

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create 16 new species in the genera *Aviadenovirus*, *Barthadenovirus* and *Mastadenovirus* (*Rowavirales*: *Adenoviridae*) | |
| **Code assigned:** | 2024.004D.N.v1.Adenoviridae\_16ns |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses | **X** | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| Adenoviridae SG |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
| Adenoviridae (11) | 10 | 0 | 1 |
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| **Submission date:** | 21/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** | DD/MM/YYYY |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Name of accompanying Excel module:** |
| 2024.004D.N.v1.Adenoviridae\_16ns.xlsx |

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:** | | **Y/N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  109 species in 6 genera in the family *Adenoviridae*.  *Proposed* *taxonomic change(s):*  Adding 16 novel species; 7 to genus *Mastadenovirus*, 5 to *Aviadenovirus*, 4 to *Barthadenovirus*.  *Justification*:  Novel adenovirus sequences have been submitted to GenBank (many from metagenomic data) reflecting very rich diversity (https://sites.google.com/site/adenoseq). From these sequences, 16 full or almost full (coding-complete) animal adenovirus genomes originating from 7 mammal, 7 bird and 2 reptilian species merit the establishment of new species for them. The phylogenetic distance of their DNA polymerase amino acid sequences is more than 15 percent to members of accepted adenovirus species (this is the main demarcation criterion). Furthermore, they originate from new hosts or from hosts different from those of existing species, or/and have a characteristic whole-genome GC% difference. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected:*  Species  *Description of current taxonomy:*  Six genera and 109 species in the family *Adenoviridae;*  genus *Mastadenovirus*: 56 species  genus *Aviadenovirus*: 23 species  genus *Barthadenovirus* (earlier Atadenovirus): 17 species  genus *Siadenovirus*: 11 species  genus *Ichtadenovirus*: 1 species  genus *Testadenovirus*: 1 species  (<https://sites.google.com/site/adenoseq>)  *Proposed taxonomic change(s):*  Establish 16 new species (total species number in the family: 125)  genus *Mastadenovirus*: 7 new species (for 7 mammalian adenoviruses; total virus species: 63)  genus *Aviadenovirus*: 5 new species (for 5 avian adenoviruses; total 28)  genus *Barthadenovirus*: 4 new species (2 viruses from birds, 2 from reptiles; total 21)  *Demarcation criteria:*  In the family *Adenoviridae*, species demarcation depends on at least two of the following characteristics (Benkő et al., 2022):  Phylogenetic distance (>10–15%, based on distance matrix or maximum likelihood analysis of the DNA polymerase amino acid sequences)  genome organization (characteristically in the right terminal region)  host range  nucleotide composition  cross-neutralization  pathogenicity.  With the advancement of sequencing techniques, the calculated phylogenetic distances became the decisive demarcation criteria. If the DNA polymerase identity is less than 15%, the need for the establishment of new species is rather clear. If the distance is between 10 and 15%, a second demarcation criterion is needed.  *Justification:*  **Proposed new species**  In recent years, several novel adenovirid genomes have been sequenced completely or almost completely from birds (Zheng et al., 2022, 2024; Karamendin et al., 2024) or have been identified from metagenomic projects (French et al., 2023; Zheng et al., 2023). Similarly, adenovirus (AdV) genomes have been identified from metagenomic studies of mammals (Buck et al., 2024; Wang et al., 2024) and reptiles (Buck et al., 2024). Sixteen of these AdVs merit the establishment of new species: 7 mastadenoviruses, 5 aviadenoviruses, and 4 barthadenoviruses (earlier called atadenoviruses). Notably, both reptilian AdVs belong to the genus *Barthadenovirus*, along with 2 from the 7 avian AdVs. These findings seem to further confirm the theory that the barthadenovirus lineage evolved in and co-evolved with the reptiles, but after a host switch from them to birds, a separate lineage exists now and evolves further in birds (Benkő et al., 2022).  In the case of the present 16 species candidates, all exemplar strains of the proposed novel species shared DNA polymerase (amino acid) sequence identity with the closest related reference strain below 85%. The second species demarcation criterion was the different host or/and the different GC content of the most similar exemplars of existing species (Table 1).  **Naming**  The ICTV requires the application of a binomial species naming system. For adenovirid species we use Latinized species epithets derived by applying different approaches (Postler et al., 2022). We first attempted to design species epithets based on host/host taxon names. When this failed due to distinct viruses sharing the same host, we applied other etymologies as detailed below and in the attached Excel table.  **Species naming after**  **Colloquial host name**  bat adenovirus (bat in Latin: *vespertilio, -onis*) *Mastadenovirus vespertilionis*  Rousettus leschenaultia is a fruit bat (fruit in Latin: *fructus, -us*) *Mastadenovirus fructus*  Cherry valley breeder duck (Pekin duck; cherry in Latin: *cerasus, -i*) *Aviadenovirus cerasi*  **Genus**  marmot, *Marmota caudata* *Mastadenovirus marmotae*  roe deer, *Capreolus capreolus* *Mastadenovirus capreoli*  vampire bat, *Desmodus rotundus* *Mastadenovirus desmodi*  heart-nosed bat, *Cardioderma cor* *Mastadenovirus cardiodermatis*  black-naped oriole*, Oriolus chinensis* *Aviadenovirus orioli*  Eurasian scops owl*, Otus scops*  *Aviadenovirus oti*  grey warbler, *Gerygone igata* *Barthadenovirus gerygones*  scaly thrush, *Zoothera dauma* *Barthadenovirus zootherae*  spiny-tailed monitor (*Varanus acanthurus acanthurus*) *Barthadenovirus varani*  viviparous lizard, *Zootoca vivipara* *Barthadenovirus zootocae*  **Family**  great cormorant, Phalacrocoracidae *Aviadenovirus phalacrocoracidae*  **Subfamily**  vole, Arvicolinae (voles, lemmings, muskrats) *Mastadenovirus arvicolinae*  **Color**  rosy-faced lovebird (Latin *roseus, -a, -um*) *Aviadenovirus roseae*  **Bioinformatics**  Complete DNA polymerase amino acid sequences were aligned using the MAFFT v7.490 G-INS-i algorithm (Katoh & Standley, 2013). The alignment was edited using the Automated1 algorithm of TrimAl (v1.3): the length of the edited alignment was 805 amino acids. The LG+I+G evolutionary model was selected using ModelTest-NG v0.1.7 (Darriba et al., 2020). The tree was inferred using RAxML-NG v1.2.2, and the robustness of the tree was determined with a non-parametric bootstrap calculation using 1000 replicates (Kozlov et al., 2019). The transfer bootstrap expectation values were applied to the tree (Lemoine et al., 2018). The phylogenetic tree was visualized using MEGA7, and it was rooted on the midpoint, with the bootstrap values ≥75% at the nodes (Kumar et al., 2016).  The same complete DNA polymerase amino acid sequences were compared pairwise to reveal their amino acid sequence identity using SDT v1.2 (Muhire et al., 2014).  The inferred phylogenetic tree is available in Fig. 1, and the DNA polymerase sequence identities in Table 1. Note that the simple pairwise comparison of the full DNA polymerase sequences finds sometimes other adenoviruses as being more similar than the sophisticated phylogenetic analysis, which furthermore applies sequences edited/truncated in the non-informative regions (deleting most columns with gaps from the multiple alignment). |

