

Whole genome constellations of five reassortant rotavirus strains detected during post-rotavirus vaccine introduction period in Rwanda

¹J.N. Mugweru, ²P.N. Mwangi, ²S.P. Rasebotsa, ²M.T. Mogotsi, ²S. Sabiu, ³J. Uwimana, ³L. Mutesa, ³N. Muganga, ³D. Murenzi, ³L. Tuyisenge, ⁴N.B. Magagula, ⁴K. Rakau, ⁴L.M. Seheri, ⁴M.J. Mphahlele, ⁵J.M. Mwenda, ²M.M. Nyaga

¹Department of Biological Sciences, University of Embu, Kenya, ²Next Generation Sequencing Unit, Division of Virology, Faculty of Health Sciences, University of the Free State, Bloemfontein, South Africa
³Kigali University Teaching Hospital, Kigali, Rwanda, ⁴South African Medical Research Council/Diarrhoeal Pathogens Research Unit, Faculty of Health Sciences, Sefako Makgatho Health Sciences University, Medunsa, Pretoria, South Africa, ⁵World Health Organization, Regional Office for Africa, Brazzaville, People's Republic of Congo

Background

In May 2012, Rwanda was the first low-income country in the world to introduce RotaTeq™ vaccine, into its national immunization program but switched to Rotarix™ in April 2017. Drastic decline in total case diarrhea was reported during the post-vaccination period. This study analyzed five reassortant strains that were detected during the post-vaccine period as part of the ongoing World Health Organization's Regional Office for Africa (WHO/AFRO) rotavirus whole genome characterization program. There has been concern about emergence of vaccine escape strains post-vaccine introduction.

Methods

Rotavirus RNA was extracted from stool samples utilizing TRI-REAGENT®-LS and purified using MinElute gel extraction kit. The RNA samples were whole genome sequenced using Illumina MiSeq platform for 600 cycles (301 x 2 paired-end reads). Genome assembly was done using Geneious software and genotyping was carried out using RotaC, to determine the genotype constellations.

Results

The whole genome constellations for each of the 5 reassortant strains detected during the post-vaccine period in Rwanda revealed: 1) RVA/Human-wt/RWA/UFS-NGS:MRC-DPRU6235/2014/G4P[4] (G4-P[4]-I1-R2-C2-M2-A2-N2-T1-E1-H2), 2) RVA/Human-wt/RWA/UFS-NGS:MRC-DPRU566/2013/G9P[4] (G9-P[4]-I1-R2-C2-M2-A1-N1-T1-E1-H1), 3) RVA/Human-wt/RWA/UFS-NGS:MRC-DPRU649/2013/G12P[4] (G12-P[4]-I1-R1-C1-M1-A1-N1-T1-E1-H1), 4) RVA/Human-wt/RWA/UFS-NGS:MRC-DPRU8020/2014/G12P[8] (G12-P[8]-I1-R2-C2-M1-A1-N2-T1-E2-H3)and5) RVA/Human-wt/RWA/UFS-NGS:MRC-DPRU6212/2014/G12P[8] (G12-P[8]-I1-R1-C1-M1-A2-N2-T2-E1-H1). This study illustrates that detection of different genotypes; in this case genotype 1 and 2 within a genotype constellation may result in novel rotavirus progeny following genome segment reassortment events, post vaccination.

Conclusions

The detection of the five-reassortant strains post-vaccine introduction in Rwanda that may be due to vaccine pressure needs follow up as part of long-term surveillance using whole genome sequencing.