

Diversity of rotavirus genotypes in Madagascar before and after rotavirus vaccine introduction

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Background

After monovalent G1P8 rotavirus vaccine (Rotarix) introduction into the Extended Program on Immunization in Madagascar in May 2014, hospitalizations due to rotavirus decreased significantly. We investigate diversity of circulating rotavirus strains from children <5 years of age, admitted at Centre Hospitalier Universitaire Mère Enfant Tsaralàlana (CHU MET).

Methods

All children <5 years old with acute watery diarrhea admitted to CHU MET between June 2013 and December 2017 were eligible for enrollment. Active rotavirus surveillance was conducted with support from WHO. Stool samples were collected from enrolled children and tested for rotavirus by EIA at sentinel site laboratory. Residual rotavirus positive specimens were genotyped at Regional Reference Laboratory by PCR targeting VP7 and VP4. For analysis, we defined June 2013-April 2014 to be the pre-rotavirus vaccine period and 2015-2017 to be the post-rotavirus vaccine period.

Results

820 samples were tested for rotavirus: 55% of 204 samples collected in period before vaccine introduction and 15% of 616 samples in 2015-2017 were positive. 135 samples were genotyped: 79 (71% of positive) were in pre-vaccine, 56 (61% of positive) in post-vaccination period. In the pre-vaccine period, G3P8 (67%), G2P4 (15%), G1P8 (14%) were the most common genotypes detected. Genotype distribution changed in period post-vaccine introduction; in 2015, G2P4 (67%) was most commonly detected and there were no G1P8 detections; G2P4 (36%), G1P8 (21%) and G21P8 (21%) were the most common in 2016; and G1P8 (50%), G2P4 (29%) and G3P6 (14%) were the most common in 2017.

Conclusion

Rotavirus genotype distribution varied by year. G2P4 and G1P8 were common genotypes before and after vaccine introduction, although G1P8 was not detected in any specimens in 2015. G1P8 increased in 2016 and 2017. Ongoing surveillance is essential monitor the circulating rotavirus genotypes especially genotype G1P8.