



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:	2011.023aV	(to be completed by ICTV officers)			
Short title: Create species <i>Turkey adenovirus B</i> in the genus <i>Aviadenovirus</i> , family <i>Adenoviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

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

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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 04, 2011

To Vertebrate Virus Subcommittee chair (A. J. Davison): Aug 12, 2011

August 18, 2011

Date of this revision (if different to above):

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	2011.023aV	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Aviadenovirus</i>	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.
Subfamily:	Unassigned	
Family:	<i>Adenoviridae</i>	
Order:	Unassigned	
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Turkey adenovirus B</i>		GU936707

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

Species demarcation criteria in the genus

- Phylogenetic distance (>5-15%, based primarily on distance matrix analysis of the DNA polymerase amino acid sequence).

The closest type from an accepted species to turkey adenovirus 1 (TAdV-1), based on the DNA polymerase sequence, is fowl adenovirus 1 (species *Fowl adenovirus A*), with a distance of 19%.

- Genome organization (characteristically in the region at the right end of the genome).
The genome organization of TAdV-1 is similar to that of FAdV-1, but there are differences. A novel ORF (ORF50) is located at the right genomic end, and its product shows no significant similarity to any protein in GenBank. FAdV-1 ORF10 and ORF16 lack homologues in TAdV-1. There are also differences at the left genomic end: TAdV-1 does not contain a homologue of FAdV-1 ORF1C, but on the other strand there is a homologue of FAdV-9 ORF24.

- RFLP analysis
Virtual restriction endonuclease profiles of TAdV-1 are very different from those of FAdVs (Zsák and Kisary, 1984).

- Host range
TAdV-1 was isolated from a bird species different from hosts of other aviadenoviruses: domesticated turkey (*Meleagris gallopavo*).

- Pathogenicity
TAdV-1 was isolated from the trachea of 10-week-old turkeys showing respiratory signs. Thus its apparent pathogenic properties are different from those of members of accepted adenovirus species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Benkő M., Harrach B., Both G., Russell W.C., Adair B., Ádám É., de Jong J., Hess M., Johnson M., Kajon A., Kidd A., Lehmkuhl H., Li Q.-G., Mautner V., Pring-Akerblom P., Wadell G.: Family *Adenoviridae*. In: Fauquet C.M., Mayo M.A., Maniloff J., Desselberger U., Ball L. (eds): *Virus Taxonomy: VIIIth Report of the International Committee on Taxonomy of Viruses*. Elsevier. New York, 213–228, 2005.
- Benkő M., Harrach B., Russell W.C.: Family *Adenoviridae*. In: van Regenmortel M.H.V., Fauquet C.M., Bishop D.H.L., Carsten E.B., Estes M.K., Lemon S.M., Maniloff J., Mayo M.A., McGeoch D.J., Pringle C.R., Wickner R.B. (eds): *Virus Taxonomy: Seventh Report of the International Committee on Taxonomy of Viruses*. Academic Press. San Diego, 227–238, 2000.
- Kaján G.L., Sameti, S., Benkő M.: Partial sequence of the DNA-dependent DNA polymerase gene of fowl adenoviruses: A reference panel for a general diagnostic PCR in poultry. *Acta Vet. Hung.*, 59. 279–285, 2011.
- Kaján G.L., Stefancsik R., Ursu K., Palya V., Benkő M.: The first complete genome sequence of a non-chicken aviadenovirus, proposed to be turkey adenovirus 1. *Virus Res.*, 153. 226-233, 2010.
- Zsák L., Kisary J.: Grouping of fowl adenoviruses based upon the restriction patterns of DNA generated by *Bam*HI and *Hind*III. *Intervirology*, 22. 110–114, 1984.

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.

