

# Distribution of Rotavirus Genotypes among Children with Diarrhea prior to Vaccine Introduction in Western Kenya, 2010-2013

J.B Ochieng<sup>1\*</sup>, S Khagayi<sup>1</sup>, B Ogwel<sup>1</sup>, E Apondi<sup>1</sup>, J Juma<sup>1</sup>, M Seheri<sup>2</sup>, I Peenze<sup>2</sup>, C Tabu<sup>3</sup>, S Kibet<sup>4</sup>, R Omore<sup>1</sup>, J Mphahlele<sup>2</sup>, G Bigogo<sup>1</sup>, K.F Laserson<sup>5</sup>, J.E Tate<sup>6</sup>, J.M Mwenda<sup>7</sup>, R.F Breiman<sup>8</sup>.

<sup>1</sup>Center for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya, <sup>2</sup>Department of Virology, South African Medical Research Council / Diarrheal Pathogens Research Unit, Sefako Makgatho Health Sciences University, Pretoria, South Africa, <sup>3</sup>Division of Vaccines and Immunization, Ministry of Health, Nairobi, Kenya, <sup>4</sup>Division of Disease Surveillance, World Health Organization Country Office, Nairobi, Kenya, <sup>5</sup>Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, GA, USA, <sup>6</sup>Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, <sup>7</sup>Division of Disease Surveillance, World Health Organization AFRO, Congo Brazzaville, <sup>8</sup>Emory Global Health Institute, Emory University, Atlanta, GA, USA

## Background

Group A rotavirus is the leading cause of diarrhea hospitalization among children worldwide. Most fatal rotavirus-associated diarrhea cases among children under 5 years occur in Africa and Asia. We investigated the molecular epidemiology of circulating rotavirus strains among children less than 5 years in western Kenya to provide baseline data on the prevalence of each genotype prior to the introduction of monovalent rotavirus vaccine in Kenya.

## Methods

From January 2010 to December 2013, stool samples were collected from 1677 children with acute gastroenteritis. All specimens were transported to Kenya Medical Research Institute, Center for Global Health Research, Enterics Laboratory and tested for rotavirus antigens using enzyme immunoassay. Rotavirus dsRNA was extracted from 234 simple randomly selected EIA positive stool samples using QIAamp viral RNA mini kit and tested by semi-nested RT-PCR for G and P genotypes using type-specific primers. The PCR products were analyzed by gel electrophoresis. Chi-square test was used to test the association between rotavirus genotypes and age.

## Results

Of the 1677 stool samples tested, 401 (23.9%) were positive for group A rotavirus antigen. Of the 234 rotavirus dsRNA extractions analyzed by PCR, 219 (93.6%) and 193 (82.5%) typed positive for at least one of the VP7 genotypes (G type) and VP4 genotypes (P types), respectively. Of the typeable, 19 were mixed G types and P types. However, 15 VP7 and 41 VP4 were nontypeable. The predominant genotypes detected included G1 (30%), G9 (27%), G8 (10%) and G3 (9%) for the G types, and P[8] (33%) and P[6] (30%) for the P types. The predominant combinations were: G1P[8] (15%), G9P[8] (12%) and G3P[6] (8%) which combined accounted for 35% of the genotypes detected.

## Conclusions

This study demonstrated the genotype diversity and dominance of G1, G3, G8 and G9 in combination with P[6] and P[8] as the most common genotypes associated with rotavirus gastroenteritis in this population. Continuous surveillance is necessary to monitor the effectiveness of the vaccine and shifts among the circulating genotypes in this region.