This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.006D*** | |  |
| **Short title:** Create five species in the genus *Mastadenovirus* and one species in the genus *Aviadenovirus*, family *Adenoviridae* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Harrach B, Kaján GL, Benkő M | | harrach.balazs@agrar.mta.hu; kajan.gyozo@agrar.mta.hu; benko.maria@agrar.mta.hu | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | | Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, H-1143 Budapest, Hungary (HB, KGL, BM) | | | | |
| **Corresponding author** | | | |
| Balázs Harrach | | | |
| **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 SG** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | 18 May 2019 |
| Date of this revision (if different to above): | | | 2 September 2019 |

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| **ICTV-EC comments and response of the proposer:** |
| Correct one accession number.  Done |

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2019.006D.A.v1.Adenoviridae\_6sp.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| 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, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

Three distinct novel adenoviruses have been isolated from straw-colored fruit bat (*Eidolon helvum*, Zambia) (Ogawa et al., 2017), Egyptian fruit bat (*Rousettus aegyptiacus*, South Africa) (Jansen van Vuren et al., 2018) and Asian particolored bat (*Vespertilio sinensis*, Japan) (Kobayashi et al., 2019). The genomes have been sequenced. These viruses are proposed now to be members of three novel species *Bat mastadenovirus H* to *Bat mastadenovirus J*, respectively (Fig. 1). As well as the >15% phylogenetic distance (one of the species demarcation criteria), several other genetic or/and biological properties differentiate these viruses from the members of the phylogenetically closest species, including different host species. Bat adenovirus strains WIV17 and WIV18 (members of *Bat mastadenovirus F*), which are the closest to straw-colored fruit bat adenovirus, originate from Leschenault's rousette (*Rousettus leschenaultii*) rather than *Eidolon helvum.* Bat adenovirus strains WIV12 and WIV13 (members of *Bat mastadenovirus D* and *Bat mastadenovirus E*, respectively), are phylogenetically the closest to Egyptian fruit bat adenovirus, are both from common bent-wing bat (*Miniopterus schreibersi*), and have extremely long and unique E3 genes. The Asian particolored bat adenovirus is closest to bat adenovirus 2, and canine adenovirus 1 and 2, but shows a sufficient phylogenetic distance from them. Bat adenovirus 2 (*Bat mastadenovirus B*) was isolated from common pipistrelle (*Pipistrellus pipistrellus*), and canine adenovirus 1 and 2 from different carnivores, and thus the host species of the closest adenoviruses are different from Asian particolored bat (*Vespertilio sinensis*).

Ovine adenovirus 8 (*Ovine mastadenovirus C*) is a new isolate obtained from sheep in Hungary (Vidovszky et al., 2019). It is phylogenetically distinct from the closest deer adenovirus 2 (*Deer mastadenovirus B*) and bovine adenovirus 3 (*Bovine mastadenovirus B*); their hosts are also different animal species.

Polar bear adenovirus 1 (*Polar bear mastadenovirus A*) is from a new host and shows a large phylogenetic distance from all other adenoviruses (Fig. 1). Furthermore, it lacks the gene of protein IX, which is unique among mastadenoviruses. It has (two) unique proteins coded in the E3 region, and further two novel ORFs in the E4 region, which show no similarity to any known proteins.

Psittacine adenovirus 1 was described first from a red-breasted parakeet (*Psittacula alexandri*) based on partial hexon sequence (Raue et al., 2005). Its complete coding genome sequence was recently derived from the liver of a dead Senegal parrot (*Poicephalus senegalus*) by a metagenomic approach (Milani et al., 2018). Only the sequences of the ITRs occupying the genome ends are missing. Phylogenetically, this virus is most similar to psittacine adenovirus 4, the only known member of species *Psittacine aviadenovirus B*, which was isolated from a red-bellied parrot (*Poicephalus rufiventris*)*.* The DNA-dependent DNA polymerase sequences show more than 10% divergence. For species demarcation in case of 5-15% difference, a second distinguishing property is needed, and this is that the viruses originated from different host species. The next available designation letter is proposed for the naming: *Psittacine aviadenovirus C.*

