

ICTV Virus Taxonomy Profile: Adenoviridae 2022

Mária Benkő¹, Koki Aoki², Niklas Arnberg³, Andrew J. Davison⁴, Marcela Echavarría⁵, Michael Hess⁶, Morris S. Jones⁷, Győző L. Kaján¹, Adriana E. Kajon⁸, Suresh K. Mittal⁹, Iva I. Podgorski¹⁰, Carmen San Martín¹¹, Göran Wadell³, Hidemi Watanabe², Balázs Harrach^{1,*} and ICTV Report Consortium

Abstract

The family *Adenoviridae* includes non-enveloped viruses with linear dsDNA genomes of 25–48 kb and medium-sized icosahedral capsids. Adenoviruses have been discovered in vertebrates from fish to humans. The family is divided into six genera, each of which is more common in certain animal groups. The outcome of infection may vary from subclinical to lethal disease. This is a summary of the ICTV Report on the family *Adenoviridae*, which is available at ictv.global/report/adenoviridae.

Table 1. Characteristics of members of the family Adenoviridae

Example:	human adenovirus 5 (AC_000008), species Human mastadenovirus C, genus Mastadenovirus
Virion	Non-enveloped icosahedral capsid 90 nm in diameter
Genome	Linear, dsDNA of 25-48 kb with inverted terminal repeats
Replication	Nuclear
Translation	From capped, polyadenylated and often spliced transcripts
Host range	Mammals, birds, reptiles, amphibians and fish; host range varies among virus genera
Taxonomy	Realm Varidnaviria, kingdom Bamfordvirae, phylum Preplasmiviricota, class Tectiliviricetes, order Rowavirales; 6 genera containing >85 species

VIRION

Adenovirus virions are non-enveloped, pseudo T=25 icosahedral particles. The capsid consists of 240 non-vertex (hexon) and 12 vertex capsomers (penton). The latter consist of the penton base and a protruding fiber protein trimer (Table 1, Fig. 1) [1, 2]. The minor, cementing proteins show genus-specific variation but LH3 (atadenoviruses) and protein IX (mastadenoviruses) share a capsid-binding motif [3].

GENOME

The genome is a single linear molecule of dsDNA of 24 630–48 395 bp [4, 5] with inverted terminal repeats of 26–721 bp (Fig. 2).

A virus-encoded terminal protein is covalently linked to the 5'-end of each DNA strand.

REPLICATION

Entry of virus into cells occurs by attachment of the fiber trimer knob to cellular receptors followed by internalization involving interaction between the penton base and cellular α_v integrins [6]. After uncoating, the virus core is delivered to the nucleus, the site of virus RNA transcription, DNA replication and assembly. Infection results in the arrest of synthesis of host DNA, mRNA and proteins. Transcription by host RNA polymerase II involves both DNA strands of the virus genome. Primary transcripts are capped and polyadenylated. Complex splicing patterns govern the

Keywords: Adenoviridae; Atadenovirus; Aviadenovirus; Ichtadenovirus; Mastadenovirus; Siadenovirus; Testadenovirus; ICTV Report; Taxonomy. Abbreviations: DBP, DNA-binding protein; E, early region; ITR, inverted terminal repeat; p, precursor protein; pol, DNA polymerase; TP, terminal protein; UXP, U-exon protein; VA, virus-associated RNA. 001721 © 2022



Received 30 November 2021; Accepted 02 December 2021; Published 09 March 2022

Author affiliations: ¹Veterinary Medical Research Institute, Budapest, Hungary; ²Hokkaido University, Sapporo, Japan; ³Umeå University, Umeå, Sweden; ⁴MRC-University of Glasgow Centre for Virus Research, Glasgow, UK; ⁵CEMIC University Hospital, CONICET, Buenos Aires, Argentina; ⁴University of Veterinary Medicine, Vienna, Austria; ⁷Naval Medical Center, San Diego, CA, USA; ⁸Lovelace Respiratory Research Institute, Albuquerque, NM, USA; ⁹Purdue University, West Lafayette, IN, USA; ¹⁰Ruđer Bošković Institute, Zagreb, Croatia; ¹¹Centro Nacional de Biotecnología, Madrid, Spain. ***Correspondence:** Balázs Harrach, balazs.harrach@gmail.com



Fig. 1. Adenovirus virion structure. Left: a model, built from a low-resolution cryo-electron microscopy reconstruction of human adenovirus 5 [9]. Yellow - penton bases, dark blue - fiber protein trimers, modelled from the crystal structure of the distal knob and the filamentous shaft [10], shaded triangle - one facet. Right: schematic of a triangular facet [1].

production of mRNA families. In primate adenoviruses, virusassociated RNA genes transcribed by cellular RNA polymerase III facilitate translation of late virus mRNAs and block the cellular interferon response.