The tentative species *Turkey adenovirus* was listed in the Seventh ICTV Report as containing the types TAdV-1 and TAdV-2 (Benkő et al., 2000). In the Eighth ICTV Report this tentative species was renamed as *Turkey adenovirus B*, as *Turkey adenovirus A* was accepted for TAdV-3 (turkey hemorrhagic enteritis virus, THEV). However, it was not recognized as an official species (Benkő et al., 2005) because of lack of genome sequence. At that stage, the tentative species category was abolished, the accepted taxonomy listing only the officially accepted species. The classification of fowl adenoviruses was recently validated by the analysis of partial DNA polymerase sequences (Kaján et al, 2011), but the TAdV types were still not included in an officially accepted virus species.

A strain of TAdV-1 was isolated in Hungary, and the whole genome was sequenced (Fig. 1; Kaján et al, 2010). The observed phylogenetic distances between TAdV-1 and members of accepted aviadenovirus species, are adequate for the acceptance of a species for TAdV-1 (Figs. 2-4). In addition to phylogenetic analyses, the genome organisation, virtual RFLP data and the known and differing host and pathogenicity also support the establishment of a new species.

Since the name of the species should reflect the name of the host, the proposed name is *Turkey adenovirus B*.

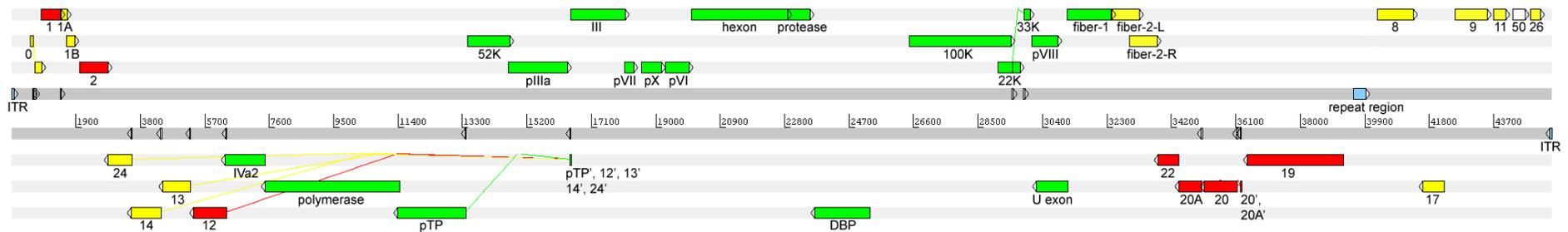


Fig. 1. Genome organisation of TAdV-1. The six lighter grey bars represent the six reading frames; exons are merged by thin lines. Genes highlighted in green are conserved in every adenovirus sequenced to date, red ones are common only to every aviadenovirus, and the homologues of yellow ones are present in certain aviadenoviruses only. The single white ORF (ORF50) shows no significant similarity to any protein sequences. Fiber-2-L and fiber-2-R represent the two resulting mutilated fiber genes originating from the break of the second fiber gene. DBP – DNA-binding protein; ITR – inverted terminal repeat; pTP – terminal protein precursor

