

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

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| **Code assigned:** | ***2023.008D*** |  |
| **Short title:** Rename genus *Atadenovirus* and add seven new species; create seven new species in genus *Aviadenovirus*, five new species in genus *Mastadenovirus,* three new species in genus *Siadenovirus*; and rename 86 adenovirid species (*Rowavirales*: *Adenoviridae*) |
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**List the ICTV Study Group(s) that have seen this proposal**

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| --- |
| ICTV Adenoviridae SG |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| ICTV Adenoviridae Study Group (11) | 11 | 0 | 0 |

**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | Y |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Barthadenovirus* | Adorján Bartha | N |
| *Mastadenovirus russelli* | William C. Russell | N |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 16, 2023 |
| Date of this revision (if different to above) | June 28, 2023 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

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| N/A |

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

**Name of accompanying Excel module**

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| --- |
| 2023.008D.N.v2.Adenoviridae\_1reng\_22ns\_86rensp.xlsx |

**Abstract**

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| We propose the renaming of genus *Atadenovirus* to *Barthadenovirus*, establishing 22 new adenovirus species in the four well populated genera, and the binominal renaming of 86 existing adenovirus species (one species already received a binomial Latinized name). We propose Latinized species names based on different principles but mostly on the hosts. This will result in 87 species in the six genera of *Adenoviridae*. |

**Text of proposal**

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| **Renaming of genus *Atadenovirus***Genus *Atadenovirus* was originally named based on the high AT content of the genomes of the first identified members of this adenovirid lineage, namely several characteristically different ruminant adenovirids (from cattle and sheep) and duck adenovirus 1 (from chicken, causing the egg drop syndrome) (Bartha and Áldásy, 1966; Harrach et al., 1997; Hess et al., 1997). However, subsequent identification of squamate reptile (snake, lizard) adenoviruses turned out to have a balanced GC content (Farkas et al., 2002, Wellehan et al., 2004, Pénzes et al., 2020). This lineage may have coevolved with squamate reptiles, and only later switched hosts to ruminants and waterfowl. Additional avian adenovirids were identified and many of them proved not to have low GC contents. The genus *Mastadenovirus* has the members with the lowest (and the highest) GC% values in the family. Thus, this original name is somewhat misleading. With the new proposed genus name, *Barthadenovirus*, we wish to honor Adorján Bartha, a Hungarian virologist, who was born 100 years ago, and who was the first to recognize that certain (bovine) adenovirids have remarkably different biological properties and who proposed a new taxonomical group (bovine “subgroup 2”) for them (Bartha, 1969). Later, his proposal was validated by the introduction of molecular techniques (DNA hybridization and finally sequencing and phylogenetic analyses). Finally, even turtles proved to have atadenoviruses (Garcia-Morante et al., 2016), thus the Bartha name could be seen also as one referring to the bovine, avian, (squamate) reptilian and turtle hosts. The name even contains the old name: Bartha. **Proposed new species**Over the last several years, novel adenovirid genomes have been sequenced completely or almost completely from birds (Mukai et al., 2019; Athukorala et al., 2020; Huang et al., 2020; Vibin et al., 2020; Gellért et al., 2022; Kobayashi et al., 2022; Kraberger et al., 2022; Shan et al., 2022; Surplis et al., 2022), and mammals (van Beurden et al., 2017; Prada et al., 2019; Dastjerdi et al., 2022; Kumagai et al., 2022; Okoh et al., 2023, Veith et al., 2023). Twenty-two of them merit the establishment of new species: seven aviadenoviruses, seven barthadenoviruses (atadenoviruses), five mastadenoviruses*,* and three siadenoviruses. In 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,
* Pathogenicity,
* Cross-neutralization, and/or
* Nucleotide composition.

