



Genetic diversity of human enterovirus 68 strains isolated in Kenya using the hypervariable 3'-end of VP1 gene_ Abstract

Abstract

Reports of increasing worldwide circulation of human enterovirus-68 (EV68) are well documented. Despite health concerns posed by resurgence of these viruses, little is known about EV68 strains circulating in Kenya. In this study, we characterized 13 EV68 strains isolated in Kenya between 2008 and 2011 based on the Hypervariable 3'-end of the VP1 gene. Viral RNA was extracted from the isolates and partial VP1 gene amplified by RT-PCR, followed by nucleotide sequencing. Alignment of deduced amino acid sequences revealed substitutions in Kenyan EV68 isolates absent in the prototype reference strain (Fermon). The majority of these changes were present in the BC and DE-loop regions, which are associated with viral antigenicity and virulence. The Kenyan strains exhibited high sequence homology with respect to those from other countries. Natural selection analysis based on the VP1 region showed that the Kenyan EV68 isolates were under purifying selection. Phylogenetic analysis revealed that majority (84.6%) of the Kenyan strains belonged to clade A, while a minority belonged to clades B and C. Overall, our results illustrate that although EV68 strains isolated in Kenya were genetically and antigenically divergent from the prototype strain (Fermon), they were closely related to those circulating in other countries, suggesting worldwide transmissibility. Further, the presence of shared mutations by Kenyan EV68 strains and those isolated in other countries, indicates evolution in the VP1 region may be contributing to increased worldwide detection of the viruses. This is the first study to document circulation of EV68 in Kenya.

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