

Complete genome analysis of the sturgeon adenovirus

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The white sturgeon adenovirus 1 (WSAdV-1) is the only adenovirus isolated from fish and the single member of the genus *Ichtadenovirus*. Full genome sequencing of WSAdV-1 revealed the largest hitherto known adenoviral genome (48,395 bp) with an average G+C content of 42.6%. Interestingly, the fiber gene was identified in an unorthodox position at the left end of the genome. Moreover, as many as four fiber-like genes were found here; three of them tandem on the *r* strand, and a fourth one in opposite direction. However, the functionality as fiber gene of all or any of these ORFs needs to be confirmed. The central genome region, consisting of the late genes and the E2 transcription units, conserved by all members of the family *Adenoviridae*, was identified in WSAdV-1. Rightward from the gene of pVIII, 28 ORFs were found, the majority of which did not have detectable homology to any genes present in public databases. Among the five exceptions were ORF4 and 9 on the *r* strand showing homology to sulfotransferase enzyme genes. Such genes have not been found in viral genomes before. Also on the *r* strand, ORF5 and 6 seemed to code for homologues of the non-structural protein (NS) of parvoviruses. One or more copies of NS-like genes, albeit in different positions, have been described in members of the *Aviadenovirus* genus only. However, their function in adenoviruses remains to be clarified. The putative protein encoded by ORF25, on the *l* strand, comprises two immunoglobulin domains. Similar genes have been found also in aviadenoviruses only. The origin and possible function of the remaining 23 ORFs, are unknown. Phylogenetic calculations with the newly determined proteins further strengthened the previously obtained results, i.e. WSAdV-1 always appeared as the most basal independent branch, clearly separated from the other four genera. (Support: OTKA K100163.)

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