*Fig. 1.* Phylogenetic tree of full DNA-dependent DNA polymerase amino acid sequences of mastadenoviruses. Maximum likelihood (RAxML) calculation with LG+I+G model (according to model selection by ProtTest). Bootstrap values are shown in percent (for 100 resamplings). From the names of adenovirus types the word “adenovirus” was deleted for clarity. Non-rooted calculation; murine adenoviruses selected as outgroup for the visualisation. The newly proposed species are shown by bold font.



avi.emf

*Fig. 2.* Phylogenetic tree of full DNA-dependent DNA polymerase amino acid sequences of aviadenoviruses. Maximum likelihood calculation (RAxML) with LG+I+G model (according to model selection). From the names of the adenovirus types the word “adenovirus” was deleted for clarity. Bootstrap values are shown in percent (for 100 resamplings). Non-rooted calculation. The newly proposed species is shown by bold font.

| **References:** |
| --- |
| Boszormenyi KP, Podgorski II, Sos E, Harrach B (2018) Genomic and phylogenetic analysis of a novel adenovirus found in polar bear (*Ursus maritimus*). GenBank accession number MF773580  Dayaram A, Tsangaras K, Pavulraj S, Azab W, Groenke N, Wibbelt G, Sicks F, Osterrieder N, Greenwood AD (2018) Novel divergent polar bear-associated mastadenovirus recovered from a deceased juvenile polar bear. mSphere 3 (4) e00171-18  Jansen van Vuren P, Allam M, Wiley MR, Ismail AR, Storm N, Birkhead M, Markotter W, Palacios G, Paweska JT (2018) A novel adenovirus isolated from the Egyptian fruit bat in South Africa is closely related to recent isolates from China. Sci Rep 8 (1) 9584  Kobayashi T, Matsugo H, Maruyama J, Kamiki H, Takada A, Maeda K, Takenaka-Uema A, Tohya Y, Murakami S, Horimoto T (2019) Characterization of a novel species of adenovirus from Japanese microbat and role of CXADR as its entry factor. Sci Rep 9 (1) 573  Milani A, Zamperin G, Fusaro A, Salviato A, Bano L, Zandonà L, Brunetta R, Monne I (2018) Complete genome sequence of psittacine adenovirus 1, identified from *Poicephalus senegalus* in Italy. Microbiol Resour Announc 7 (11) e01037-18  [Ogawa H](https://www.ncbi.nlm.nih.gov/pubmed/?term=Ogawa%20H%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Kajihara M](https://www.ncbi.nlm.nih.gov/pubmed/?term=Kajihara%20M%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Nao N](https://www.ncbi.nlm.nih.gov/pubmed/?term=Nao%20N%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Shigeno A](https://www.ncbi.nlm.nih.gov/pubmed/?term=Shigeno%20A%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Fujikura D](https://www.ncbi.nlm.nih.gov/pubmed/?term=Fujikura%20D%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Hang'ombe BM](https://www.ncbi.nlm.nih.gov/pubmed/?term=Hang%27ombe%20BM%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Mweene AS](https://www.ncbi.nlm.nih.gov/pubmed/?term=Mweene%20AS%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Mutemwa A](https://www.ncbi.nlm.nih.gov/pubmed/?term=Mutemwa%20A%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Squarre D](https://www.ncbi.nlm.nih.gov/pubmed/?term=Squarre%20D%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Yamada M](https://www.ncbi.nlm.nih.gov/pubmed/?term=Yamada%20M%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Higashi H](https://www.ncbi.nlm.nih.gov/pubmed/?term=Higashi%20H%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Sawa H](https://www.ncbi.nlm.nih.gov/pubmed/?term=Sawa%20H%5BAuthor%5D&cauthor=true&cauthor_uid=29207524), [Takada A](https://www.ncbi.nlm.nih.gov/pubmed/?term=Takada%20A%5BAuthor%5D&cauthor=true&cauthor_uid=29207524) (2017) Characterization of a novel bat adenovirus isolated from straw-colored fruit bat (*Eidolon helvum*). Viruses 9 (12) E371  Raue R, Gerlach H, Müller H (2005) Phylogenetic analysis of the hexon loop 1 region of an adenovirus from psittacine birds supports the existence of a new psittacine adenovirus (PsAdV). Arch Virol 150 (10) 1933-1943  Vidovszky MZ, Szeredi L, Doszpoly A, Harrach B, Hornyák Á (2019) Isolation and complete genome sequence analysis of a novel ovine adenovirus type representing a possible new mastadenovirus species. Arch Virol 164 (8) 2205-2207 |