This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

Part 1: **TITLE, AUTHORS, etc**

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| **Code assigned:** | ***2017.016D*** | | | | (to be completed by ICTV officers) |
| **Short title:** 4 new species in the family *Adenoviridae* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Balázs Harrach, Mária Benkő | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Balázs Harrach: harrach.balazs@agrar.mta.hu | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | **Adenoviridae Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
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| Date first submitted to ICTV: | | | | 12 October 2017 | |
| Date of this revision (if different to above): | | | |  | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.016D.U.v1.Adenoviridae\_4sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| Abendroth B, Höper D, Ulrich RG, Larres G, Beer M. A red squirrel associated adenovirus identified by a combined microarray and deep sequencing approach. Arch Virol. 2017 Jul 6. doi: 10.1007/s00705-017-3463-5. [Epub ahead of print]  Malmberg M, Rubio-Guerri C, Hayer J, García-Párraga D, Nieto-Pelegrín E, Melero M, Álvaro T, Valls M, Sánchez-Vizcaíno JM, Belák S, Granberg F (2017) Phylogenomic analysis of the complete sequence of a gastroenteritis-associated cetacean adenovirus (bottlenose dolphin adenovirus 1) reveals a high degree of genetic divergence. Infect. Genet. Evol. 53: 47-55. doi: 10.1016/j.meegid.2017.05.008.  Miller MM, Cornish TE, Creekmore TE, Fox K, Laegreid W, McKenna J, Vasquez M, Woods LW (2017) Whole-genome sequences of Odocoileus hemionus deer adenovirus isolates from deer, moose and elk are highly conserved and support a new species in the genus *Atadenovirus*. [J. Gen. Virol](https://www.ncbi.nlm.nih.gov/pubmed/?term=Complete+genomic+sequence+of+cervid+adenovirus+1). 98 (9) 2320-2328. doi: 10.1099/jgv.0.000880.  Ridpath JF, Neill JD, Palmer MV, Bauermann FV, Falkenberg SM, Wolff PL. (2017) Isolation and characterization of a novel cervid adenovirus from white-tailed deer (*Odocoileus virginianus*) fawns in a captive herd. Virus Res. 238: 198-203. doi: 10.1016/j.virusres.2017.06.020.  van Beurden SJ, IJsseldijk LL, van de Bildt MWG, Begeman L, Wellehan JFX Jr, Waltzek TB, de Vrieze G, Gröne A, Kuiken T, Verheije MH, Penzes JJ (2017) A novel cetacean adenovirus in stranded harbour porpoises from the North Sea: detection and molecular characterization. Arch. Virol. 162 (7) 2035-2040.  Woods LW, Swift PK, Barr BC, Horzinek MC, Nordhausen RW, Stillian MH, Patton JF, Oliver MN, Jones KR, MacLachlan NJ (1996) Systemic adenovirus infection associated with high mortality in mule deer (*Odocoileus hemionus*) in California. Vet. Pathol. 33 (2) 125-132.  Zakhartchouk A, Bout A, Woods LW, Lehmkuhl HD, Havenga MJ (2002) Odocoileus hemionus deer adenovirus is related to the members of Atadenovirus genus. Arch. Virol. 147 (4) 841-847. |

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| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

An adenovirus (Odocoileus adenovirus 1, syn. deer adenovirus 1) has been identified in mule deer (*Odocoileus heimonus*) associated with high mortality in California (Woods et al., 1996). Later it was detected in multiple other deer species, and was identified as belonging to the genus *Atadenovirus* (Zakhartchouk et al., 2002). Finally, it was isolated and sequenced from several deer species (Miller et al., 2017). Recently, also a mastadenovirus was isolated from white-tailed deer (*Odocoileus virginianus*) and named “cervid adenovirus 1 strain 1339” (Ridpath *et al.*, 2017). However, as this is the second adenovirus type from an Odocoileus species, it seems to be more appropriate to call it deer adenovirus 2. Its full genome was sequenced (Ridpath *et al.*, 2017). They are proposed now to be members of novel species *Deer atadenovirus A* and *Deer mastadenovirus B*, respectively (Fig. 1 and 2). Besides the >15% phylogenetic distance (one of the species demarcation criteria), several other genetic or/and biological properties differentiate them from the phylogenetically closest species. Deer adenovirus 1 is phylogenetically closest to bovine and ovine atadenoviruses (Fig. 1), but those are from different host species (cattle and sheep). Bovine adenovirus 3 is the phylogenetically closest virus to deer adenovirus 2 (Fig. 2), but it is from a different host species, i.e., from cattle, furthermore its E3 region contains a 14.7K homologue occurring in primate adenoviruses but missing from deer adenovirus 2.

Squirrel adenovirus 1 is from a new host and shows adequate phylogenetic distance to the closest virus, equine adenovirus 2 (Fig. 2). Furthermore, squirrel adenovirus 1 has a unique gene (called ORF10) in its E3 region.

