

Understanding Pediatric Norovirus Epidemiology: A decade of study among Ghanaian children

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Background

Noroviruses are a highly diverse group of diarrheagenic RNA viruses and a cause of acute gastroenteritis (AGE) in all age groups with the elderly and young children usually experiencing severe clinical outcomes. Following better diagnostic techniques, earnest research and development of prospective vaccine candidates, noroviruses have received increasing recognition as important etiological agents of severe acute gastroenteritis especially in children under five years old. The study aimed to describe the epidemiology of noroviruses and norovirus strain diversity in the pediatric population of Ghana.

Methods

Diarrhoeic stool samples collected between 2008 and 2017 as part of an ongoing national rotavirus surveillance from children <5 years were used for this study. Samples were tested for norovirus antigen by EIA. Partial polymerase and capsid gene typing was performed by Sanger sequencing of positive diarrhoeic stool specimens. Genotypes were assigned with the RIVM genotyping tool while sequence and phylogenetic analysis were performed with MEGA 7 v0.26 software.

Results

Of the 1,334 stool samples tested, 36.1% (482/1334) of children were found to be shedding the virus. A high rate of norovirus infection was observed post-rotavirus vaccination era in Ghana. Overall, 365 of 482 (75.7%) positive samples belonged to GII, 69 of 482 (14.3%) belonged to GI and 47 of 482 (9.8%) were mixed infections of both genogroups I & II. The most consistently and commonly detected norovirus strain was GII.P4-GII.4 (54.1%) and GII.P21-GII.3 (8.0%). The remaining ~40.0% of typed samples were a diverse mixture of genotypes some of which were detected more in some years. Phylogenetic analysis of Ghanaian GII.4 strains showed 64.0% of them clustering with the GII.4 Sydney_2012 variants associated with current global norovirus diarrhoeal epidemics whilst 30.0% remained unassigned.

Conclusion

The highly diverse nature of norovirus genotypes and strains necessitates its continuous monitoring and in-depth genetic analysis to better understand their evolution and implication for efforts being made towards vaccine discovery.