

## Post-vaccine circulating group a rotavirus strains in under 5 years children with acute diarrhea during 2015–2018 in Center region Cameroon

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Rotavirus infection caused more than 500,000 deaths in children under five before vaccine introduction in 2014 in developed and developing countries. The objective of this work was to determine the circulating genotypes of rotavirus in Center Region Cameroon after the introduction of the vaccine during 2015-2018.

A retrospective study was conducted as part of a comprehensive review of unpublished and unpublished data on genotypes of rotavirus G and P circulating in the Center Region of Cameroon. The descriptive data were expressed in the form of frequency tables and proportions.

A total of 439/2220 rotavirus positive cases were analyzed. In all, 385/439 strains were characterized for the P (VP4) specificity. Three different VP4 genotypes were observed, including P [4], P [6] and P [8]. The most predominant P genotypes were P [6] at 45.0% and P [4] at 23.6%. Mixed infections were observed at 4.6%, whereas 7.3% of the strains were P non-typeable. A total of 302/439 rotavirus strains were characterized for the G (VP7) specificity. VP7 genotypes G1, G2, G3, G4, G9 and G12 were observed. G2 (28.6%), G3 (14.6%) and G12 (14.2%) were the predominant G genotypes. 13.5% of all strains were G non-typeable whereas 17.4% were mixed G genotypes. A total of 431 strains were characterized for both G and P genes, from which 30 different G–P combinations were observed. Overall, G2P[4] (16.6%) was identified as the predominant rotavirus strain circulating in Cameroon followed by G12P [6] (13.0%).

In conclusion, we observed that the genotypes identified in Cameroon during 2015–2018 were partially covered by the two WHO recommended rotavirus vaccines. This review provides comprehensive up-to-date information on rotavirus strain surveillance in Cameroon during the post-vaccination era.

**Keywords:** rotavirus, genotypes, Center Region, Cameroon, vaccine