PATHOGENESIS

Human infections are usually subclinical but can, especially in immunosuppressed patients, induce acute respiratory symptoms, adenoidal–pharyngeal conjunctivitis, epidemic keratoconjunctivitis, hepatitis, acute gastroenteritis (infantile virus-caused diarrhoea), persistent interstitial infection in the kidney and haemorrhagic cystitis. Mastadenovirus infections in animals are



Fig. 2. Genome organization of the mastadenovirus human adenovirus 5. Coloured arrows depict genes conserved in all genera (black), present in more than one genus (blue) or restricted to mastadenoviruses (red). Rectangles mark the inverted terminal repeats.

References

- 1. San Martín C. Latest insights on adenovirus structure and assembly. *Viruses* 2012;4:847–877.
- Pénzes JJ, Menéndez-Conejero R, Condezo GN, Ball I, Papp T, et al. Molecular characterization of a lizard adenovirus reveals the first atadenovirus with two fiber genes and the first adenovirus with either one short or three long fibers per penton. J Virol 2014;88:11304–11314.
- Marabini R, Condezo GN, Krupovic M, Menéndez-Conejero R, Gómez-Blanco J, et al. Near-atomic structure of an atadenovirus reveals a conserved capsid-binding motif and intergenera variations in cementing proteins. Sci Adv 2021;7:eabe6008.
- Doszpoly A, Harrach B, LaPatra S, Benkő M. Unconventional gene arrangement and content revealed by full genome analysis of the white sturgeon adenovirus, the single member of the genus *lchtadenovirus*. *Infect Genet Evol* 2019;75:103976.
- Harrach B, Tarján ZL, Benkő M. Adenoviruses across the animal kingdom: a walk in the zoo. FEBS Lett 2019;593:3660–3673.

common, but disease usually appears only when predisposing factors are present [7]. Canine adenovirus 1 is the causative agent of infectious canine hepatitis (a life-threatening disease of puppies). Skunk adenovirus 1 also infects African pigmy hedgehog, porcupine, racoon and a New World monkey. Both viruses share ancestry with bat adenoviruses [8]. In chickens, hepatitis-hydropericardium syndrome is associated with fowl adenovirus 4 and gizzard erosion with fowl adenovirus 1. Additional aviadenoviruses cause inclusion body hepatitis. The atadenovirus duck adenovirus 1 is the causative agent of egg drop syndrome in chickens, and deer adenovirus 1 infection has resulted in the death of thousands of deer in California (USA). A siadenovirus causes turkey haemorrhagic enteritis.

TAXONOMY

Current taxonomy: ictv.global/taxonomy. Genus and species demarcation is based mainly on phylogenetic criteria but also on genome organization and biological characteristics. Genus *Mastadenovirus*: >50 species (members infecting mammals); *Aviadenovirus*: >14 species (birds); *Atadenovirus*: >9 species (reptiles, birds, ruminants and marsupials); *Siadenovirus*: >7 species (birds, frogs and tortoises); *Ichtadenovirus*: 1 species (white sturgeon); *Testadenovirus*: 1 species (red-eared slider) [4, 5].

RESOURCES

Full ICTV Report on the family *Adenoviridae*: ictv.global/report/ adenoviridae.

Sequenced adenoviruses: sites.google.com/site/adenoseq.

Funding information

Production of this Profile, the ICTV Report and associated resources was funded by a grant from the Wellcome Trust (WT108418AIA). Support was also provided by the National Research, Development and Innovation Office, Hungary (NN140356) to B.H.

Acknowledgements

Members of the ICTV Report Consortium are Stuart G. Siddell, Elliot J. Lefkowitz, Sead Sabanadzovic, Peter Simmonds, F. Murilo Zerbini, Donald B. Smith and Arvind Varsani.

Conflicts of interest

The authors declare that there are no conflicts of interest.

- Lenman A, Liaci AM, Liu Y, Frängsmyr L, Frank M, et al. Polysialic acid is a cellular receptor for human adenovirus 52. Proc Natl Acad Sci U S A 2018;115:E4264–E4273.
- Standorf K, Cortés-Hinojosa G, Venn-Watson S, Rivera R, Archer LL, et al. Phylogenetic analysis of the genome of an enteritis-associated bottlenose dolphin mastadenovirus supports a clade infecting the cetartiodactyla. J Wildl Dis 2018;54:112–121.
- Doszpoly A, Hornyák Á, Bányai K. Complete genome analysis confirms that the pygmy marmoset adenovirus is a variant of the skunk adenovirus 1 - Short communication. *Acta Vet Hung* 2020;68:323–327.
- Liu H, Jin L, Koh SBS, Atanasov I, Schein S, et al. Atomic structure of human adenovirus by cryo-EM reveals interactions among protein networks. Science 2010;329:1038–1043.
- van Raaij MJ, Mitraki A, Lavigne G, Cusack S. A triple beta-spiral in the adenovirus fiber shaft reveals a new structural motif for a fibrous protein. *Nature* 1999;401:935–938.