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Arch Virol 168(2):68, PMID: 36656447, doi: [10.1007/s00705-022-05647-9](https://doi.org/10.1007/s00705-022-05647-9)  [Zheng](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zheng+W&cauthor_id=35537575) W, [Li](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Li+Y&cauthor_id=35537575) Y, [Tang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Tang+W&cauthor_id=35537575) W, [Wei](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Wei+M&cauthor_id=35537575) M, [Li](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Li+Y&cauthor_id=35537575) Y, [Shi](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Shi+P&cauthor_id=35537575) P, [Jiang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Jiang+L&cauthor_id=35537575) L, [Zhu](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zhu+H&cauthor_id=35537575) H, [Yu](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Yu+X&cauthor_id=35537575) X, [Chen](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Chen+G&cauthor_id=35537575) G, [Wang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Wang+J&cauthor_id=35537575) J, [Zhang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zhang+J&cauthor_id=35537575) J, [Zhang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zhang+X&cauthor_id=35537575) X (2022) Whole genome analysis of a novel adenovirus discovered from *Oriolus chinesis*. Virus Res 317: 198799, PMID: 35537575, doi: [10.1016/j.virusres.2022.198799](https://doi.org/10.1016/j.virusres.2022.198799)  [Zheng](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zheng+W&cauthor_id=38368638) W, [Teng](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Teng+X&cauthor_id=38368638) X, [Jiang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Jiang+T&cauthor_id=38368638) T, [Tang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Tang+W&cauthor_id=38368638) W, [Jiang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Jiang+L&cauthor_id=38368638) L, [Zhu](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zhu+H&cauthor_id=38368638) H, [Yu](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Yu+X&cauthor_id=38368638) X, [Chen](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Chen+G&cauthor_id=38368638) G, [Wang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Wang+J&cauthor_id=38368638) J, [Zhang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zhang+J&cauthor_id=38368638) J, [Qu](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Qu+M&cauthor_id=38368638) M, [Zhang](https://pubmed.ncbi.nlm.nih.gov/?sort=date&term=Zhang+X&cauthor_id=38368638) X (2024) Genome analysis of a novel avian atadenovirus reveals a possible horizontal gene transfer. Virology 593: 109999, doi: 10.1016/j.virol.2024.109999 |

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| **Tables, Figures:** |

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**Fig. 1. Phylogenetic tree of viruses of all accepted and proposed adenovirid species based on complete DNA polymerase amino acid sequences.** Proposed species are emphasized in bold type and red letters.



