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## Molecular characterization of Norovirus strains circulating in rural communities of the Limpopo province of South Africa

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Data supporting the role of NoV in diarrheal disease are limited in the African continent. This study determines the estimated viral burden of NoV in symptomatic and asymptomatic children and investigates NoV genotypes diversity in outpatient children from rural communities of Vhembe district, South Africa. Between July 2014 and April 2015, 303 stool specimens were collected from young children with diarrhea (n=253) and without (n=50) diarrhea. NoVs were identified using real-time one-step RT-PCR and Nucleotide sequencing methods were performed to genotype the strains. One hundred and four (41.1%) NoVs were detected. NoV detection rates in symptomatic and asymptomatic children (OR=1.24; 95% CI 0.66–2.33) were not significantly different. Comparison of the median CT values for NoV in symptomatic and asymptomatic children revealed significant statistical difference of estimated GII viral load from both groups. The sequence analyses demonstrated multiple NoV genotypes including GI.4 (13.8%), GI.5 (6.9%), GII.14 (6.9%), GII.4 (31%), GII.6 (3.4%), GII.P15 (3.4%), GII.P21 (3.4%) and GII.Pe (31%). The most prevalent NoV genotypes were GII.4 Sydney 2012 variants (n=7) among the capsid genotypes, GII.Pe (n=9) among the polymerase genotypes and GII.Pe/GII.4 Sydney 2012 (n=8) putative recombinants among the RdRp/Capsid genotypes. Though not proven predictive of diarrhea disease in this study, the results suggest that the difference between asymptomatic and symptomatic children with NoV may be at the level of the viral load of NoV genogroups involved. The findings revealed continuous pandemic spread and predominance of GII.Pe/GII.4 Sydney 2012, indicative of increased NoV activity in the study region.

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