This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2016.012aD***	(to be completed by ICTV officers)

Short title: a new species in the genus *Siadenovirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

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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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	*Adenoviridae*

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: July 22, 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

Code	***2016.012aD***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Siadenovirus***
Subfamily:	**Unassigned**
Family:	***Adenoviridae***
Order:	**Unassigned**

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate:** (only 1 per species please)	**GenBank sequence accession number(s)**
Penguin siadenovirus A	chinstrap penguin adenovirus 2 (CSPAdV-2)	KP144329

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 11

Complete genome sequences and biological properties of two chinstrap penguin (*Pygoscelis antarctica*) and two gentoo penguin (*Pygoscelis papua*) adenoviruses were analyzed and published (Lee et al., 2014 and 2016). According to phylogenetic calculations and the genome organization, these four viruses are very similar to each other and belong to the genus *Siadenovirus*. Phylogenetic analyses (based on the complete amino acid sequence of the DNA-dependent DNA polymerase) prove clear distance of these penguin AdVs of the proposed new species from members of the previously accepted species (Figure 1). In the calculation shown in the Annex, we applied only one representative of the four very similar proteins, namely from the chinstrap penguin adenovirus 2 (CSPAdV-2), which also appears in the RefSeq data base. One of the species demarcation criteria in the family *Adenoviridae* is a 5-15% phylogenetic distance in the amino acid sequence of the DNA polymerase. The distance of CSPAdV-2 is more than 15% from the closest virus belonging to an accepted species, i.e. turkey adenovirus 3 (TAdV-3). Another species demarcation criterion is a new host. These four siadenoviruses were detected in penguins of two species in the wild life at the Antarctica. We can safely suppose that they indeed belong to this penguin hosts, from which no AdVs have been reported yet. A third species demarcation criterion is the genome organization. The four sequenced penguin AdV genomes have the peculiar property of lacking the sialidase gene otherwise present in every siadenovirus sequenced so far.

Considering the phylogenetic distance, the new host, and the specific genome organization, CSPAdV-2 seems to merit the establishment of a new species.

We propose the name of *Penguin siadenovirus A* as its members occur at least in two different penguin species. This name is in-line with the earlier naming policy in *Adenoviridae* family.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Lee, S.Y., Kim, J.H., Park, Y.M., Shin, O.S., Kim, H., Choi, H.G., Song, J.W. (2014). A Novel Adenovirus in Chinstrap Penguins (*Pygoscelis antarctica*) in Antarctica. Viruses **6** (5) 2052–61 doi: 10.3390/v6052052.

Lee, S.Y., Kim, J.H., Seo, T.K., No, J.S., Kim, H., Kim, W.K, Choi, H.G., Kang, S.H.Song, J.W. (2016). Genetic and Molecular Epidemiological Characterization of a Novel Adenovirus in Antarctic Penguins Collected between 2008 and 2013. PLoS One. **11** (6) e0157032. doi: 10.1371/journal.pone.0157032.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1. Properties of the members of the newly proposed species (highlighted with bold) compared to the phylogenetically closest fully sequenced siadenoviruses

Species (virus)	G+C content (%)	Host species	sialidase gene
Penguin siadenovirus A (2 chinstrap penguins /KP144329, KP144330/ and 2 gentoo penguins /KP279746, KP279747/)	35.5-35.6	chinstrap penguin (*Pygoscelis antarctica*), gentoo penguin (*Pygoscelis papua*)	missing
Turkey siadenovirus A (turkey AdV-3)	34.99	domestic turkey (*Meleagris gallopavo domesticus*)	present
Raptor siadenovirus A (raptor AdV-1)	38.48	Bengal eagle owl (*Bubo bengalensis*), Verreaux's eagle owl (*Bubo lacteus*) and Harris hawk (*Parabuteo unicinctus*)	present
Skua siadenovirus A (South Polar skua AdV-1)	34.23	South Polar skua *(Stercorarius maccormicki)*	present

