ABSTRACT

Background: Rotavirus group A genomic characterization is critical for understanding the mechanisms of rotavirus diversity, such as assortment events and possible interspecies transmission. However, little is known about the genetic diversity and genomic relationship of the rotavirus group A strains circulating in Tanzania. The genetic and genomic relationship of RVA genotypes was investigated in children under the age of five. A total of 169 fecal samples were collected from under-five with diarrhea in Mbeya, Iringa and Morogoro regions of Tanzania. The RVA were screened in children under five with diarrhea using reverse transcription PCR for VP7 and VP4, and the G and P genotypes were determined using Sanger dideoxynucleotide cycle sequencing. Whole-genome sequencing was performed on selected genotypes. The overall RVA rate was 4.7% (8/169). The G genotypes were G3 (7/8) and G6 (1/8) among the 8 RVA positives, while the P genotypes were P [6] (4/8) and P[8] (2), and the other two were untenable. G3P [6] and G3P [8] were the identified genotype combinations. The genomic analysis reveals that the circulating G3P [8] and G3P [6] isolates from children under the age of five with diarrhea had a DS-1-like genome configuration (I2-R2-C2-M2-axe-N2-T2-E2-H2). The phylogenic analysis revealed that all 11 segments of G3P [6] were closely related to human G3P [6] identified in neighboring countries such as Uganda, Kenya, and other African countries, implying that G3P [6] strains descended from a common ancestor. Whereas, G3P [8] were closely related to previously identified equine-like G3P [P8] from Kenya, Japan, Thailand, Brazil, and Taiwan, implying that this strain was introduced rather than assortment events. We discovered amino acid differences at antigenic epitopes and N-linked glycosylation sites between the wild type G3 and P [8] compared to vaccine strains, implying that further research into the impact of these differences on vaccine effectiveness is warranted. The phylogenic analysis of VP7 also identified a bovine-like G6. For the first time in Tanzania, we report the emergence of novel equine-like G3 and bovine-like G6 RVA strains, highlighting the importance of rotavirus genotype monitoring and genomic analysis of representative genotypes.