq vaccine strain. Our results also indicate that considerable genetic exchange is occurring in Sabahan strains. Sabah is home to a number of different ethnic groups, some of which culturally are in close contact with animals, which might contribute to the evolution of diverse rotavirus strains. Sabah is also a popular tourist destination, and a large number of tourists from different countries possibly contributes to the diversity of circulating rotavirus genotypes. Considering all these factors which are contributing rotavirus genotype diversity, continuous surveillance of rotavirus strains is of utmost importance to monitor the pre- and post-vaccination efficacy of rotavirus vaccines in Sabah.