With the advancement of sequencing techniques, the calculated phylogenetic distances became the decisive demarcation criterion. 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. In the case of the present 22 candidates, all but one reference strain of proposed novel species shared DNA polymerase sequence identity with the closest related reference strain below 85%. The only exception, reindeer adenovirus 1 (Dastjerdi et al., 2022), shared 85.56% with the reference strain of *Deer mastadenovirus B*. The second species demarcation criterion was the different host in all except one case: the species *Siadenovirus carbocapituli* and *Great tit siadenovirus A* were demarcated, in addition to the vast evolutionary distance, based on the different presumed pathogenicity of their members infecting great tit (Gellért et al., 2022).**Naming and renaming**ICTV requires the application of a binomial species naming system. One species in family *Adenoviridae* has been named already following this system (*Aviadenovirus leucophthalmi* for [white-eyed parakeet](https://en.wikipedia.org/wiki/White-eyed_parakeet) adenovirus 2, GenBank #MN153802). Aside from assigning binomial names to 22 novel species proposed here, we propose to rename the remaining 86 adenovirid species using 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** **the old species name***Human mastadenovirus A*: Adam, the first man *Mastadenovirus adami**Human mastadenovirus B*: Blackbeard (the pirate,  viruses act as pirates) *Mastadenovirus blackbeardi**Human mastadenovirus C*: Caesar (emperor,  human adenovirus (AdV) 2 and 5 rule almost all AdV labs) *Mastadenovirus caesari**Human mastadenovirus D*: dominating, most abundant *Mastadenovirus dominans**Human mastadenovirus E*: exotic single HAdV type  in the species (among chimp AdVs) *Mastadenovirus exoticum**Human mastadenovirus F*: detectable mainly in faeces *Mastadenovirus faecale*(We are not following this scheme for *Human mastadenovirus G* because HAdV-52 was not confirmed as a human virus, and there seems to be no need to implicate this group of viruses in having medical importance when they originate from Old World monkeys. Instead, we propose to rename the species after a respected adenovirologist from Scotland, William C. Russell.)**scientist**Russell (simian AdV-1, +many SAdVs; human AdV-52) *Mastadenovirus russelli***Colloquial host name**Asian particolored bat (Vs9), *Vespertilio sinensis* *Mastadenovirus asiense*bearded dragon, *draco* *Barthadenovirus draconis*bottlenose dolphin (dolphin AdV-1), *delphinus* *Mastadenovirus delphini*crane, *grui* *Aviadenovirus gruis*deer, *cervus* (Odocoileus AdV-1) *Barthadenovirus cervi*duck AdV-2, *anas* (Muscovy duck, *Cairina moschata*) *Aviadenovirus anatis*eastern spinebill, a honeyeater (bird), honey: *mel* *Barthadenovirus mellis*falcon, *falco* (several falcon species) *Aviadenovirus falconis*frog, *rana* *Siadenovirus ranae*goose, *anser* *Aviadenovirus anseris*hen (fowl AdV-2, -3, -9, -11), *gallina* *Aviadenovirus gallinae*horse (equine AdV-1) (host swich from bat, pathogenic) *Mastadenovirus equi*lemur (from *lamia*, “ghost” in Latin; etymological origin of lemur) *Mastadenovirus lamiae*Mexican beaded lizard, *lacerta* *Barthadenovirus