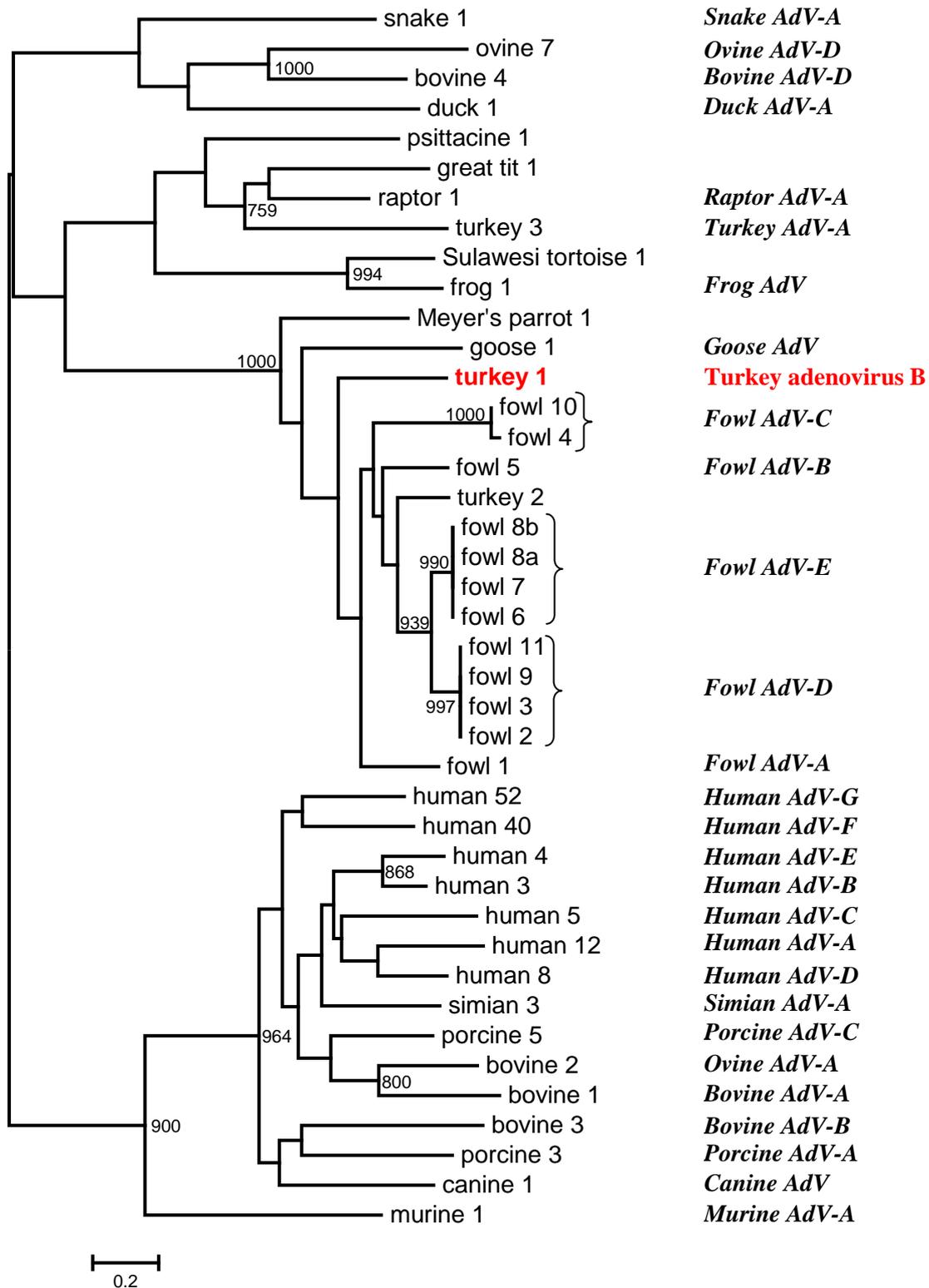


Fig. 3. Phylogenetic tree constructed by distance matrix analysis of partial DNA polymerase sequences from adenoviruses. The calculation was non-rooted, and the tree was rooted at the midpoint. TAdV-1 is shown in red. Numbers at the nodes refer to the level of confidence as determined by bootstrap analysis from 1000 samplings (when they confirmed the initial phylogenetic calculation). Scale bar indicates an evolutionary distance of 0.2 aa substitution per position.

