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

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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

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.