

Rotavirus group A characterization before and after nationwide vaccine introduction in Kenya, 2010-2018

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Background

Group A rotavirus (RVA) is the major cause of gastroenteritis in children worldwide. Kenya introduced the RotarixTM vaccine into the infant immunization schedule in July 2014. Continuous surveillance of RVA in diarrhea admissions in Kenya has been undertaken since 2010. Herein, we report the trends and distribution of RVA genotypes in Kenya before and after vaccine deployment.

Methods

Stool samples were collected from diarrheic children <13 years hospitalized between 2010-2018 across three sentinel sites (Kilifi, Lwak and Kibera) in Kenya. Sequences were obtained from the VP7 (encoding G gene) and VP4 (encoding P gene) of the RVA positive stool samples and genotypes determined by the VIPR online genotyping tool.

Results

A total of 645 (67%) samples were successfully genotyped for both G and P genes. During the pre-vaccine era, the most frequent RVA strains were G1P[8] (52%), G8P[4] (18%), G9P[8] (11%) and G2P[4] (10%). In the post-vaccine introduction era, the most frequent strains observed were G1P[8] (52%), G2P[4] (21%) and G3P[8] (17%). These dominant genotypes were observed across all the surveillances sites with several other unusual and diverse genotypes circulating in low proportions. Temporal genotype pattern analysis showed a re-emergence and dominance of heterotypic G2P[4] and G3P[8] strains in the post-vaccine introduction period (2016-2018).

Conclusion

Although there is detection of the non-vaccine strains in the post-vaccine introduction period, the inconsistency in the circulation pattern of the strains might not be as a result of selective pressure from vaccine use, following vaccine introduction and this requires further monitoring. Further work is necessary to determine potential source of the re-emerging strains