The prevalence and molecular characterization of norovirus strains circulating in children under 5 years hospitalized for diarrhoea in Southern and Eastern African countries during 2015

Leshabana AM[1], Esona MD[1], Weldegebriel G [2], Mukaratirwa A[3], Rahajamanana VL[4] Abebe A[5], Maphalala G[6], Simwaka J[7], Mwenda J[8], Mphahlele J[1], Seheri LM[1]

[1]SMU Diarrhoeal Pathogens Research Unit, Department of Virology, Sefako Makgatho Health Sciences University, South Africa, [2]WHO IST East and Southern Africa, Harare, Zimbabwe [3]Department of Medical Microbiology (University of Zimbabwe-College of Health Sciences) [4]Department of Child Health, Teaching Hospital, Centre HospitalierUniversitaireMère Enfant Tsaralàlana, Antananarivo, Madagascar, [5]Ethiopian Public Health Institute, [6]The National Clinical Laboratory Service, Mbabane, Swaziland, [7]University Teaching Hospital, Department of Pathology and Microbiology, Virology Laboratory, Lusaka, Zambia, [8]African Rotavirus Surveillance Network, Immunization, Vaccines and Development Cluster, WHO African Regional Office, Brazzaville, Congo

Background

Noroviruses are major causative agents of foodborne and waterborne disease outbreaks, and the most common cause of viral gastroenteritis in adults and children worldwide. The characterization and molecular epidemiology of norovirus infection in children less than 5 years of age in Africa is not well defined. Thus, the aim of this study was to investigate the prevalence and characterization of the circulating norovirus strains in children less than 5 years of age hospitalized for diarrhoea in some of selected Southern and Eastern African countries during 2015.

Methods

Archival diarrhoeal stool samples collected from Ethiopia, Kenya, Lesotho Madagascar, South Africa, Swaziland, Tanzania, Zambia and Zimbabwe during 2015 rotavirus season were used for this study. A total number of 401 stool specimens were tested for norovirus using conventional reverse-transcriptase polymerase chain reaction (RT-PCR). The PCR products were subjected to nucleotide sequencing for genogroups and genotypes identification. Furthermore, a subset of 89 stool samples were used to evaluate sensitivity and specificity of Ridascreen® Norovirus 3rd Generation enzyme linked immunosorbent assay (ELISA) and conventional RT-PCR assays.

Results

Norovirus was detected in 21/401 (5.2%) of the stool samples analysed using conventional RT-PCR. Our study shows that norovirus GII.Pe (53%) was the most predominant strain, followed by GII.P4 (16%), GII.P17 (16%), GII.Pa (5%), GI.P7 (5%) and GI.Pb (5%). Phylogenetic analysis and nucleotide sequencing indicated that most of norovirus strains that were detected belonged to GII.4 variants (GII.Pe and GII.P4). These strains were mainly circulating in Madagascar and Tanzania. Of the 89 stool samples tested with Ridascreen ELISA, 12 (13.5%) were norovirus positive and 15 (16.9%) were norovirus RNA positive by conventional RT-PCR. The estimated sensitivity and specificity of Ridascreen Elisa was 80% and 100%, respectively.

Conclusions

The findings revealed that norovirus detection rate was very low (5.2%) as previously speculated in Southern and Eastern African countries. Further robust norovirus surveillance studies are required to determine the burden of norovirus diseases in order to enhance the current understanding of the epidemiology of norovirus infection. Furthermore, our data indicate that GII.Pe and GII.P4 were the most common cause of severe diarrhoea in children < 5 years of age indicating its geographical distribution in the continent.