

Diversity of Circulating Rotavirus Genotypes in Ethiopia, 2011-2017

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Introduction

Group A rotaviruses, family *Reoviridae* are major etiologic agents for pediatric gastroenteritis, characterized by severe dehydrating diarrhea in infants & young children leading to deaths particularly in sub-Saharan Africa region. Prevalence of pathogenic serotypes varies worldwide and serotypes are continually changing. Rotavirus vaccine (Rotarix) was introduced in Ethiopian EPI system in November 2013. In his paper, analysis of diversity of circulating rotavirus genotypes in Ethiopia, pre and post vaccination era, is presented using data from the enteropathogenes sentinel surveillance system.

Methods

Stool specimens were collected among children <5 years of age enrolled in three hospital based enteropathogenes sentinel surveillance sites in Ethiopia 2011-2017. Detection of the presence of Rotavirus in the stool was done using an antigen capture enzyme immunoassay technique. Rotavirus positive samples were further characterized by rotavirus genotyping methods to identify the predominant circulating genotypes (G and P types).

Results

A total of 1620 children <5 years of age were enrolled between 2011- 2017 from the three sentinel sites in Addis Ababa, Ethiopia. Out of which 156 from pre and 147 from post-vaccination periods were Rotavirus positive samples and were further characterized by rotavirus genotyping methods. The most prevalent circulating strains were G12P [8] in 2011 (36%) and in 2012 (27%), G2P [4] (35%) in 2013, G9P [8] (19%) in 2014, G3P [6] and G2P [4] (19%) each in 2015, and G3P [8] (29%) in 2016. Highest genotype combinations circulating in 2017 were also identified to be G3P [8] (44%) followed by G12 P [8] (16%) and G12 P [6] (12%).

Conclusion

The introduction of rotavirus vaccine in Ethiopia has greatly reduced rotavirus associated hospitalizations in children <5 years. A wide variety of rotavirus strains continued to circulate throughout the surveillance periods in Addis Ababa. Decrease in genotypes prevalence of G1P[8] and comparably increased prevalence of G3P[6] and G3P[8] strains in the post vaccine era have been observed. Uninterrupted monitoring of the rotavirus genotypes is required so as to clearly understand continuous change in genotype distribution.