**Table 1.** **Pairwise sequence identity analysis of the exemplar strains of proposed new adenovirid species based on complete DNA polymerase amino acid sequences**

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| --- | --- | --- | --- | --- |
| **Proposed new species** | | **Most similar (representatives of) accepted or proposed species** | **Pairwise amino acid sequence identity (%; <85)** | **Further species demarcation criteria**  **(GC% difference)** |
| **Type name, GenBank accession number**  **(host species)** | **Proposed species name** |
| marmot AdV-1, PP098964 (*Marmota caudata*) | *Mastadenovirus marmotae* | *Mastadenovirus sciuri*  (squirrel AdV-1, KY427939) | 76.40 | new host |
| roe deer AdV, BK066828  (*Capreolus capreolus*) | *Mastadenovirus capreoli* | *Mastadenovirus bosprimum*  (bovine AdV-1, cattle) | 82.24 | new host |
| bat AdV 33390, BK066631  (unspecified bat from Vietnam) | *Mastadenovirus vespertilionis* | *Mastadenovirus chalinolobi*  (Gould’s wattled bat) | 78.21 | 7.0 |
| vampire bat AdV, BK066905  (*Desmodus rotundus*) | *Mastadenovirus desmodi* | *Mastadenovirus canidae*  (canine AdV-1, Y07760) | 68,87 | new host  4.9 |
| heart-nosed bat AdV, PP711818  (*Cardioderma cor*) | *Mastadenovirus cardiodermatis* | *Mastadenovirus canidae*  (canine AdV-1,Y07760) | 68.55 | new host  10.3 |
| Leschenault’s rousette AdV, OR998962 (*Rosettus leschenaultii*) | *Mastadenovirus fructus* | *Mastadenovirus equi*  (equine AdV-1, JN418926) | 59.9 | new host  17.7 |
| vole AdV-1 BK066403  (species not specified; Ukraine) | *Mastadenovirus arvicolinae* | *Mastadenovirus marmotae* (marmot AdV-1, PP098964) | 69.46 | different host  8.3 |
| great cormorant AdV-1 OR529407  (*Phalacrocorax carbo*) | *Aviadenovirus phalacrocoracidae* | *Aviadenovirus gallinae*  (fowl AdV-9, AF083975 chicken) | 70.13 | new host  4.1 |
| Eurasian scops owl AdV-1 ON843719  (*Otus scops*) | *Aviadenovirus oti* | *Aviadenovirus bubonis*  (owl AdV-1, LC638697, Indian eagle-owl, *Bubo bengalensis*) | 80.79 | new host |
| black-naped oriole AdV MZ819701 | *Aviadenovirus orioli* | *Aviadenovirus leucophthalmi*  (white-eyed parakeet AdV-2, *Psittacara leucophthalmus*, MN153802) | 76.72 | new host  2.9 |
| psittacine AdV-12 ON843719  (rosy-faced lovebird, *Agapornis roseicollis*) | *Aviadenovirus roseae* | *Aviadenovirus senegalense*  (psittacine AdV-1, MH580295, Senegal parrot, *Poicephalus senegalus*) | 75.30 | different host |
| duck AdV-6, MK757473  (Cherry valley breeder of Pekin/domestic duck, *Anas platyrhychos domesticus*) | *Aviadenovirus cerasi* | *Aviadenovirus quintum*  (fowl AdV-5, chicken,KC493646) | 82.04 | different host |
| grey warbler AdV-1 OQ986611  (*Gerygone igata*) | *Barthadenovirus gerygones* | *Barthadenovirus mellis* (Eastern spinebill AdV, MT674683, *Acanthorhynchus tenuirostris*) | 53.7 | new host  9.6 |
| scaly thrush AdV-1 OR233592  (*Zoothera dauma*) | *Barthadenovirus zootherae* | *Barthadenovirus sternae* (tern AdV-1,OL692338, common tern, *Sterna hirundo*, Laridae) | 59.94 | new host  5.1 |
| varanus adenovirus 37597 BK066675  (*Varanus acanthurus acanthurus*) | *Barthadenovirus varani* | *Barthadenovirus galloanserae*  (duck AdV-1, chicken, water fowl, Y09598) | 54.95 | new host  12.6 |
| viviparous lizard AdV-1 BK066448  (*Zootoca vivipara*) | *Barthadenovirus zootocae* | *Barthadenovirus lacertae* (lizard AdV-2, Mexican  beaded lizard,KJ156523) | 60.39 | new host  4.0 |