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Phylogenomic analysis of the complete sequence of a gastroenteritis-associated cetacean adenovirus (bottlenose dolphin adenovirus 1) reveals a high degree of genetic divergence

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Abstract

Adenoviruses are common pathogens in vertebrates, infecting a wide range of hosts, but only having rarely been detected and correlated with disease in cetaceans. This article describes the first complete genomic sequence of a cetacean adenovirus, bottlenose dolphin adenovirus 1 (BdAdV-1), detected in captive bottlenose dolphin population (*Tursiops truncatus*) suffering from self-limiting gastroenteritis. The complete genome sequence of BdAdV-1 was recovered from data generated by high-throughput sequencing and validated by Sanger sequencing. The genome is 34,080 bp long and has

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