Whole genome analysis of African G12P[6] and G12P[8] rotaviruses provides evidence of porcine-human reassortment at NSP2, NSP3 and NSP4

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Group A rotaviruses (RVA) represent the most common cause of pediatric gastroenteritis in children <5 years, worldwide. There has been an increase in global detection and reported cases of acute gastroenteritis caused by RVA genotype G12 strains. Our study sought to determine the possible origin and genomic relationship between African G12 strains and globally circulating rotaviruses. Therefore, the whole genome sequences of 34 RVA G12P[6] and G12P[8] strains detected from the southern (South Africa, Zambia and Zimbabwe), eastern (Ethiopia and Uganda), central (Cameroon) and western (Togo) African regions, were sequenced using the Sanger and Ion Torrent PGM methods. The majority of the strains possessed a Wa-like backbone with consensus genotype constellation of G12-P[6]/P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1, while a single strain (MRC-DPRU861) from Ethiopia displayed a DS-1-like genetic constellation of G12-P6-I2-R2-C2-M2-A2-N2-T2-E2-H2. In addition, three Ethiopian strains (MRC-DPRU850,MRC-DPRU5010 and MRC-DPRU5002) and a single strain (MRC-DPRU309) from South Africa had DS-1-like inter-genogroup reassortment with genetic constellation of G12-P[8]-I1-R1-C1-M1-A1-N1-T2-E1H1 and G12P[8]-I1-R1-C1,C2-M1-A1,A2-N1,N2-T1,E1,E2-H1, respectively. Overall, 10 gene segments (VP1-VP4, VP6 and NSP1-NSP5) of African G12 strains were determined to be genetically related to cognate gene sequences from globally circulating human G12, G9 and G1 strains with nucleotide identities of 94.1%-99.9%, 88.5%-98.5% and 89.8%-99.0%, respectively. Phylogenetic analysis showed that strain G12P[6] (MRC-DPRU861) from Ethiopia possessing a DS-1 like backbone consistently clustered with G2P[4] from Senegal and G3P[6] from Ethiopia. Notably, the non-structural gene segments, NSP2, NSP3 and NSP4 of the strains examined in the study exhibited the closest relationship with porcine and human-like porcine strains as well as human strains suggesting the occurrence of reassortment between human and porcine strains. Our results underpin the potential role interspecies transmission plays in generating human rotavirus diversity through reassortment events and provide insights into the evolutionary dynamics of G12 strains spreading across the African continent