Genetic Relatedness Of Rotavirus Group A G1[P8] Strains Isolated Pre- And Post-Vaccine Introduction In Africa

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Background
Currently, in sub-Saharan Africa, most countries use Rotarix® vaccine for prevention of rotavirus-associated disease. However, despite this vaccine being derived from an attenuated G1[P8] strain, some countries in Africa using this vaccine have continued to experience significant rotavirus disease from G1[P8] strains. This prompted us to investigate the source(s) and genetic diversity of G1[P8] strains circulating in these countries post-vaccine introduction.

Method
Alone and with all other G1 and P[8] viruses collected across the globe, the phylogenetic relationships of G1 and P[8] sequences from South Africa, Malawi, and Kenya available in public sequence databases were examined in the context of (i) pre- versus post-vaccine introduction period and (ii) local versus global relatedness to identify their potential geographic origin in post-vaccine era. Nucleotide sequence diversity within and between pre- and post-vaccine introduction strains was investigated for presence of antigenic changes that can result in vaccine escape.

Results
Whereas pre-vaccine sequences in these three countries formed multiple distinct clades, post-vaccine they formed monophyletic clades. Whereas for South Africa and Malawi, pre-vaccine and post-vaccine introduction G1 and P[8] sequences clustered closely on the global phylogeny indicating potential local persistence through the vaccine introduction period, the Kenyan pre- and post-vaccine sequences that were interspersed with sequences with other countries strongly depicting an external origin of post-vaccine sequences. Although non-synonymous nucleotide changes were observed between pre- and post-vaccine sequences in all three countries, most of the changes were also observed between the pre-vaccine introduction sequences thus precluding our inference that their occurrence in post-vaccine era was related to vaccine escape.

Conclusion
The factors sustaining continued G1[P8] transmission in the Africa may be different between countries that have introduced the Rotarix® vaccine and a longer-term, systematic multi-country investigation is required. Although amino acid changes were observed in G1 and P[8] sequences collected between the pre- and post-Rotarix® vaccine introduction periods, these are difficult to confirm to be vaccine immunity escape related.