ABSTRACT

 BACKGROUND:

The World Health Organization has recommended that rotavirus (RV) vaccines be included in all national immunization programs as part of a strategy to control RV-associated diarrheal diseases. Hospital-based surveillance of RV infection is therefore crucial in monitoring the impact pre- and post-vaccine introduction and also to document changes in genotype distribution. This study sought to determine the RV genotypes circulating in the eastern region of Kenya before introduction of the RV vaccine.

METHODS:

During September 2009 to August 2011, 500 stool samples were collected from children <5 years of age admitted for acute diarrhea in hospitals in the eastern region of Kenya and analyzed for the presence of group A RV using an enzyme immunoassay. G and P genotypes were determined using hemi-nested reverse transcriptase polymerase chain reaction.

RESULTS:

One hundred and eighty nine out of 500 (38%) samples analyzed were positive for rotavirus. The following G types were detected: G9 (50.9%), G1 (26.8%), G8 (12.1%), G12 (3.1%), G2 (0.6%), mixed G (1.3%) and 5.1% were G nontypeable. P types detected included: P[8] (63.7%), P[4] (12.1%), P[6] (4.5%), mixed P (7.6%) and 12.1% were P nontypeable. The most dominant strain was G9P[8] (35%), followed by G1P[8] (26.8%), G8P[4] (9.6%), G12P[6] (2.5%), G9P[6] (1.9%), G9P[4] (1.3%), G8P[8] (1.3%), and G2P[4] (0.6%).

CONCLUSIONS:

The present study demonstrates the recurring changing genotypes of RV circulating in Kenya, with genotypes G9, G1 and G8 being the dominant strains circulating in the eastern region of Kenya between 2009 and 2011. Additionally, G12 genotype was detected for the first time in Kenya.