

Genetic diversity of norovirus in children from 0 to 5 years old with acute diarrhea in Mozambique (2014 – 2015)

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Background

Norovirus (NoV) is the second most important cause of diarrheal disease in children worldwide after rotavirus, and is estimated to be responsible for 18% of acute diarrhea. NoV is classified into 7 genogroups (GI - GVII) and > 40 genotypes. Despite the burden of NoV in diarrheal disease, there are no published studies describing genotypes in Mozambique. This study aimed to determine the NoV genotypes in Mozambique.

Methodology

Stool specimens collected from children under the age of 5 years, between May 2014 and December 2015 within the Mozambique National Surveillance of Acute Diarrhea, were tested for NoV genogroup I (GI) and GII using conventional reverse transcriptase-polymerase chain reaction (RT-PCR). Positive specimens were sent to South Africa (Department of Medical Virology, University of Pretoria) for confirmation using real-time RT-PCR (qRT-PCR) and genotyping. Nucleotide sequences were aligned using MAFFT, phylogenetic analyses were performed using MEGA 7.

Results

During this period, 203 stool specimens were tested for NoV, 57.6% (117/203) from males and 87.2% (177/203) from children < 2 years of age. The rate of NoV detection was 13.8% (28/203). Twenty-three specimens (82.1%; 23/28) were confirmed by real time RT-PCR and NoV GII predominated (69.6%; 16/23). NoV strains in 23 positive specimens, 95.7% (22/23) could be genotyped by nucleotide sequence analysis. NoV GII.4 Sydney 2102 was the predominant genotype detected (n=7), other genotypes detected were: GII.3 (n=3), GII.7 (n=2), GII.17 (n=1), GII.21 (n=1), GII.4 not assigned (1), GI.7 (n=3), GI.3 (n=2) and GI.2 (n=2).

Conclusion

This study showed a high genetic diversity of NoV in Mozambican children and emphasises the need to continue to determine the role of NoV after rotavirus vaccine introduction in the country.