lacertae*mice, *mus* (numerous virus variants) *Mastadenovirus muris*Old World monkey, *simia* (SAdV-3) *Mastadenovirus simiae*owl (Indian eagle-owl, *Bubo bengalensis), bubo*  *Aviadenovirus bubonis*pigeon AdV-1, *columba* *Aviadenovirus columbae*polar bear, *ursus* *Mastadenovirus ursi*raptor (Accipitriformes and Strigiformes) derived from the  Latin word [*rapio*](https://en.wiktionary.org/wiki/rapio#Latin), meaning "to seize or take by force" *Siadenovirus raptoris*rhesus macaque *Macaca mulatta* (king in the Iliad) (SAdV-54) *Mastadenovirus rhesi*Senegal parrot (psittacine AdV-1) *Aviadenovirus senegalense*sheep (ovine AdV-7) *Barthadenovirus ovis*snake, *serpens* *Barthadenovirus serpentis*squirrel, *sciurus* *Mastadenovirus sciuri*swine (porcine AdV-3), *porcus* *Mastadenovirus porci*reindeer, *tarandrus* *Mastadenovirus tarandri*titi monkey, black-capped squirrel monkey New Worldmonkeys, Platyrrhini, "flat nosed", *simulus* *Mastadenovirus simuli*trush, *turdus* *Aviadenovirus turdi*white sturgeon, *acipenser* *Ichtadenovirus acipenseris***Species**bat AdV-2 *Pipistrellus pipistrellus* *Mastadenovirus pipistrelli*common brushtail possum *Trichosurus vulpecula*, “little fox" *Barthadenovirus vulpeculae*little corella (*Cacatua sanguinea*) *Siadenovirus sanguineae*Egyptian fruit bat (*Rousettus aegyptiacus*) *Mastadenovirus aegyptiaci*Eurasian siskin (*Spinus spinus*) *Aviadenovirus spinus* Radde's warbler (bird, *Phylloscopus schwarzi*)  German astronomer *Barthadenovirus schwarzi*Senegal parrot (*Poicephalus senegalus*) *Aviadenovirus senegalense*yellow baboon (*Papio cynocephalus*) "dog-faced" (SAdV-19) *Mastadenovirus cynocephali*yellow-browed warbler (bird, *Phylloscopus inornatus*) „plain” *Barthadenovirus inornati***Genus**common tern, *Sterna hirundo Barthadenovirus sternae*duck AdV-4, Muscovy duck, *Cairina moschata* *Aviadenovirus cairinae*Gould's wattled bat, *Chalinolobus gouldii* (lobe, *lobus*) *Mastadenovirus chalinolobi*grivet, *Chlorocebus aethiops* (SAdV-17, -18) *Mastadenovirus chlorocebi*guinea pig, *Cavia porcellus* *Mastadenovirus caviae*kangaroo rat, *Dipodomys* *Mastadenovirus dipodomysis*macaque, *Macaca* sp. (SAdV-13) *Mastadenovirus macacae*pond slider, *Trachemys scripta* *Testadenovirus trachemysis*porpoise, *Phoecoena* *Mastadenovirus phocoenae*Southern mealy amazon, *Amazona farisona* *Barthadenovirus amazonae*straw-colored fruit bat, *Eidolon helvum* *Mastadenovirus eidoli*tree shrew, *Tupaia* *Mastadenovirus tupaiae***Family**bat AdV-4 *Mastadenovirus rhinolophidae*bat AdV-7, WIV12 *Mastadenovirus miniopteridae*bat AdV-9, WIV17 *Mastadenovirus pteropodidae*bottlenose dolphin (dolphin AdV-2) *Mastadenovirus dolphinae*bovine AdV-2 (+ovine AdV-2, -3, -4) *Mastadenovirus bovidae*California sea lion *Mastadenovirus otariidae*canine AdV-1, -2 *Mastadenovirus canidae*chinstrap penguin and other penguin species *Siadenovirus spheniscidae*common murre *Siadenovirus uriae*duck AdV-1, (chicken, waterfowl) *Barthadenovirus galloanserae*frogmouth (bird) Tasmania *Aviadenovirus podargidae*great tit AdV-1 (great tit, blue tit) *Siadenovirus paridae*horse (equine AdV-2, coevolved with horse) *Mastadenovirus equidae*pigeon AdV-2 *Aviadenovirus columbidae*South Polar skua*Siadenovirus