

Diversity of circulating rotavirus strains pre-vaccination amongst under five children presenting with diarrhoea at the University of Ilorin teaching hospital, North-Central Nigeria from 2013-2018

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Background

Rotavirus remains the leading cause of diarrhoea related hospitalizations and death globally. Vaccination is an effective strategy for its prevention. Knowledge of the local rotavirus genotype diversity is important pre and post vaccine introduction. This study aims to describe rotavirus genotype diversity following six year pre-vaccine introduction surveillance.

Method

The study was conducted at University of Ilorin Teaching Hospital in North-Central Nigeria. Children aged less than five years hospitalized with diarrhoea were recruited consecutively. Relevant clinical data was collected. Stool samples were collected and tested for rotavirus by ELISA. Rotavirus ELISA positive samples were analysed at a regional reference laboratory for rotavirus strains by polymerase chain reaction (PCR). Data was entered into the WHO Rotavirus surveillance module and analysed using EPI-Info.

Results

903 subjects were recruited over the period January 2013 – December 2018. Two hundred and eighty six samples (31.7%) tested ELISA positive for rotavirus. Genotype results for 260 (90.9%) were available. The commonest G-types were G1(129; 49.6%) and G2(39;15.0%). The commonest P-types were P[8](88;33.8%) and P[6](88;33.8%). The most frequent combinations were G1P[8] in 73 samples (28.1%), G1P[6] in 27 (10.4%) and G2P[6] in 22(8.5%). There were a high proportion of samples with mixed genotypes. There were wide variations in predominant strains annually.

Conclusion

The most frequent rotavirus genotypes in Ilorin are similar to reports from most African countries, however there is a wide variability in predominant genotypes.