

**Protection and Molecular Characterization of Rotavirus Strains
Title: Isolated from Children Attending Selected Health Facilities in
Kiambu District**

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Despite numerous health intervention measures available, severe dehydrating rotavirus diarrhea remains a major contributor towards childhood mortality particularly in developing countries. Global rotavirus surveillance is vital towards the development of safe, effective and efficacious vaccines to control the associated high infection rates. In Kenya, however, there is little corroborated data on rotavirus epidemiology, burden of disease and strains in circulation. The objective of this study was to determine the prevalence and molecular characteristics of rotavirus strains responsible for severe gastroenteritis in children in Kiambu District, Kenya. A total of 232 fecal samples were collected between August 2008 and May 2011 from children below 5 years old with diarrhea hospitalized at Kiambu District Hospital and Karuri Health Centre. The specimens were screened for group A rotavirus using Enzyme Linked Immunosorbent Assay (ELISA). RNA from ELISA-positive specimens was separated by polyacrylamide gel electrophoresis (PAGE) to determine rotavirus electropherotypes. Reverse Transcription Polymerase Chain Reaction (RT-PCR) was used to determine rotavirus G and P genotypes. The ELISA screen gave 36.6% positive results for group A rotavirus among the diarrheal cases. Rotavirus was detected most frequently in infants and young children aged below 2 years with a peak at 6 to 11 months ($X^2 = 12.162$; $df = 4$; $P = 0.016$). The virus was found year-round with slight peaks and valleys in some months ($X^2 = 96$; $df = 90$; $P \text{ value} = 0.313$). Of the 85 ELISA positive samples, 58 (68.1%) gave visible RNA profiles whereas 28 (32.9%) gave invisible profile. Of the visible RNA profiles, 92.9%, 5.3% and 1.8% displayed long, short and more than 11 RNA segments electropherotypes respectively ($X^2 = 344.621$; $df = 1$; $P = 0.001$). Five different G genotypes were determined in 55 of 85 of the specimens analysed ($X^2 = 447.48$; $df = 1$; $P = 0.001$). G1 was predominated among the strains at 44.7%. Other usual global genotypes; G2, G4 and G9 were detected at 10.60%, 4.7% and 1.2% respectively. G8, an African-specific strain was isolated at 8.2%. Three different P genotypes were determined in 55.3% of the specimens analysed ($X^2 = 376.379$; $df = 1$; $P = 0.001$). P [8] and P [4] predominated at 28.2% and 25.9% respectively. P [6], an African-specific strain was isolated in one sample. Data generated from this study will add crucial information on the burden of the rotavirus disease and genotype distribution in the country. Such information will not only aid in seeking advocacy for rotavirus vaccine introduction in the country's national immunization programme, but will also help in the evaluation of the efficacy of these vaccines in relation to the rotavirus genotypes in circulation. The heterogeneity and ever-changing epidemiology of rotavirus observed in this and other related studies underscores the need for continued surveillance of rotavirus strains throughout Kenya to ensure that vaccination programmes being advocated for provide optimal protection.