

Genetic Diversity of Norovirus Strains in Outpatient Children from Rural Communities of Vhembe District, South Africa, 2014-2015

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Abstract : Norovirus is now considered the most common cause of outbreaks of nonbacterial gastroenteritis. Limited data are available for Norovirus strains in Africa, especially in rural and peri-urban areas. Despite the excessive burden of diarrhea disease in developing countries, Norovirus infections have been to date mostly reported in developed countries. There is a need to investigate intensively the role of viral agents associated with diarrhea in different settings in Africa continent. To determine the prevalence and genetic diversity of Norovirus strains circulating in the rural communities in the Limpopo Province, South Africa and investigate the genetic relationship between Norovirus strains, a cross-sectional study was performed on human stools collected from rural communities. Between July 2014 and April 2015, outpatient children under 5 years of age from rural communities of Vhembe District, South Africa, were recorded for the study. A total of 303 stool specimens were collected from those with diarrhea (n=253) and without (n=50) diarrhea. NoVs were identified using real-time one-step RT-PCR. Partial Sequence analyses were performed to genotype the strains. Phylogenetic analyses were performed to compare identified NoVs genotypes to the worldwide circulating strains. Norovirus detection rate was 41.1% (104/253) in children with diarrhea. There was no significant difference (OR=1.24; 95% CI 0.66-2.33) in Norovirus detection between symptomatic and asymptomatic children. Comparison of the median CT values for NoV in children with diarrhea and without diarrhea revealed significant statistical difference of estimated GII viral load from both groups, with a much higher viral burden in children with diarrhea. To our knowledge, this is the first study reporting on the differences in estimated viral load of GII and GI NoV positive cases and controls. GII.Pe (n=9) were the predominant genotypes followed by GII.Pe/GII.4 Sydney 2012 (n=8) suspected recombinant and GII.4 Sydney 2012 variants(n=7). Two unassigned GII.4 variants and an unusual RdRp genotype GII.P15 were found. With note, the rare GIIP15 identified in this study has a common ancestor with GIIP15 strain from Japan previously reported as GII/untypeable recombinant strain implicated in a gastroenteritis outbreak. To our knowledge, this is the first report of this unusual genotype in the African continent. Though not confirmed predictive of diarrhea disease in this study, the high detection rate of NoV is an indication of subsequent exposure of children from rural communities to enteric pathogens due to poor sanitation and hygiene practices. The results reveal that the difference between asymptomatic and symptomatic children with NoV may possibly be related to the NoV genogroups involved. The findings emphasize NoV genetic diversity and predominance of GII.Pe/GII.4 Sydney 2012, indicative of increased NoV activity. An uncommon GII.P15 and two unassigned GII.4 variants were also identified from rural settings of the Vhembe District/South Africa. NoV surveillance is required to help to inform investigations into NoV evolution, and to support vaccine development programmes in Africa.

Keywords : asymptomatic, common, outpatients, norovirus genetic diversity, sporadic gastroenteritis, South African rural communities, symptomatic

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