Rotavirus group A genotype circulation patterns across Kenya before and after nationwide vaccine introduction, 2010-2018

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Abstract

Background: Kenya introduced the monovalent G1P[8] Rotarix® vaccine into the infant immunization schedule in July 2014. We examined trends in rotavirus group A (RVA) genotype distribution pre- (January 2010 - June 2014) and post- (July 2014-December 2018) RVA vaccine introduction.

Methods: Stool samples were collected from children aged <13 years from four surveillance sites across Kenya: Kilifi County Hospital, Tabitha Clinic, Lwak Mission Hospital, and Siaya County Referral Hospital (children aged <5 years only). Samples were screened for RVA using enzyme linked immunosorbent assay (ELISA) and G and P genes sequenced to infer genotypes.

Results: We genotyped 614 samples in pre-vaccine and 261 in post-vaccine introduction periods. During the pre-vaccine introduction period, the most frequent RVA genotypes were G1P[8] (45.8%), G8P[4] (15.8%), G9P[8] (13.2%), G2P[4] (7.0%) and G3P[6] (3.1%). In the post-vaccine introduction period, the most frequent genotypes were G1P[8] (52.1%), G2P[4] (20.7%) and G3P[8] (16.1%). Predominant genotypes varied by year and site in both pre and post-vaccine periods. Temporal genotype patterns showed an increase in prevalence of heterotypic commonly DS-1-like G2P[4] (7.0 to 20.7%, P <.001) and G3P[8] (1.3 to 16.1%, P< .001) genotypes in the post-vaccine introduction period. Additionally, we observed a decline in prevalence of genotypes G8P[4] (15.8 to 0.4%, P <.001) and G9P[8] (13.2 to 5.4%, P <.001) in the post-vaccine introduction period.

Conclusion: Genotype prevalence varied from before to after vaccine introduction. Such observations emphasize the need for long-term surveillance to monitor vaccine impact. These changes may represent natural secular variation or possible immuno-epidemiological changes arising from the introduction of the vaccine. Full length sequencing could provide insights into post-vaccine evolutionary pressures and antigenic diversity.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures
Temporal rotavirus genotype distribution in the three surveillance sites across Kenya; a - Kilifi County Hospital in Kilifi County, b - Tabitha Clinic in Kibera, Nairobi County, c - Siaya County (combined genotype data from Lwak Mission Hospital and Siaya Referral Hospital) and d - combination of the three Counties in Kenya between 2010 to 2018.
Comparison of prevalence of the dominant genotypes (G1P[8], G2P[4], G3P[8], G8P[4] and G9P[8]) at 95% confidence interval (CI) during the pre- (Jan 2010-Jun 2014) and post-(July 2014 – Dec 2018) vaccine introduction periods in Kenya. The predominant genotypes were selected based on their frequency as indicated in Table 3.

Supplementary Files
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