Norovirus predominates in pediatric diarrhea after rotavirus vaccine introduction in Burkina Faso

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Background and aims

Norovirus (NoV) and Rotavirus (RV) are the two major viral enteropathogens of childhood. In Burkina Faso, national RV vaccination program using the pentavalent RV5 vaccine from Merck was implemented in October 2013. We have previously reported the reduction of RV gastroenteritis (GE) cases in the first 3 years after RV vaccination in Burkina Faso. This study describes the prevalence of NoV and RV after RV vaccine implementation in Burkina Faso.

Methods

From January to December 2015, we enrolled 146 children <5 years of age hospitalized with acute gastroenteritis (AGE) at Hôpital du District de Bogodogo (HBD) in Ouagadougou, the capital of Burkina Faso. Stool specimens were collected and screened for RV and NoV. RVs were detected by ELISA, and RV positive samples were G and P genotyped using sequencing and/or end-point multiplex RT-PCR assays. NoV was detected and genogrouped using a duplex TaqMan real-time PCR and genotyped by sequencing of the NS region. Phylogenetic trees were constructed with Maximum Likelihood using MEGA software.

Results

RVs were found in 14% (20/146) and NoVs in 20% (29/146) of the fecal samples of children hospitalized for diarrhea. No simultaneous infection was observed for both NoV and RVA. RV predominated during January to May while NoV was detected year round. RV G2P[4] was the most prevalent RV genotype (30%) followed by G12P[6] (25%) and G12P[8] (20%).

NoV GII.4 strains were the predominant 58% (11/19). Others NoVs genotypes observed in this study were globally rare: GII.12 11% (2/19), GII.14 5% (1/19), GII.15 5% (1/19), GII.3 11% (2/19), GII.6 5% (1/19), GII.9 5% (1/19). Only two NoVs genogroup GI were found: GI.3 66.7% (2/3) and GI.5 33.3% (1/3). 7 NoVs were not possible to genotype.

Conclusions

We conclude that the introductions of RV vaccination have reduced the prevalence of RV in the community in Burkina Faso and that NoV now is detected more frequently with a high diversity of circulating genotypes. This study highlights the need for further assessment of NoV following RV vaccine introduction.

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