

Molecular epidemiology of rotavirus genotype and corresponding trends in Kenya since 1975

¹Atunga Nyachieo, ¹Nicholas M. Kiulia, ¹Mary Galo, ¹E. Omolo, ¹Jason M. Mwenda.
¹Enteric Viruses Research Group, Institute of Primate Research, Karen, Nairobi, Kenya

Background

Globally over 215 000 children <5years die annually due to rotavirus (RV) infection with over 80% occurring in Sub-Sahara Africa. Since the introduction of rotavirus vaccine, there has been a decline. Nevertheless, molecular epidemiology still remains important in Kenya to determine accurately the burden of rotavirus disease and the emerging new genotypes and understand genotype trends pre and post vaccine era.

Objective: To evaluate the trends of rotavirus strains/genotypes since 1975.

Methods

Rotavirus data was evaluated from published articles (including our data) since 1975. The methods of assay, the genotype trends and seasonality were evaluated.

Results

The analysis showed that rotavirus prevalence was 6-56% with diarrhoea occurring throughout the year and generally exhibiting distinct peaks during the dry months. Among the common genotype, G1 was the most predominant up to the year 2002 but more recently there has been an emergence of genotype G9 as the most predominant genotype and to a less extent G8.

Conclusion

The overall prevalence and the obtained trends of rotavirus infection in young children with diarrhea indicate that rotavirus still plays an important role and in some cases its even severe.