

Abstract

Molecular Characterization of Human Enterovirus 68 Strains Circulating in Kenya between 2008 and 2010

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Background: Human enterovirus 68 (HEV-68) is a rarely detected viral pathogen associated with acute respiratory illness. It is unique among enteroviruses because it shares common biological properties with human rhinoviruses. In 2008-2010, an upsurge of acute respiratory illnesses associated with HEV-68 were reported in many parts of the world including Asia, Europe and the United States. Activity of human respiratory enterovirus infections have not been well characterized in the region including Kenya

Objective: To molecularly characterize HEV-68 strains isolated in Kenya between 2008 and 2010, targeting the VP1 gene.

Methods: A total of six (6) HEV-68 strains isolated in Kenya 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 compared to corresponding regions of prototype Fermon strain and other previously characterized EV-68 strains deposited in Genbank.

Results: Pair-wise comparison of VP1 sequences of Kenyan EV-68 strains revealed 87.2-99.5% nucleotide identity. The Kenyan viruses shared 86.0-88.4% and 91-99% nucleotide identities with Fermon and recently characterized EV-68 strains reported in Gen Bank respectively. Alignment of partial VP1 sequences of Kenyan isolates with Fermon revealed 12 amino acid substitutions and one deletion in five of the isolates and 11 amino acid substitutions. Phylogenetic analysis showed that five of the Kenyan isolates clustered closely to EV-68 strains that circulated in New York City, USA and Yamagata, Japan. One Kenyan isolate clustered closely to viruses which circulated in Netherlands, Europe. All the Kenyan isolates clustered away from Fermon EV-68 strain indicating divergence from the prototype strain.

Conclusions: This study confirms circulation of HEV-68 strains in Kenya during the period 2008 to 2010. Most Kenyan isolates were similar to viruses which circulated in New York City, USA and Yamagata, Japan. The viruses had genetically evolved from Fermon prototype reference strain but remained antigenically similar.

Monitoring of evolution patterns of respiratory viruses such as HEV-68 is essential for early prediction of viruses with epidemic potential.

Key words: Human enterovirus-68, VP1 gene, Kenya

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