

Variability of the P-types in stable genotype constellations pre- and post-vaccine introduction in Rwanda

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Background

Rotaviruses (RVs) are the primary etiological agents of viral-induced gastroenteritis in infants and children <5 years. Fluctuations in RV genotype combinations have been reported in several countries during post-vaccination period. In this study, we analyzed RV strains detected in Rwanda in the course of the ongoing WHO/AFRO whole genome characterization for possible genotype fluctuations.

Methods

Rotavirus - ELISA positive samples from children hospitalized between 2011 and 2015 in Rwanda were included in this analysis. Whole genome sequencing (Illumina MiSeq) was performed on 158 samples comprising 46 (29.1%) and 112 (70.9%) from the pre- and post-vaccine periods, respectively. The resulting sequences were analyzed using Geneious (V.11.0.5) complemented with RotaC (V.2.0).

Results

During the pre-vaccine period, 33.3% each of G2P[4], G8P[4] and G8P[6] strains constituted the DS-1-like constellation, while G1P[8] (25%), G4P[6] (7.5%), G9P[8] (60%) and G12P[6] (7.5%) were identified for the Wa-like. In sharp contrast to this observation, fluctuations were evident in the P-genotypes with 66.7% G8P[4] (DS-1-like) and Wa-like (G1P[6] (7.4%), G4P[8] (3.7%), G9P[6] (1.2%) and G12P[8] (39.5%)) constellations observed, post-vaccination. Provisional analysis revealed no genomic evidence that the emergence and variability of P-genotypes was due to vaccine escape mutants.

Conclusions

This study showed high variability frequency and emergence of P-types in stable DS-1- and Wa-like constellations in the post-vaccine period in Rwanda. Although, it is unclear if the observed variability in the P-genotypes is related to vaccine introduction, or attributable to normal genotype fluctuations, analysis of antigenic regions and comparison with cognate reference strains to provide genomic evidence to ascertain this is underway. Continued whole genome sequence surveillance pre- and post-vaccination will be pivotal to monitor circulating rotavirus strains over time and detect unusual/emerging genotypes.