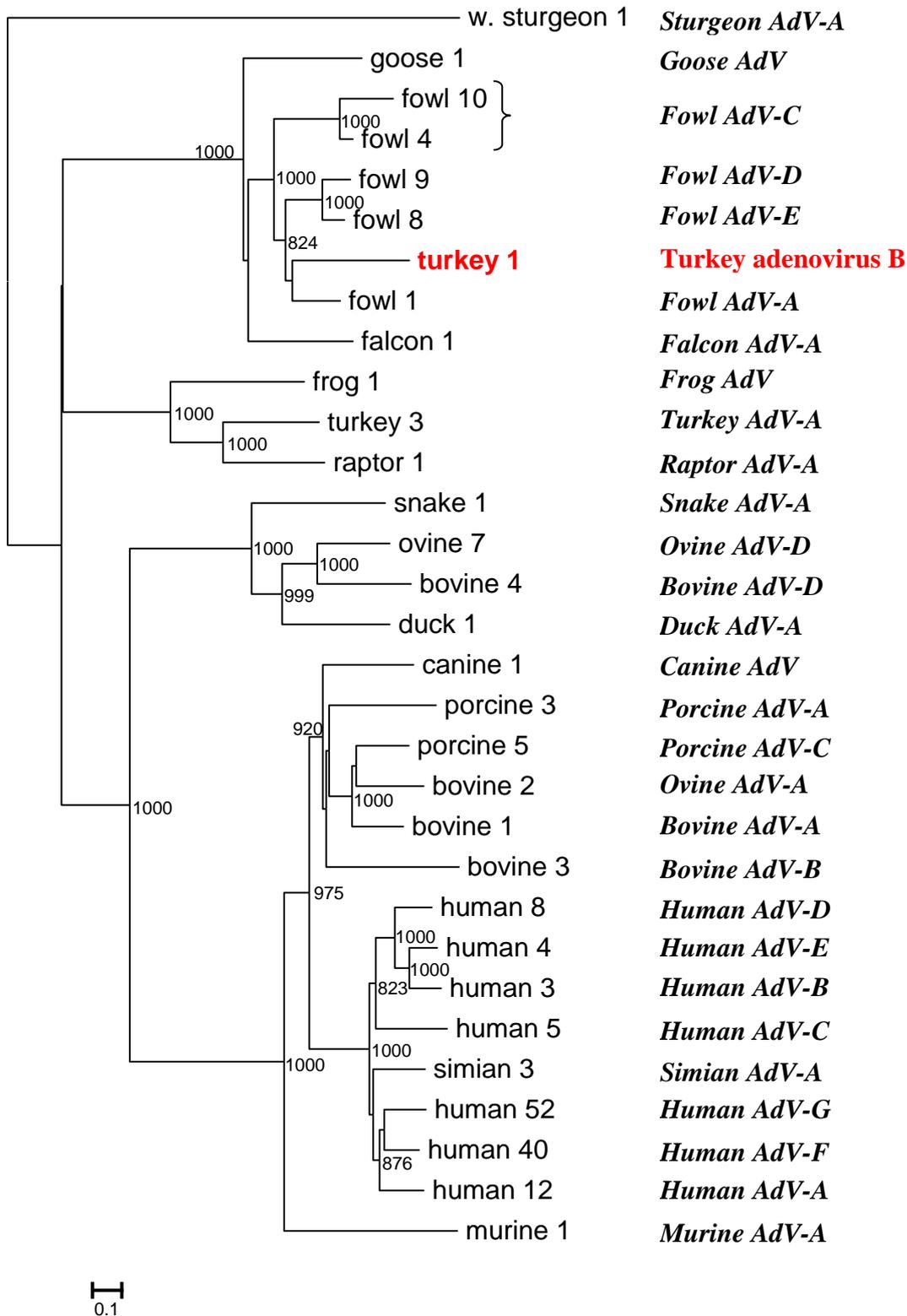


Fig. 4. Phylogenetic tree constructed by distance matrix analysis from derived aa sequence alignment of the complete hexon gene. The calculation was non-rooted, and the tree was rooted at the midpoint. TAdV-1 is shown in red. Numbers at the nodes refer to the level of confidence as determined by bootstrap analysis from 1000 samplings (when they confirmed the initial phylogenetic calculation). Scale bar indicates an evolutionary distance of 0.1 aa substitution per position.