stercorariidae*wallaby *Barthadenovirus macropodidae*wild duck, *Anas platyrhynchos,* and  Pacific black duck, *A. superciliosa* (duck AdV-5) *Aviadenovirus anatidae***Disease**hen (fowl AdV-1), gizzard erosion, *ventriculus* *Aviadenovirus ventriculi*hen (fowl AdV-4), hydropericardium syndrome *Aviadenovirus hydropericardii*hen (fowl AdV-6, -7, -8a, -8b) inclusion body hepatitis *Aviadenovirus hepatitidis*murine AdV-1, fatal encephalomyelitis *Mastadenovirus encephalomyelitidis***Tropism**heart, *cor* (murine AdV-3 from striped field mouse) *Mastadenovirus cordis***Colors**blue-throated macaw, psittacine *AdV*-11, *caeruleum* *Barthadenovirus caerulei*golden snub-nosed monkey, golden-haired: *flavus* *Mastadenovirus flavi*grey parrot (PsAdV-2): *cinereum**Siadenovirus cinerei*Pacific parrotlet, a small green p. (PsAdV-5): *viride**Siadenovirus viridis*red-bellied parrot *Poicephalus rufiventris* (PsAdV-4) *Aviadenovirus rubri***Fantasy names**bat AdV-3 *Myotis ricketti* *(*Neo-Latin construction from the Greek „mouse-eared”: „*mus auritus*” *Mastadenovirus musauriti*bat AdV-8 WIV13, lowest GC% among AdVs, *humilis*, *Mastadenovirus humile*cattle (bovine AdV-1) *primum* *Mastadenovirus bosprimum*cattle (bovine AdV-3) *tertium* *Mastadenovirus bostertium*cattle (bovine AdV-4) *quartum* *Barthadenovirus bosquartum*cattle (bovine AdV-6) *sextum* *Barthadenovirus bossextum*cattle (bovine AdV-7) *septimum* *Barthadenovirus bosseptimum*cattle (bovine AdV-10) *decimum* *Mastadenovirus bosdecimum*chicken (fowl AdV-5) *quintum* *Aviadenovirus quintum*crab-eating or long-tailed macaque *Macaca fascicularis*:  "*longum cauda*" *Mastadenovirus longumcaudae*great tit AdV-3 (Hungarian name: „coal-headed”) *Siadenovirus carbocapituli*pig (porcine AdV-1, -2, -3): *porcus* + third: *tertium* *Mastadenovirus porcustertium*pig (porcine AdV-4): *porcus* + fourth: *quartum* *Mastadenovirus porcusquartum*pig (porcine AdV-5): *porcus* + fifth: *quintum* *Mastadenovirus porcusquintum*Rafinesque's big-eared bat, North America, bat AdV-11 *Mastadenovirus magnauris*sheep (ovine AdV-1) *primum* *Mastadenovirus ovisprimum*sheep (ovine AdV-8) *octavum* *Mastadenovirus ovisoctavum*simian AdV-16 has unique HAG properties (IV), “foreigner” *Mastadenovirus alienum*simian AdV-20 (twenties) *vigesimum* *Mastadenovirus simiavigesimum*skunk (Canada), four-toed hedgehog (Africa, Japan, USA) pygmy marmoset (South America, Hungary),  North American porcupine, grey fox (N. America):  fatal and crosses (species) boundaries like the  Treaty of Trianon *Mastadenovirus trianonum*turkey AdV-1 *Meleagris gallopavo primum* *Aviadenovirus gallopavoprimum*turkey (TAdV-3) *Meleagris gallopavo tertium* *Barthadenovirus* gallopavotertiumturkey (TAdV-4) *Meleagris gallopavo quartum* *Aviadenovirus gallopavoquartum*turkey (TAdV-5) *Meleagris gallopavo quintum* *Aviadenovirus gallopavoquintum***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 784 amino acids. The LG+I+G evolutionary model was selected using ModelTest-NG v0.1.5 (Darriba et al., 2020). The tree was inferred using RAxML-NG v1.1.0, and the robustness of the tree was determined with a non-parametric bootstrap calculation using 100 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. |

