

JOINT EVENT

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Molecular epidemiology of noroviruses in fewer than five year children with acute gastroenteritis in Yaoundé, Cameroon**Akongnwi E Mugyia¹, Valentine N Ndze^{2,5}, Jane Francis T K Akoachere¹, Lucy M Ndip¹, Hannah Browne⁴, Angeline Boula³, Mathew D Esona⁴, Paul Koki Ndombo^{2,3} and Jan Vinjé⁴**¹University of Buea, Cameroon²University of Yaoundé I, Cameroon³Rotavirus National Reference Laboratory, Cameroon⁴Centers for Disease Control and Prevention, USA⁵Metabiota, Cameroon

Background: Norovirus is a major cause of acute gastroenteritis among children in developing countries. Limited data are available on the burden of norovirus gastroenteritis and genotype distribution in Cameroon, where early childhood mortality due to acute gastroenteritis is common.

Methodology: Stool specimens from 903 hospitalized children under 5 years of age hospitalized with acute diarrhea were collected in Yaoundé, Cameroon between January 2010 and December 2013. Clinical data were analyzed and the stool specimens were tested for noroviruses by duplex conventional RT-PCR. Positive samples were genotyped by nucleotide sequence analysis.

Results: Overall 99 (10.7%) samples tested positive for noroviruses and 76 were successfully sequenced. Two (2.6%) samples were genogroup I (GI) positive and 74 (97.4%) samples were genogroup II (GII) positive. Sequence analyses demonstrated co-circulation of 10 different norovirus genotypes including GI.2 (1.3%); GI.6 (1.3%) and 8 GII genotypes. The predominant genotype was GII.4 causing 80.3% of the infections and three different GII.4 variants were detected: GII.4Apeldoorn, GII.4NewOrleans and GII.4Sydney. Other genotypes included GII.1 (1.3%); GII.2 (1.3%); GII.3 (3.6%); GII.6 (1.3%), GII.16 (2.6%); GII.17 (2.6%); GII.21 (5.3%). The relatively rare GII.21 (5.3%) was the second most prevalent genotype. Norovirus was detected throughout the year with peaks in October and November. A higher percentage of children less than 12 months of age were positive for noroviruses.

Conclusion: A single genotype (GII.4) caused the majority of the infections. GII.4Sydney was detected in samples collected in 2010, 2 years before the Sydney reference strain was first described, which suggests that young children may serve as a reservoir from which new norovirus epidemic strains emerge and spread. This was further supported by the presence of GII.17 Kawasaki viruses that a few years later (2014) emerged as the predominant cause of outbreaks in East Asia.

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