Interspecies transmission of rotaviruses and its evolutionary implication: a view from Africa

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Background
The rotavirus genome is notoriously diverse and evolves through rapid point mutations, genetic reassortment and interspecies transmission (IT). RVAs in Africa are considerably different from the ones circulating elsewhere in the world in that, apart from the globally common strains the prevalence of unusual genotypes is high. These unusual genotypes at a glance, are suggestive of animal rotavirus origin. While there is always a vague speculation that frequent IT events occur in Africa because people and animals live closely together, precise analysis to decipher the evolutionary history of the novel strains are limited. What remains unknown include but not limited to: 1) How frequent do IT events occur in Africa? 2) How readily are those animal RVA strains that cross the host species barrier able to establish a transmission chain within the human population?

Methods
We examined at the whole genome level, unusual genotypes such as G6P[6] and G8 using molecular phylogeny We explored and identified specific features of RVAs on the African continent and placed the observations made in the context of existing knowledge.

Results
We showed that the G6 VP7 possessed by G6P[6] strains in Africa as well as Europe originated from a single ancestral VP7 from a human G6P[9] strain around the year 1998 and not directly from bovine G6 strains or bovine-like human G6P[14] strains. What appeared to be African specific G8 VP7 lineages were divided into at least two; while their origin was of bovine, they seemed to have been transmitted only from human to human which was made possible by the acquisition of either the human RVA Wa-like or DS-1-like genetic backbone. Those G8 strains that gained the Wa-like genetic backbone seem to have died out from Africa after prevailing for some time on the continent. Also noted were the ever-diversifying NSP4 lineages within the E2 genotype which were mostly due to the introduction of the NSP4 sequences of animal rotavirus origin; these lineages were however short-lived with limited geographical distribution.

Conclusion
In summary, proximity of people and animals in Africa provides opportunities for animal rotaviruses to cross species barriers, however, many of such events are dead-end infections with no human to human transmission event; only a few IT events do so after gaining human rotavirus backbone genes. The lifespan of such novel lineages within human rotavirus is short and limited geographically as they might be out-competed by the co-circulating parental strains. Nevertheless, such IT events coupled with genetic reassortment provide the source of rich genetic diversity, whether transient or permanent, in African rotavirus strains we observe today.