

The Detection and Molecular Characterization of Human Rotavirus G12 Genotypes in the Eastern Part of Kenya

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He is currently working as a Enteric Viruses Researcher at Enteric Viruses Research Group, the Institute of Primate Research in Kenya, primarily working on the molecular characterization of selected enteric viruses in human and environmental samples in Kenya.

He is a young scientist who has contributed significantly to the surveillance of enteric viruses both in clinical and environmental water samples in Kenya. His research work has provided crucial data on the circulating enteric viruses in the Kenyan community especially in the field of health-related water microbiology and epidemiology of enteric viruses in Kenya. His work has been published in international peer reviewed journals and presented in various international symposiums.

Report

As we had proposed in the Research plan to Small Grant Program, we have generated important and very interesting data. The work was concluded in September 2010. Part of the results was presented as a poster at the Equitable Global Health symposium held in Bochum, Germany 7th and 8th October 2010. We are now in the process of publishing the data in an international peer-reviewed journal.

Background

Globally, rotaviruses (RVs) are the most common cause of severe infantile viral diarrheal disease in infants and children < 5 years of age with ~ 527,000 deaths occurring annually in the less developed countries (WHO, 2007). In Africa alone approximately 300,000 young children < 5 years die each year due to RVs (Sanchez-Padilla *et al.*, 2009). In Kenya, it is estimated that RV infection causes 19% hospitalizations, 16% of clinics visit for diarrhea among children < 5 years and about 4,500 deaths annually. Nationally RV cost the health care system about \$10.8 million annually. It has been argued that introduction of RV vaccine will avert 55 % of death, 65 % of hospitalization due to RV infection (Tate *et al.*, 2009).

Prospective surveillance is required to monitor and characterize rotavirus infections, including viral and clinical data, and to detect the emergence of potentially epidemic strains.

Objectives

The objective of this surveillance was to determine the epidemiology and the disease burden caused by hospitalization due to rotavirus in children <5 years of age in the Eastern region and to ascertain whether the distribution of rotavirus serotypes in circulation differs from the available rotavirus vaccines strain

Methods

Hospital surveillance data for rotavirus infections among children aged < 5 years of age was started September 2009 in the Eastern region of Kenya. Cases of acute watery diarrhoea lasting 7 days or less, who are below 5 years of age and had been admitted to the Hospital were enrolled for surveillance. Children with bloody diarrhoea and those who acquired diarrhoea in the ward were excluded. A standard case report form (questionnaire) was used to record the children's socio-demographic data.

Diarrhoea faecal samples collected from children under 5 years of age with acute gastroenteritis were analyzed by enzyme immunoassays (EIA) and the positive samples genotyped by reverse transcriptase/polymerase chain reaction (RT-PCR) with RV specific primer pairs used for amplification of the VP7 and VP4 gene.

Results

From this study G12 was detected for the first time with a G/P combination as G12P [6]. The other genotypes detected were G9 P[4] and G9 P[8]. The common strain detected was G2 P[4]. It was interesting to see that most of the common strains G1 P[8] and G3 P[8] that are already included in the licensed rotavirus vaccines were not identified in this study.

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Small Grant Report of Nicholas Kiulia

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ISID Small Grant Program Report *continued*

Conclusion

Rotavirus is an important cause of acute watery diarrhoea in the Eastern region of Kenya among the under five children. The detection of G12 strains from different parts of the world in recent years suggests the possibility of its emergence as an important global genotype. Thus, monitoring of cocirculating rotavirus strains and detection of emerging strains is important in the context of the availability of rotavirus vaccines.

Owing to the recent emergence of G12 rotavirus, the findings from this study are important since they provide new information concerning the local and global spread of rotavirus genotypes. This study has extended our knowledge on the circulating G-genotype circulating in the eastern region of Kenya.

It is important to continue the surveillance of rotavirus strains and to determine accurately the burden of rotavirus disease in Kenya and the emerging new genotypes as this will assist policy makers in decision making on rotavirus vaccine introduction and determining the impact of the vaccine.

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