Identification of Rotavirus Strains circulating in the South West Region of Cameroon after Vaccine Introduction

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Background
Group A Rotavirus (RVA) remains the major cause of diarrhea in children below 5 years with an estimated annual death of 233,000 worldwide. Two oral RVA vaccines, RotaTeq® (RV5) and Rotarix® (RV1), have been licensed and adopted into routine immunization programs of more than 100 countries worldwide. In April 2014, Cameroon integrated RV1 in the national vaccination program but updated knowledge of circulating RVA strains in many regions post vaccine licensure from the country are still lacking. Pre-vaccine introduction RVA strain surveillance studies from Cameroon revealed a great diversity of RVA strains circulation, with the predominance of the G1P[8], and the emergence of unusual genotypes including G6, G8 and G12 with the following combination G6P[8], G12P[6], G8P[4] and G12P[8]. These findings raise the need to continue RVA strain surveillance in Cameroon in order to provide comprehensive, up-to-date data on circulating strains after vaccine introduction. The present study is a description of RVA strains circulating in the South West region of Cameroon in 2017.

Methods
Sixty-seven diarrhea stool samples were collected between the months of JulyNovember 2017 from children admitted or consulting for diarrhea in healthcare centers in the Kumba District Hospital, the Baptist Health Centre, the Ekona District Hospital and Bambini Pediatric Foundation. These samples were screened for RVA antigen using Rotaclone (Premier RotaClone) ELISA and then screened with NSP3 qRT-PCR. The positive samples were subjected to VP4 and VP7 nested RT-PCR, the amplicons were purified using a Qiagen PCR purification kit. The purified amplicons were sequenced by Sanger method and the genotypes were determined by the BLASTN program at the National Center for Biotechnology Information website (available at: http://www.ncbi.nlm.gov/BLAST/).

Results
Out sixty-seven samples, 59 (86.4%) were positive by both ELISA and NSP3 qRTPCR assays, with majority from vaccinated children. G1P[8] was the predominant (51%) circulating RVA strain. Other strains detected included G12P[6] (28%), G12P[8] (4.5%), G1P[6] (3%), and GntP[6] (1.5%). The G1P[6], G12P[6], and G12P[8] genotypes were not reported in this region prior to vaccine-introduction. The current vaccine may have a reduced effectiveness against these genotypes, particularly G12P[6], since neither RV1 or RV5 protects against these G and P-types.

Conclusion

This study reveals the emergence of the G12P[6] strain and predominance of G1P[8] strain in a vaccinated population in Cameroon. Continued surveillance is necessary to monitor these emergent genotypes.