Arch Virol (2007) 152: 1201–1208
DOI 10.1007/s00705-006-0934-5
Printed in the Netherlands

Archives of Virology

Brief Report

Molecular phylogeny of modern coxsackievirus A16

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Received November 14, 2006; accepted December 21, 2006; published online February 19, 2007

Summary

A phylogenetic analysis of VP1 and VP4 nucleotide sequences of 52 recent CVA16 strains demonstrated two distinct CVA16 genogroups, A and B, with the prototype strain being the only member of genogroup A. CVA16 G-10, the prototype strain, showed a nucleotide difference of 27.7–30.2% and 19.9–25.2% in VP1 and VP4, respectively, in relation to other CVA16 strains, which formed two separate lineages in genogroup B with nucleotide variation of less than 13.4% and less than 16.3% in VP1 and VP4, respectively. Lineage 1 strains circulating before 2000 were later displaced by lineage 2 strains.

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Hand, foot, and mouth disease (HFMD) is a common febrile illness of children associated with infections of species A enteroviruses from the genus *Enterovirus* within the family *Picornaviridae*. Lesions on the skin and oral mucosa typically characterize the illness, with herpangina also presented in some patients. Several enterovirus serotypes have been associated with this disease, the majority of these being members of human enterovirus A, such as coxsackieviruses (CV) A2, A4, A5, A8, A10, A16 and human enterovirus (HEV) 71 [17, 20, 15]. Of these, CVA16 and HEV71 are the major causative agents associated with HFMD, and co-circulation of both of these serotypes during outbreaks of HFMD