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

Ernest Apondi Wandera, Satoshi Komoto, Shah Mohammad, Tomihiko Ide, Martin Bundi, James Nyangao, Cyrus Kathiiko, Erick Odoyo, Amina Galata, Gabriel Miring’u, Saori Fukuda, Riona Hatazawa, Takayuki Murata, Koki Taniguchi, and Yoshio Ichinose

KEMRI/Nagasaki University, Institute of Tropical Medicine, Kenya Research Station, Nairobi, Kenya
Department of Virology and Parasitology, Fujita Health University School of Medicine, Toyoake, Aichi, Japan, National Biosafety Authority, Nairobi, Kenya, Center for Virus Research, KEMRI, Nairobi, Kenya

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