Abstract

Background: Human enteroviruses (genus Enterovirus, family Picornaviridae) are common infectious agents grouped into HEV-A, HEV-B, HEV-C and HEV-D species. They comprise >100 serotypes and are responsible for a wide range of human pathologies including upper and lower respiratory tract infections. There’s scanty information about serotype diversity of HEV circulating in Kenya. Objective: To molecularly type human enteroviruses isolated in Kenya between 2008 and 2011 using hypervariable 3′-end of the VP1 gene. Methods: A total of 200 HEV isolates obtained in the country from nasopharyngeal specimens were analyzed. Viral RNA was extracted and partial VP1 gene amplified using RT-PCR followed by sequencing. The resulting VP1 sequences were evaluated by sequence homology and phylogenetic analysis relative to those of prototypes retrieved from GenBank. Results: Overall, 22 different enteroviral serotypes were detected. The majority (72%) of the serotypes were from HEV-B species (72%) followed by HEV-D (21.3%) and HEV-A (6.5%). None of the identified serotypes belonged to HEV-C species. The most frequently detected serotypes were enterovirus-68 (EV68), Coxsackie-virus types -B2, -B1, -B4 and B3. The most prevalent serotypes were enterovirus-68 (EV68), Coxsackievirus types -B2, -B1, -B4 and -B3. Conclusions: Findings from this study demonstrate the existence of high serotype diversity among HEVs that circulated in Kenya between 2008 and 2011. The viruses belonging to HEV-A, HEV-B and HEV-D species played a key role in enteroviral infections in the country during this period. The absence of HEV-C known to frequently recombine with poliovirus vaccine strains indicates a low risk of emergence of vaccine derived poliovirus (VDPV) in Kenya. Typing of HEV is important in determining temporal and spatial patterns of the circulating serotypes. This information is necessary for healthcare planning and outbreak investigation studies.