

TITLE: FULL GENOTYPE CONSTELLATION OF G8 ROTAVIRUS STRAINS DETECTED IN BRAZIL, 2009-2017

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ABSTRACT:

Reassortment events between human and animal rotavirus (RVA) strains play an important role in RVA natural evolution. G8 genotype is widely distributed in animal species. Detection of G8 strains in humans is rare, nevertheless reported worldwide, including in Brazil. The aim of the present study is to conduct the molecular characterization and phylogenetic analysis of the 11 segments (genomic constellation) of 12 RVA G8 strains detected in Brazil between 2009 and 2017, targeting to reveal the true origin of these strains. So far, five structural proteins (VP1-4 and VP7) and three non-structural proteins (NSP1, NSP3 and NSP4) of 2 G8P[8] (detected in 2017), 4 G8P[4] (detected in 2010) and 6 G8P[6] (detected in 2009-2010) RVA strains were amplified by conventional RT-PCR and sequencing. Genotyping and genetic diversity was carried out by phylogenetic analysis. All G8P[8], G8P[6] and G8P[4] strains showed the potential DS-1-like genetic background (G8-P[4]/P[6]/P[8]-Ix-R2-C2-M2-A2-Nx-T2-E2-Hx). Sequence analysis of Brazilian G8P[4] strains revealed nucleotide similarity to G8P[4], G2P[4] and G8P[6] strains isolated in USA, South Korea and Democratic Republic of Congo, respectively. The Brazilian G8P[8] strains shared nucleotide identities with equine-like DS-1-like G3P[8] strains from Germany and Spain; DS-1-like G9P[8] strains from Thailand; DS-1-like G1P[8] strains from Japan; and DS-1-like G8P[8] strains from Czech Republic, South Korea, Thailand and Japan, including those Asian G8P[8] strains which had emerged following genetic reassortment between bovine and human RVA. Brazilian G8P[6] strains clustered with South America (Argentina) and Africa (Democratic Republic of Congo) G8P[6] RVA strains. Phylogenetic analysis of Brazilian G8P[6] strains suggests that a gene flow could be occurring between Africa and South America countries. On the other hand, there is no evidence for the introduction of a particular RVA G8P[4] variant in the country. Brazilian DS-1-like G8P[8] strains clustered together with DS-1-like RVA strains from distinct continents, indicating that DS-1-like G8P[8] strains circulating in Brazil were closely related to those pool of newly emergent DS-1-like strains circulating worldwide. The impact of these unusual RVA DS-1-like strains reassortments on RVA vaccines efficacy worldwide requires to be carefully evaluated.

Keywords: Gastroenteritis, interspecies transmission, genotyping, sequencing

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