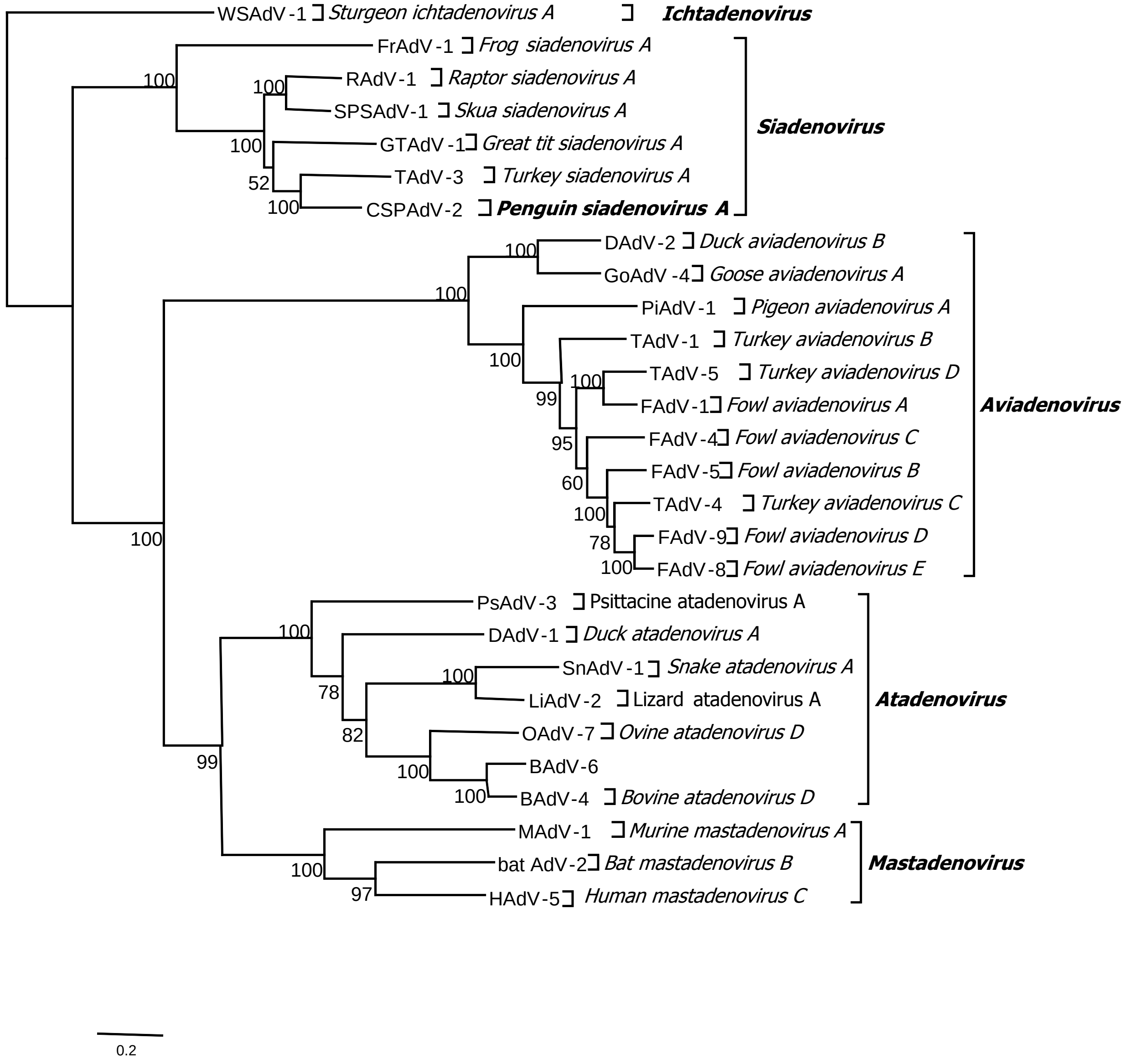

Fig. 1. Maximum likelihood analysis of the complete amino-acid sequences of the DNA-dependent DNA polymerase shows the genetic distance between CSPAdV-2 (highlighted with bold) and its closest relative, TAdV-3. Only three selected types were included in the calculations from the members of the genus *Mastadenovirus*. According to the result of model selection (performed by ProtTest on the following server: http://darwin.uvigo.es/), the LG+I+G+F model was used in the maximum likelihood analysis (PhyML). Bootstrap analysis with 100 replicates was performed, and the values are shown as percentage. The scale bar shows an evolutionary distance of 0.2 aa substitution per position. Abbreviations: WSAdV – white sturgeon adenovirus; FrAdV – frog adenovirus; RAdV – raptor adenovirus; SPSAdV – South Polar skua adenovirus; GTAdV – great tit adenovirus; TAdV – turkey adenovirus; **CSPAdV – chinstrap penguin adenovirus**; DAdV – duck adenovirus; GoAdV – goose adenovirus; PiAdV – pigeon adenovirus; FAdV – fowl adenovirus; PsAdV – psittacine adenovirus; SnAdV – snake adenovirus; LiAdV – lizard adenovirus; OAdV – ovine adenovirus; BAdV – bovine adenovirus; MAdV – murine adenovirus; HAdV – human adenovirus.