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**Supporting evidence**

AY771780

 *Human mastadenovirus G*

KP329565

 *Simian mastadenovirus C*

L19443

 *Human mastadenovirus F*

FJ025931

 *Simian mastadenovirus F*

HQ241819

 *Simian mastadenovirus B*

KP329564

 *Simian mastadenovirus E*

J01917

 *Human mastadenovirus C*

AJ854486

 *Human mastadenovirus D*

DQ086466

 *Human mastadenovirus B*

AY487947

 *Human mastadenovirus E*

X73487

 *Human mastadenovirus A*

KP329563

 *Simian mastadenovirus D*

KM190146

 *Simian mastadenovirus H*

KX505867

 *Simian mastadenovirus I*

AY598782

 *Simian mastadenovirus A*

HQ605912

 *Simian mastadenovirus G*

HQ913600

 *Platyrrhini mastadenovirus A*

MK518392

 *Ovine mastadenovirus C*

 AC\_000002

 *Bovine mastadenovirus B*

KY306667

 *Deer mastadenovirus B*

 **MZ507556**

***Mastadenovirus tarandri***

KJ563221

 *Sea lion mastadenovirus A*

MK774519

 *Porcine mastadenovirus B*

AF258784

 *Tree shrew mastadenovirus A*

KT698853

 *Bat mastadenovirus C*

 **OQ081771 *Mastadenovirus lamiae***

KT698852

 *Bat mastadenovirus E*

KT698856

 *Bat mastadenovirus D*

MG551742

 *Bat mastadenovirus I*

AP018374

 *Bat mastadenovirus H*

KX961095

 *Bat mastadenovirus F*

 **MK472072**

***Mastadenovirus chalinolobi***

JN418926

 *Equine mastadenovirus A*

KP238322

 *Skunk mastadenovirus A*

GU226970

 *Bat mastadenovirus A*

KX871230

 *Bat mastadenovirus G*

JN252129

 *Bat mastadenovirus B*

LC385827

 *Bat mastadenovirus J*

AC\_000003

 *Canine mastadenovirus A*

KY427939

 *Squirrel mastadenovirus A*

KT160425

 *Equine mastadenovirus B*

AC\_

000189

 *Porcine mastadenovirus A*

KR024710

 *Dolphin mastadenovirus A*

 **KY352473**

***Mastadenovirus phocoenae***

LT841149

 *Dolphin mastadenovirus B*

AF289262

 *Porcine mastadenovirus C*

 AC\_000191

 *Bovine mastadenovirus A*

AC\_000001

 *Ovine mastadenovirus A*

 **ABRO02087964**

***Mastadenovirus dipodomysis***

MF773580

 *Polar bear mastadenovirus A*

MN986925

 *Guinea pig mastadenovirus A*

AC\_

000012

 *Murine mastadenovirus A*

EU835513

 *Murine mastadenovirus C*

HM049560

 *Murine mastadenovirus B*

*Mastadenovirus*

 **MT138101**

***Barthadenovirus inornati***

 **MT138103**

***Barthadenovirus schwarzi***

 **MT674683**

***Barthadenovirus mellis***

 **MT138098**

***Barthadenovirus caerulei***

KJ675568

 *Psittacine atadenovirus A*

 AC\_000004

 *Duck atadenovirus A*

 **OL692338**

***Barthadenovirus sternae***

KJ156523

 *Lizard atadenovirus A*

DQ106414

 *Snake atadenovirus A*

MT050041

 *Lizard atadenovirus B*

 **OQ792214**

***Barthadenovirus macropodidae***

JQ345700

 *Bovine atadenovirus E*

AF036092

 *Bovine atadenovirus D*

KY748210

 *Deer atadenovirus A*

U40839

 *Ovine atadenovirus D*

 **LC597488**

***Barthadenovirus bosseptimum***

*Atadenovirus*

*(Barthadenovirus)*

HM585353

 *Skua siadenovirus A*

EU715130

 *Raptor siadenovirus A*

MK227353

 *Psittacine siadenovirus E*

MK695679

 *Psittacine siadenovirus D*

AF074946

 *Turkey siadenovirus A*

KP144329

 *Penguin siadenovirus A*

FJ849795

 *Great tit siadenovirus A*

 **MW508338**

***Siadenovirus carbocapituli***

 **MN480433**

***Siadenovirus uriae***

 **MZ562791**

***Siadenovirus cinerei***

AF224336

 *Frog siadenovirus A*

*Siadenovirus*

*Testadenovirus*

JN632576

 *Pond slider testadenovirus A*

*Ichtadenovirus*

MK101347

 *Sturgeon ichtadenovirus A*

 **LC469780**

***Aviadenovirus gruis***

 **MW380865**

***Aviadenovirus anatidae***

KJ469653

 *Duck aviadenovirus B*

JF510462

 *Goose aviadenovirus A*

KX121164

 *Pigeon aviadenovirus B*

FN824512

 *Pigeon aviadenovirus A*

MN153802

 *Aviadenovirus leucophthalmi*

 **MT138099**

***Aviadenovirus spinus***

 **MT138100**

***Aviadenovirus turdi***

 **ON642334**

***Aviadenovirus podargidae***

GU936707

 *Turkey aviadenovirus B*

 **MN733730**

***Aviadenovirus cairinae***

KX577802

 *Psittacine aviadenovirus B*

MH580295

 *Psittacine aviadenovirus C*

 **LC638697**

***Aviadenovirus bubonis***

 AC\_000014

 *Fowl aviadenovirus A*

KF477313

 *Turkey aviadenovirus D*

HE608152

 *Fowl aviadenovirus C*

KC493646

 *Fowl aviadenovirus B*

KF477312

 *Turkey aviadenovirus C*

AF083975

 *Fowl aviadenovirus D*

KT862808

 *Fowl aviadenovirus E*

*Aviadenovirus*

100

84

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97

0.2

**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.

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

If the closest related adenoviral strain was the reference strain of a newly proposed species, the reference strain of the closest related already accepted species was also indicated. A second species demarcation criterion (host species or pathogenicity) is included for unclear cases.

