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Characterisation and comparative analyses of the Equine adenovirus 1 and 2 complete genome sequences

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Equine Adenovirus 2 (EAdV-2)causes a mild gastrointestinal disease in foals. The primary isolate of EAdV-2 was Frecently sequenced and the genomic organisation characterised. The results indicate that EAdV-2 does not display the characteristic Mastadenovirus genome organisation one would expect. A particularly unique feature was the identification of two E1B_55K coding regions, of which one was typical of the Mastadenoviruses. The other E1B_55K region appeared to be a fusion of a partial pIXcoding sequence to anE1B_55K coding sequence more typical of the Atadenoviruses. In addition ten open reading frames ranging from 300 to 1362bpin length were identified for which no homologue could be identified for the encoded polypeptides. The evolution of this virus appears to be unique amongst the other Mastadenoviruses including Equine adenovirus 1 (EAdV-1).In comparison to EAdV-2, the EAdV-1 genome organisation, sequenced and characterisedin a previous study,was more typical of the Mastadenoviruses. The encoded EAdV-1 polypeptides had a high degree of similarity to homologues from Canine adenoviruses 1 and 2 and also Bat adenovirus TJM (BtAdV-TJM). Phylogenetic reconstructions suggested that EAdV-1 may share a common ancestor with these viruses.Collectively the results of these studiesprovide insight into the evolution of EAdV-2.

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