

Molecular surveillance of rotavirus infection in Central African Republic, 2017-2018

¹Banga-Mingo Virginie, ²Chrysostom Gody Jean, ³Bowen Michael D, ⁴Mwenda Jason M, ⁵Ndjapou Severin, ⁶Waku-Kouomou Diane, ⁷Esona Mathew D, ⁸Guifara Gilbert

¹Institut Pasteur de Bangui, Central African Republic, ²Complexe Pédiatrique de Bangui, Central African Republic, ³Centers for Disease Control and Prevention (CDC), Atlanta, Georgia 30333, United States, ⁴World Health Organization, African region, Brazzaville, Congo, ⁵Ministry of Public Health, Bangui, Central African Republic, ⁶Page Nicola National Institute for Communicable Disease (NICD), South Africa, ⁷Centers for Disease Control and Prevention (CDC), Atlanta, Georgia 30333, United States, ⁸Fandema Jean Institut Pasteur de Bangui, Central African Republic, ⁸World Health Organization, Bangui, Central African Republic

Background

Rotavirus diarrhea is widespread, approximately 215 000 of children less than 5 years of age die each year due to severe dehydration.

In Africa, the detection rates of rotavirus diarrhea vary widely from region to region and country to country. In Central African Republic (CAR), the sentinel surveillance of rotavirus gastroenteritis was established in 2011. The main objective of the surveillance was to assess the burden of rotavirus gastroenteritis and identify rotavirus strains circulating in CAR before the introduction of rotavirus vaccine.

Methods

This surveillance was conducted as part of the World Health Organization (WHO) supported control of rotavirus diarrhea disease. Stool specimens were collected from children <5 years with diarrhea following WHO criteria at the sentinel site, Complexe Pédiatrique de Bangui (2017-2018). The samples were first screened for group A rotavirus antigen by enzyme immunoassay (EIA) using the ProSpecT™ Rotavirus kit. Positives were subjected to semi nested RT-PCR at Institut Pasteur de Bangui for genotyping. Ten percent of specimens were sent to NICD and CDC for quality control.

Results

Between 2017 and 2018, 277 (46%) out of 604 stools specimens were confirmed positive by EIA. The most prevalent G-types were G12 (27.8%), and G1 (25.6%). Predominant P-Types were P[6] (51.26%) and P[8] (28.15%). NT genotypes were detected, G-type 14.4%, P-type 15.8%. The most common G-P combinations were G12P[6] (23,4%), G1P[8] (13.7%). Quality control results showed 93% concordance in 2018.

Conclusion

G12 P[6] was the predominant genotype in CAR during the last 2 years pre vaccine introduction.