Genomic characterization of uncommon human G3P[6] rotavirus strains that have emerged in Kenya after rotavirus vaccine introduction

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A monovalent rotavirus vaccine (RV1) was introduced to the national immunization program in Kenya in July 2014. There was increased detection of uncommon G3P[6] strains that coincided temporally with the timing of this vaccine introduction. Here, we sequenced and characterized the full genomes of two post-vaccine G3P[6] strains, RVA/Human-wt/KEN/KDH1951/2014/G3P[6] and RVA/Human-wt/KEN/KDH1968/2014/G3P[6], as representatives of these uncommon strains. On full-genomic analysis, both strains exhibited a DS-1-like genotype constellation: G3-P[6]- I2-R2-C2-M2-A2-N2-T2-E2-H2. Phylogenetic analysis revealed that all 11 genes of strains KDH1951 and KDH1968 were very closely related to those of human G3P[6] strains isolated in Uganda in 2012-2013, indicating the derivation of these G3P[6] strains from a common ancestor. Because the uncommon G3P[6] strains that emerged in Kenya are fully heterotypic as to the introduced vaccine strain regarding the genotype constellation, vaccine effectiveness against these G3P[6] strains needs to be closely monitored.

Keywords: Group A rotaviruses; Whole genomic analysis; RV1; Post-vaccine; G3P[6] genotype; DS-1-like genotype constellation; Kenya