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| **Proposed new species** | **Closest related accepted(and proposed) species** | **Pairwise amino acidsequence identity** |
| **Accession number and type name** | **Proposed species name** |
| MZ507556 reindeer adenovirus 1(host: *Rangifer tarandus*, reindeer) | *Mastadenovirus tarandri* | KY306667 *Deer mastadenovirus B*(host: *Odocoileus virginianus*, white-tailed deer) | 85.56% |
| MT138099 Eurasian siskin adenovirus 2 | *Aviadenovirus spinus* | MN153802 *Aviadenovirus leucophthalmi* | 83.22% |
| MT138100 Naumann's thrush adenovirus 1 | *Aviadenovirus turdi* | MN153802 *Aviadenovirus leucophthalmi* | 78.83% |
| MT138101 yellow-browed warbler adenovirus 1 | *Barthadenovirus inornati* | MT138103 *Barthadenovirus schwarzi* | 76.98% |
| AF289262 *Porcine mastadenovirus C* | (47.04%) |
| MT138103 Radde's warbler adenovirus 1 | *Barthadenovirus schwarzi* | MT138101 *Barthadenovirus inornati* | 76.98% |
| AC\_000004 *Duck atadenovirus A* | (46.39%) |
| KY352473 harbour porpoise adenovirus 1(host: *Phocoena phocoena*, harbour porpoise) | *Mastadenovirus phocoenae* | KR024710 *Dolphin mastadenovirus A*(host: *Tursiops truncatus*, bottlenose dolphin) | 74.91% |
| MT138098 psittacine adenovirus 11(host: *Ara glaucogularis*, blue-throated macaw) | *Barthadenovirus caerulei* | KJ675568 *Psittacine atadenovirus A*(host: *Amazona farinosa*, southern mealy amazon) | 74.54% |
| MN733730 duck adenovirus 4 | *Aviadenovirus cairinae* | AF083975 *Fowl aviadenovirus D* | 72.69% |
| LC638697 Indian eagle-owl adenovirus 1 | *Aviadenovirus bubonis* | AC\_000014 *Fowl aviadenovirus A* | 70.56% |
| MW380865 duck adenovirus 5(host: *Anas platyrhynchos*, wild duck) | *Aviadenovirus anatidae* | KJ469653 *Duck aviadenovirus B*(host: *Cairina moschata*, Muscovy duck) | 69.45% |
| MK472072 Gould's wattled bat adenovirus 1 | *Mastadenovirus chalinolobi* | AF289262 *Porcine mastadenovirus C* | 68.62% |
| OQ081771 lemur adenovirus | *Mastadenovirus lemuris* | AF258784 *Tree shrew mastadenovirus A* | 68.57% |
| LC597488 bovine adenovirus 7(host: *Bos taurus*, cattle) | *Barthadenovirus bosseptimum* | U40839 *Ovine atadenovirus D*(host: *Ovis aries*, domestic sheep) | (68.04%) |
| ON642334 tawny frogmouth adenovirus | *Aviadenovirus podargidae* | MN733730 *Aviadenovirus cairinae* | 67.02% |
| AF083975 *Fowl aviadenovirus D* | 67.00% |
| MW508338 great tit adenovirus 3(pathogenicity: nephritis) | *Siadenovirus carbocapituli* | FJ849795 *Great tit siadenovirus A*(pathogenicity: enteritis) | 65.28% |
| MN480433 common murre adenovirus | *Siadenovirus uriae* | HM585353 *Skua siadenovirus A* | 64.64% |
| MZ562791 psittacine adenovirus 2 | *Siadenovirus caeruli* | HM585353 *Skua siadenovirus A* | 62.83% |
| OL692338 common tern adenovirus 1 (“tern atadenovirus 1”) | *Barthadenovirus sternae* | AC\_000004 *Duck atadenovirus A* | 58.99% |
| ABRO02087964 Ord's kangaroo rat adenovirus | *Mastadenovirus dipodomysis* | AC\_000191 *Bovine mastadenovirus A* | 58.95% |
| OQ792214 agile wallaby adenovirus 1 | *Barthadenovirus macropodidae* | AF036092 *Bovine atadenovirus D* | 58.93% |
| LC469780 crane adenovirus 1 | *Aviadenovirus gruis* | AF083975 *Fowl aviadenovirus D* | 53.13% |
| MT674683 eastern spinebill adenovirus 1 (“passerine adenovirus 1”) | *Barthadenovirus mellis* | AF289262 *Porcine mastadenovirus C* | 45.33% |

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