Molecular characterization of rotavirus strains using whole genome sequencing reveals unique changes post-rotavirus vaccine introduction in Zambia

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Background

To monitor the impact of rotavirus (RV) vaccination in Africa beyond conventional G and P-typing, the WHO/AFRO is supporting whole genome characterization in partnership with the UFS-NGS Unit. Rotavirus strains circulating in Zambia from 2009-2016 pre- and post-rotavirus vaccine introduction were analyzed.

Methods

Samples (n=126; 37 pre and 89 post-vaccine) were subjected to cDNA synthesis using the Maxima H Minus Double-Stranded cDNA Synthesis Kit. The Nextera XT DNA Library Preparation Kit was used to prepare the DNA libraries and then MiSeq sequencing was performed for 600 cycles (301 x 2 paired-end reads) to generate data in fastq format files. Raw sequence data was processed using Geneious software and determination of genome constellations done using RotaC.

Results

There was stability in predominating genome constellations pre- and post-vaccine introduction. However, five reassortant strains were identified post-vaccination whereby three of the post-vaccine reassortant strains were mono-reassortants. Their NSP2 gene segment was genotype N2 within a Wa-like backbone for two Wa-like strains (RVA/Human-wt/ZAM/UFS-NGS:MRC-DPRU13232/2016/G1P[8] and RVA/Human-wt/ZAM/UFS-NGS:MRC-DPRU13541/2016/G1P[8]) ansd genotype N1 within a DS-1-like backbone for the other strain (RVA/Human-wt/ZAM/UFS-NGS:MRC-DPRU13327/2016/G2P[4]). Additionally, two uncommon strains, a G5P[6] exhibited genotype A8 in its NSPI and a unique G2P[8] within a pure DS-1-like backbone. The detection of reassortant strains post-vaccine introduction is indicative of RV evolution mechanisms to escape vaccine protection.

Conclusions

While the cyclical changes in circulating RV genome constellations might be attributable to natural annual RV evolution mechanisms, immunological pressure posed by the vaccine cannot be ruled out.The detection of the five reassortant strains post-vaccination in this study reignites the debate on strain changes due to vaccine pressure. There is need to maintain long-term surveillance and promote use of whole genome sequencing to address this phenomenon.