

Genetic Diversity of Norovirus Strains isolated from Stool Samples of Ethiopian Children under the Age of Five Years

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Background

Following the rotavirus vaccine introduction, norovirus has emerged as a leading cause of severe gastroenteritis in children. Despite Ethiopia's high burden of gastroenteritis, there is limited data on the prevalence and genetic diversity of circulating norovirus strains in the region. This study aimed to investigate the molecular characteristics of norovirus strains detected in stool samples from children hospitalized with severe gastroenteritis in Ethiopia between 2021 and 2022.

Materials and Methods

A total of 102 faecal samples were tested for norovirus using RT-PCR targeting the ORF1/ORF2 region. Positive samples were confirmed by agarose gel electrophoresis and submitted for Sanger sequencing. The sequences were genotyped using the online Norovirus Typing Tool. Phylogenetic analysis was performed using MEGA 11 software with the maximum likelihood method to assess genetic relationships between Ethiopian strains and global reference sequences.

Results

Norovirus was detected in 16 of 102 samples, yielding a prevalence of 15.7% among children under five years of age. Fourteen samples were successfully sequenced and 11 were genotyped. Genogroup II (GII) predominated (82%, 9/11), while Genogroup I (GI) accounted for 18% (2/11). Nine GII genotypes (GII.2, GII.3, GII.4, GII.6, GII.P4, GII.P17, GII.17, GII.P30, and GII.P31) and two GI genotypes (GI.P4 and GI.P5) were identified. GI.P4 clustered with strains from Spain and France, whereas GII.6 aligned with West African sequences.

Conclusion

This study demonstrates high genetic diversity of norovirus among hospitalized children in Ethiopia. Continued surveillance of norovirus alongside rotavirus is

recommended to monitor emerging strains and better control norovirus-associated gastroenteritis in this region.