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:	***2012.016aV***	(to be completed by ICTV officers)

Short title: Create species *Skua adenovirus A* in the genus *Siadenovirus*, family *Adenoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

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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-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	To SG chair: 29 June 2012 To Vertebrate Virus Subcommittee chair (A. J. Davison): 1st July 2012
Date of this revision (if different to above):	3rd July 2012

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2012.016aV***	(assigned by ICTV officers)

To create one 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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Skua adenovirus A	HM585353

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 9

The proposed species contains an adenovirus type, South Polar skua adenovirus 1, that shows more than 15% phylogenetic distance (based on DNA polymerase protein) from the members of all other established adenovirus species (Fig. 1). The species would be only the fifth accepted species in the genus *Siadenovirus* (following *Frog adenovirus A*, *Turkey adenovirus A*, *Raptor adenovirus A* and *Great tit adenovirus A*). The host of the founder member of the proposed species belongs to the order of Charadriiformes. The hosts of the members of the previously established siadenovirus species include one amphibian, and several birds that belong to Galliformes, Falconiformes, Strigiformes and Passeriformes, respectively. The phylogenetic relationships and the specific hosts reflect an evolutionary distance that justifies the establishment of this species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Davison AJ, Harrach B (2011) Siadenovirus. *Adenoviridae*. Tidona CA, Darai G (eds) The Springer Index of Viruses, Springer, New York pp 49-56.

Harrach B, Benkő M, Both GW, Brown M, Davison AJ, Echavarría M, Hess M, Jones MS, Kajon A, Lehmkuhl HD, Mautner V, Mittal SK, Wadell G (2011) Family *Adenoviridae*. King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Virus Taxonomy: Classification and Nomenclature of Viruses. Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, San Diego pp 125-141.

Kovács ER, Benkő M (2011) Complete sequence of raptor adenovirus 1 confirms the characteristic genome organization of siadenoviruses. Infect Genet Evol 11:1058-1065.

Park, Y.M., Kim, J.H., Gu, S.H., Lee, S.Y., Lee, M.G., Kang,Y.K., Kang, S.H., Kim, H.J., Song, J.W. (2012) Full genome analysis of a novel adenovirus from the South Polar skua (*Catharacta maccormicki*) in Antarctica. Virology 422:144-150.

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.

South Polar skua adenovirus 1 (SPSAdV-1) has been detected by PCR in the tissues of six South Polar skuas (*Catharacta maccormicki,* previously known as *Stercorarius maccormicki*) found dead in Antarctica. The carcasses were collected on the King George Island during 2007 to 2009. The DNA was extracted from different internal organs. The sequence of the genome fragments (DNA polymerase, penton base, hexon) amplified by PCR from the six carcasses proved to be identical. The different sampling dates prove that this is a circulating virus capable of infecting (and possibly killing) South Polar skuas. The virus seems to be specific for South Polar skuas, since it has not been found in any other avian samples including 10 further species (but no other skuas) from the suborder Laridii. Although the virus could not be isolated because of the lack of adequate cell culture, its repeated detection in carcasses of the same bird species constitute a strong evidence for its existence. Live skuas have not been screened yet.

The whole genome (26.340 bp) of one of the newly found South Polar skua adenoviruses was sequenced by serial PCRs (Park et al., 2012). The genome ends were determined by RACE PCR. The genome organization and the genes show the characteristics of siadenoviruses (Davison and Harrach, 2011; Harrach et al., 2011; Kovács and Benkő, 2011). These include the lack of protein V, and IX, as well as the presence of the sialidase, ORF4, and siadenovirus-specific E3, ORF7 and ORF8 genes, and a siadenovirus-specific protease cleavage signal in pVII (cleavage signal I; LV/IGG'), and splicing in the gene of the DNA binding protein. The classification was also supported by phylogenetic analyses (Fig. 1).

We propose that the new species be named *Skua adenovirus A*, since similar AdVs might occur in other skua species as well.

