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:** | ***2011.025aV*** | (to be completed by ICTV officers) |

**Short title:** Create species *Great tit 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:**

Mária Benkő (benko@vmri.hu)
Endre Kovács (ekovacs@vmri.hu)
on behalf of the Study Group: Balázs Harrach (harrach@vmri.hu)

**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: August 12, 2011<br>To Vertebrate Virus Subcommittee chair (A. J. Davison): Aug 14, 2011 |
| Date of this revision (if different to above): | August 18, 2011 |

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 | ***2011.025aV*** | (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:** |
|---|---|
| *Great tit adenovirus A* | FJ849795 |

**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, great tit adenovirus 1, that shows adequate phylogenetic distance (based on DNA polymerase protein) from the members of all other established adenovirus species. The species would be only the fourth accepted species in the genus *Siadenovirus* (following *Frog adenovirus*, *Turkey adenovirus A* and *Raptor adenovirus A*). The host of the founding member of the proposed species belongs to the order of Passeriformes. The hosts of the members of the previously established siadenovirus species include one amphibian, and several birds that belong to Galliformes, Falconiformes or Strigiformes, respectively. The phylogenetic relationships and the specific hosts reflect an evolutionary distance that justifies the creation 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-Verlag, New York (in press)

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 95-111 (in press)

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

Kovács ER, Jánoska M, Dán Á, Harrach B, Benkő M (2010) Recognition and partial genome characterization by non-specific DNA amplification and PCR of a new siadenovirus species in a sample originating from *Parus major*, a great tit. J Virol Methods 163:262-268.


**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.

Great tit adenovirus 1 (GTAdV-1) has been detected by PCR in four great tits (*Parus major*) found dead in the wild in Hungary. Two of the dead birds were collected in 2006 and two in 2011, all from different locations. The DNA to be tested by PCR was extracted from a mixture of the internal organs. The different locations and times of the sample collection prove that this is a real virus capable of infecting (and possibly killing) great tits. This virus seems to be specific for great tits. After having screened more than a thousand samples (from several hundreds of avian species), this virus has not been found in any other bird species. This seemingly strict host-specificity is a further supporting evidence for the existence of this virus. Although the virus has not yet been isolated because of the lack of adequate cell culture, its repeated detection in the same bird species reflects the generally tight host specificity of adenoviruses.

Genome sequencing of GTAdV-1 has been started and has thus far resulted in the determination of roughly half of the genome sequence: 13,628 bp from the middle of the IVa2 gene to almost the end of the hexon gene (Kovács et al., 2010). The genome organization and the genes show the characteristics of siadenoviruses (Davison and Harrach, 2011; Kovács and Benkő, 2011). These include the lack of protein V, as well as the presence of the siadenovirus-specific protease cleavage signals in pVII. GTAdV-1 is shown in the Ninth ICTV Report in the "List of other related viruses which may be members of the genus *Siadenovirus* but have not been approved as species", together with budgerigar adenovirus 1 [AB485763], psittacine adenovirus 2 [EU056825], and Sulawesi tortoise adenovirus 1 [EU056826] (Harrach et al., 2011). However, there is not yet enough sequence data from the latter three candidate siadenoviruses to support a formal proposal for their classification into species.

We propose that the new species be named *Great tit adenovirus A*, as GTAdV-1 has been detected to date only in great tits.

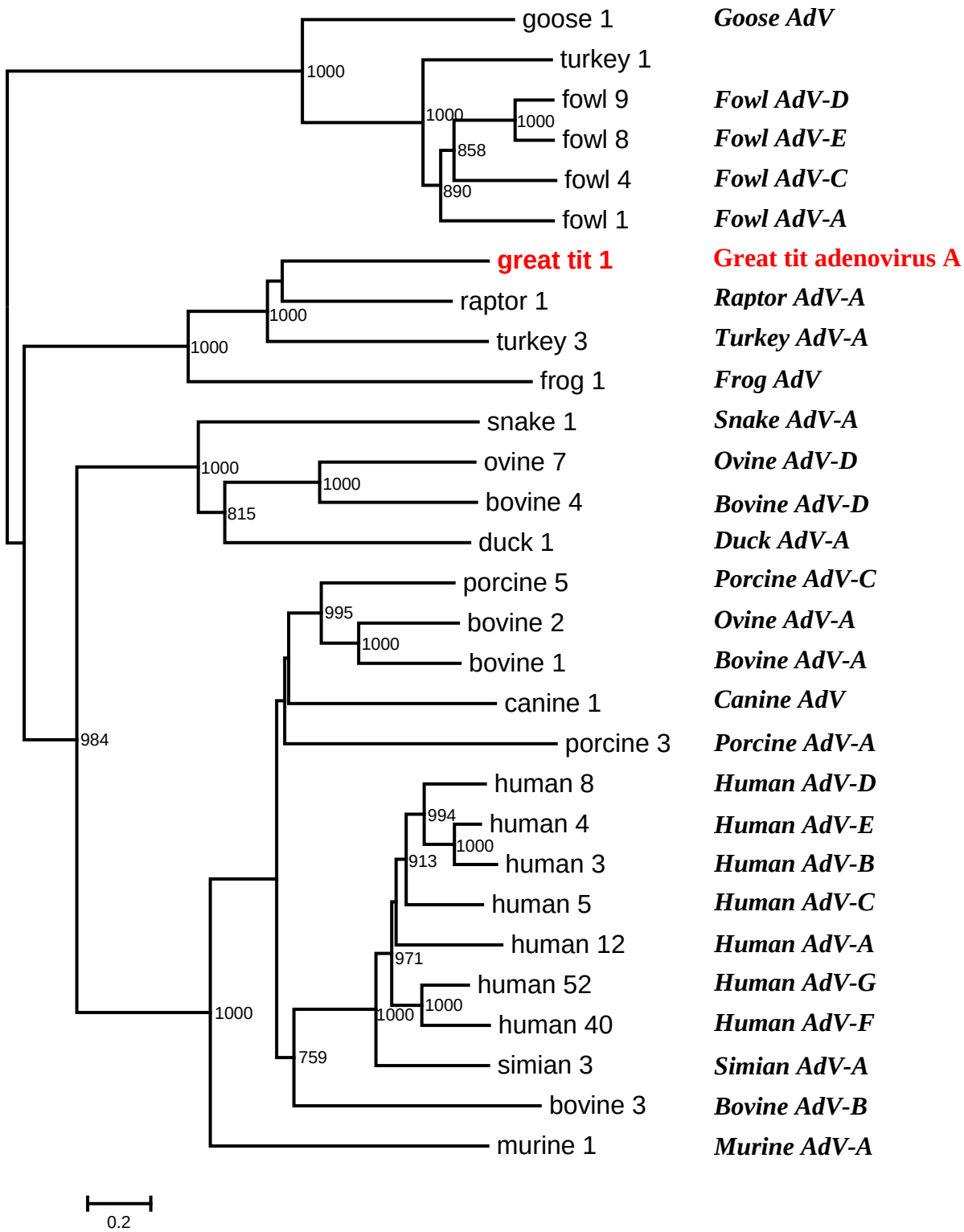


Fig. 1. Phylogenetic tree constructed by distance matrix analysis from derived aa sequence alignment of the DNA-dependent DNA polymerase gene. The calculation was non-rooted, and the tree was rooted at the midpoint. GTAdV-1 is shown in red. Numbers at the nodes refer to the level of confidence as determined by bootstrap analysis from 1000 samplings (when they confirmed the initial phylogenetic calculation). Scale bar indicates an evolutionary distance of 0.2 aa substitution per position.