

Analysis of G1P[8] whole genome constellations identified a vaccine-derived strain in Rwanda

¹S.P. Rasebotsa, ¹P.N. Mwangi, ¹M.T. Mogotsi, ^{1,2}S. Sabiu, ¹L.P. Mosime, ³N.B. Magagula, ³K. Rakau, ⁴J. Uwimana, ⁴L. Mutesa, ⁴N. Muganga, ⁴D. Murenzi, ⁴L. Tuyisenge, ³M.J. Mphahlele, ³L.M. Seheri, ⁵J.M. Mwenda, ¹M.M. Nyaga

¹Next Generation Sequencing Unit, Division of Virology, Faculty of Health Sciences, University of the Free State, Bloemfontein, South Africa, ²Biotechnology and Food Technology Department, Faculty of Applied Sciences, Durban University of Technology, Durban, South Africa, ³South African Medical Research Council/Diarrhoeal Pathogens Research Unit, Faculty of Health Sciences, Sefako Makgatho Health Sciences University, Medunsa, Pretoria, South Africa, ⁴Kigali University Teaching Hospital, Kigali, Rwanda ⁵World Health Organization, Regional Office for Africa, Brazzaville, People's Republic of Congo

Background

Rwanda was the first African country to introduce RotaTeq™ vaccine into its Expanded Program of Immunization (EPI) in May 2012 but switched to Rotarix™ in April 2017. The WHO/AFRO in collaboration with UFS-NGS Unit has introduced whole genome sequencing of rotaviruses from the African rotavirus network. This study analyzed G1P[8] strains pre- and post-vaccination to determine any incidence of atypical Wa-like constellations as evidenced in some countries that introduced Rotarix™ vaccine in their EPI.

Methods

Samples (n=38) were conventionally genotyped and whole genome sequenced using MiSeq Illumina platform. Assembly of raw sequence reads were assembled and aligned using Geneious and further analyzed by MEGA7 software.

Results

Genome sequences (n=10) were pure Wa-like constellations in the pre-vaccination period, while 27 genotypes were from the post-vaccine period. No atypical Wa-like genotype constellation was identified in both periods. However, strain RVA/Human-wt/RWA/UFSNGS:MRC-DPRU442/2012/G1P[8] was a vaccine-derived strain with a RotaTeq™-like constellation of G1-P[8]-I2-R2-C2-M2-A3-N2-T6-E2-H3. All the genome segments of the pentavalent RotaTeq™ were determined during assembly.

Conclusions

Although some countries that introduced Rotarix™ vaccine have detected atypical Wa-like constellations, post vaccination, this was not the case in this study where RotaTeq™ vaccine was used for 5 years before switching to Rotarix™. Interestingly, the detection of the G1P[8] vaccine-derived strain, circulating amongst wild type strains with atypical genotype 2 for proteins I, R, C, M, N and E in addition to genotype 3, 6 and 3 for A, T and H, respectively, poses questions on whether genetic recombination is occurring between the vaccine and the wild type strains that may affect effectiveness of the current rotavirus vaccine.