The dolphin adenovirus 1 isolate BdAdV-1\_2014 published by Malmberg et al. (2017) is phylogenetically adequately different from the other bottlenose dolphin adenovirus strain Tt11018 isolated and sequenced in the USA (NCBI accession no. KR024710) and from the harbour porpoise sequenced partially (van Beurden et al., 2017) (Fig. 2). Porpoise is a different host and porpoises belong to a different family of vertebrates than dolphins. The American dolphin adenovirus strain has a unique (very short) gene (E3 11.5K) in its E3 region. The other strain (BdAdV-1\_2014) has another unique but surprisingly long gene (ORF1) in its E3 region.

*Lizard atadenovirus A*

lizard-2

*Snake atadenovirus A*

snake-1

*Psittacine atadenovirus A*

psittacine-3

*Duck atadenovirus A*

duck-1

*Ovine atadenovirus D*

ovine-7

**Deer atadenovirus A**

deer-1

bovine-6

*Bovine atadenovirus D*

bovine-4

100

100

97

87

100

0.1

*Fig. 1.* Phylogenetic tree of full DNA polymerase amino acid sequences of atadenoviruses. Maximum likelihood calculation (PhyML) with WAG+I+G model (according to model selection in Topali platform). From the names of the adenovirus types the word “adenovirus” was deleted for clarity. Bootstrap values are shown in percent (for 100 resamplings). The newly proposed species is shown by red and bold font.

***Murine mastadenovirus B***

murine-2

***Murine mastadenovirus C***

murine-3

***Murine mastadenovirus A***

murine-1

***Equine mastadenovirus B***

equine-2

**Squirrel mastadenovirus A**

squirrel-1

canine-1

canine-2

***Canine mastadenovirus A***

***Bat mastadenovirus B***

bat-2

***Bat mastadenovirus A***

bat-3

**Bat mastadenovirus G**

bat-11 strain 250-A

***Skunk mastadenovirus A***

skunk-1

***Equine mastadenovirus A***

equine-1

***Bovine mastadenovirus A***

bovine-1

***Ovine mastadenovirus A***

bovine-2

***Porcine mastadenovirus C***

porcine-5

***Dolphin mastadenovirus A***

dolphin-2 USA

porpoise-1 (partial genome)

**Dolphin mastadenovirus B**

dolphin-1 Spain

***Porcine mastadenovirus A***

porcine-3

***Tree shrew mastadenovirus A***

tree shew-1

**Bat mastadenovirus C**

bat-4 strain WIV9

***Sea lion mastadenovirus A***

sea lion-1

**Bat mastadenovirus D**

bat-7 strain WIV12

**Bat mastadenovirus E**

bat-8 strain WIV13

bat-WIV17

bat-WIV18

**Bat mastadenovirus F**

***Bovine mastadenovirus B***

bovine-3

**Deer mastadenovirus B**

deer-2 strain1339

***Platirrhini mastadenovirus A***

titi monkey-1

**Simian mastadenovirus I**

simian-55

***Simian mastadenovirus G***

simian-20

simian-48

simian-6

simian-3

***Simian mastadenovirus A***

***Simian mastadenovirus H***

SAdV-54

***Simian mastadenovirus D***

SAdV-13

***Human mastadenovirus A***

HAdV-12

***Human mastadenovirus C***

HAdV-5

***Human mastadenovirus D***

HAdV-8

***Human mastadenovirus E***

HAdV-4

***Human mastadenovirus B***

HAdV-3

***Simian mastadenovirus E***

SAdV-16

***Simian mastadenovirus B***

SAdV-8

***Simian mastadenovirus C***

SAdV-19

***Human mastadenovirus G***

HAdV-52

***Simian mastadenovirus F***

SAdV-18

***Human mastadenovirus F***

HAdV-40

marten-associated aviadenovirus (partial genome)

100

95

87

100

87

100

100

100

97

99

61

100

99

100

99

78

86

84

100

99

100

100

100

100

42

100

100

100

100

86

65

83

100

85

99

84

100

58

11

16

46

29

46

88

84

0.2

*Fig. 2.* Phylogenetic tree of full DNA polymerase amino acid sequences of selected types representing all official and proposed Mastadenovirus species. Maximum likelihood (PhyML) calculation with RTRev+I+G model (according to model selection in the Topali platform). From the names of the AdV types the word “AdV” was deleted for clarity. Bootstrap values are shown in percent (for 100 resamplings). Non-rooted calculation; marten-associated aviadenovirus selected as outgroup for the visualisation. The newly proposed species are shown by red and bold font, those that were proposed earlier this year but are not yet fully accepted are shown by blue letters (https://talk.ictvonline.org/files/proposals/animal\_dna\_viruses\_and\_retroviruses/m/animal\_dna\_ec\_approved/6934).