Rotavirus genotype distribution during the pre-vaccine period in Cameroon: 2011-2013

Ngoya Ebiguide Roger¹, Boula Angeline¹, Ngoh Rose¹, Njiki Kinkela Mina¹, Kemajou Grace¹, Nkolo Mviena Gaston¹, Baonga Ba Pouth², Nimpa Marcellin³, Mwenda Jason⁴, Koki Ndombo Paul¹.

¹Mother and Child Centre, Chantal BIYA Foundation Yaoundé, Cameroon
²Expanded Programme on Immunization, Ministry of Public Health, Cameroon
³WHO, Country office, Cameroon. ⁴WHO- AFRO, Brazzaville, Congo

Introduction
Group A Rotaviruses are responsible for 125 million cases of infantile gastroenteritis and approximately 453000 deaths each year, 82 % of them occurring in developing countries. The monovalent attenuated human oral rotavirus was introduced in Cameroon in 2014. We describe the molecular epidemiology of circulating strains before vaccine introduction.

Methods
Sentinel surveillance was conducted between January 2011 to December 2013 at four participating hospitals in Cameroon. Group A rotavirus (RVA) was testing by using enzyme-linked-immunosorbent assay and G and P were tested by RT-PCR method.

Results
In 2011, of the 242 rotavirus positive cases genotyped, VP7 genotype G3 (26%) was predominant followed by genotypes G2 (22%). On the other hand, the VP4 genotype P[6] (37%) was predominant, followed by P[8] (35%) and P[4] (13%). The G-P rotavirus genotype combination showed strain G3P[6] (21%) to be common, followed by strains G2P[4] (13%)
In 2012, of the 348 rotavirus cases genotyped, the VP7, G1 genotype (72%) was predominant followed by G3 (33,3%). Genotype P[8] (53%) was also predominant, followed by genotypes P[6] (33%). The G-P rotavirus genotype combination showed that strain G1P[8] (39%) was the most encountered, followed by G3P[6] (21%).
While in 2013, (one year pre-vaccine period), of the 484 rotavirus positive cases genotyped, the VP7 genotypes G1 (53.7%) and G3 (24.4%) were the predominant rotavirus A genotypes, followed by G2 (14%) and G4 (3.1%). The VP4 P[6](49%) genotype was the most predominant followed by P[8] (37.5%) and P[4] (8%). The G-P rotavirus genotype combination showed that strain G1P[8] (34.5%) was most predominant followed G3P[6] (22.3%) and G2P[6] (13%)

Conclusion
During the 3-year pre-vaccine period, substantial diversity of rotavirus co-circulating strains was observed. Our data demonstrate the changes in circulating strains at this period

Key words: gastroenteritis, genotype, strains, pre-vaccine