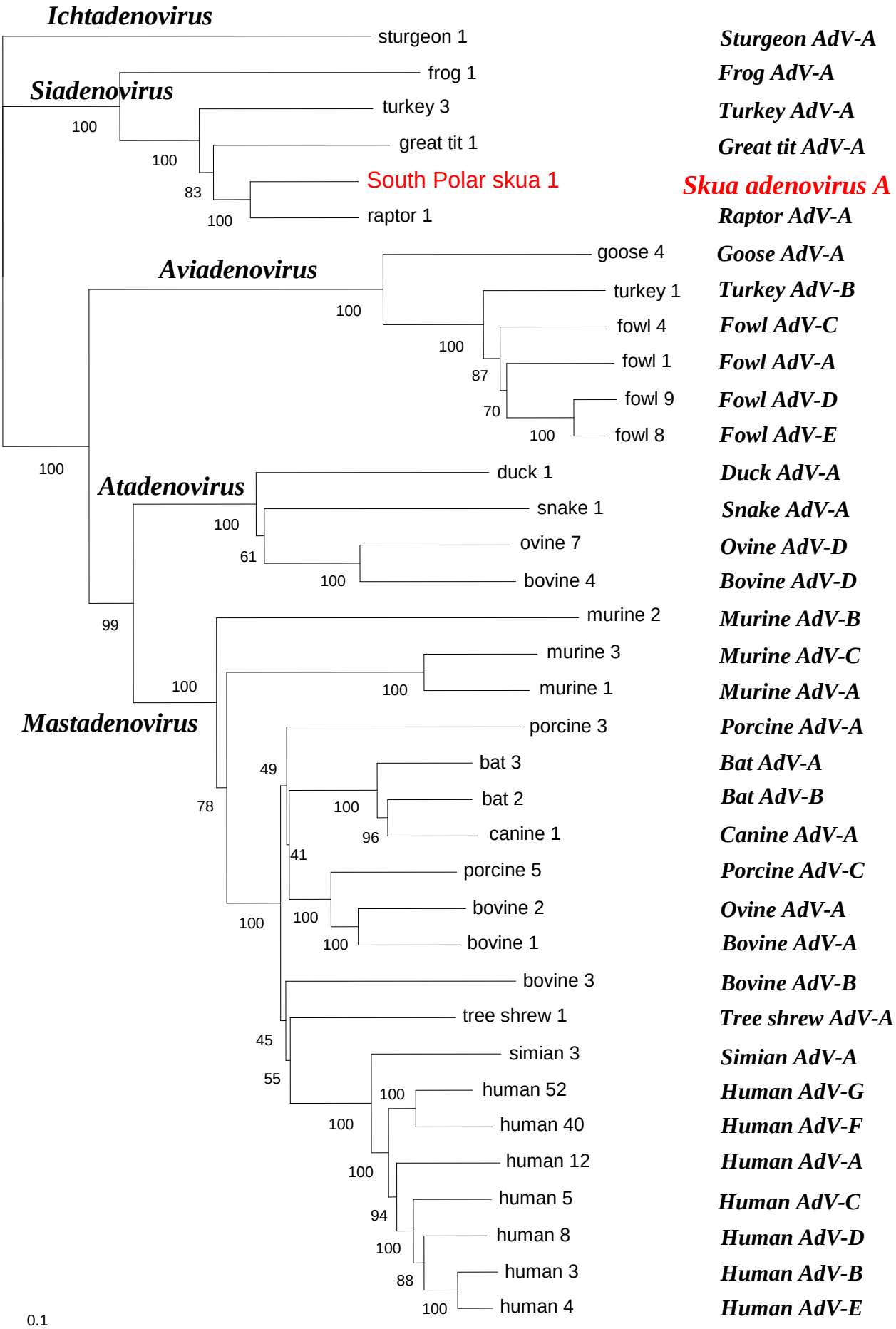
Ichtadenovirus
sturgeon 1
Siadenovirus
frog 1
turkey 3
great tit 1
South Polar skua 1
raptor 1
Aviadenovirus
goose 4
turkey 1
fowl 4
fowl 1
fowl 9
fowl 8
Atadenovirus
duck 1
snake 1
ovine 7
bovine 4
Mastadenovirus
murine 2
murine 3
murine 1
porcine 3
bat 3
bat 2
canine 1
porcine 5
bovine 2
bovine 1
bovine 3
tree shrew 1
simian 3
human 52
human 40
human 12
human 5
human 8
human 3
human 4
100
100
83
100
100
100
87
70
100
100
100
99
100
100
61
100
78
49
100
96
41
100
100
100
45
55
100
100
100
94
100
88
100
0.1
Sturgeon AdV-A
Frog AdV-A
Turkey AdV-A
Great tit AdV-A
Skua adenovirus A
Raptor AdV-A
Goose AdV-A
Turkey AdV-B
Fowl AdV-C
Fowl AdV-A
Fowl AdV-D
Fowl AdV-E
Duck AdV-A
Snake AdV-A
Ovine AdV-D
Bovine AdV-D
Murine AdV-B
Murine AdV-C
Murine AdV-A
Porcine AdV-A
Bat AdV-A
Bat AdV-B
Canine AdV-A
Porcine AdV-C
Ovine AdV-A
Bovine AdV-A
Bovine AdV-B
Tree shrew AdV-A
Simian AdV-A
Human AdV-G
Human AdV-F
Human AdV-A
Human AdV-C
Human AdV-D
Human AdV-B
Human AdV-E

Fig. 1. Phylogenetic tree constructed by distance matrix analysis from derived aa sequence alignment of the DNA-dependent DNA polymerase gene. The calculation (Protdist with JTT model, followed by Fitch with global rearrangements) was non-rooted, and the tree was rooted with sturgeon adenovirus 1. South Polar skua adenovirus 1 is shown in red. From the names of the adenovirus types, the word “adenovirus” was omitted for clarity. Genus and species names are shown (the accepted species names in abbreviated form). Numbers at the nodes refer to the level of confidence as determined by bootstrap analysis from 100 samplings.