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:	***2015.005aD***	(to be completed by ICTV officers)

Short title: 4 new species in the genus *Aviadenovirus*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

Győző Kaján
Iva Podgorski
Balázs Harrach

Corresponding author with e-mail address:

Győző Kaján, kajan.gyozo@agrar.mta.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 Study Group

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

Date first submitted to ICTV:	June 15, 2015
Date of this revision (if different to above):	September 3, 2015

ICTV-EC comments and response of the proposer:

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	***2015.005aD***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Aviadenovirus***
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)**
Duck aviadenovirus B	duck adenovirus 2 strain GR	KJ469653
Pigeon aviadenovirus A	pigeon adenovirus 1 strain IDA4	FN824512
Turkey aviadenovirus C	turkey adenovirus 4 strain TNI1	KF477312
Turkey aviadenovirus D	turkey adenovirus 5 strain 1277BT	KF477313

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

Hereby, we propose to establish the following four new aviadenovirus species: *Duck aviadenovirus B, Pigeon aviadenovirus A, Turkey aviadenovirus C, Turkey aviadenovirus D* according to Marek et al. (2014a, 2014b).

Species demarcation criteria in the genus *Aviadenovirus* are more than 5−15% phylogenetic distance (based on the amino acid sequence of the DNA-dependent DNA polymerase), differences in host range, organization and G+C content of the genome, and lack of cross-neutralization (Harrach et al., 2011).

The following features support the establishment of the four new species (the prototype strain of each species has been fully sequenced):

Phylogenetic distance

The phylogenetic distance, measured on the basis of complete DNA polymerase sequences, exceeds 15% with any representative of other AdV species (Table 1, Fig. 1).

Unique features in genome organization and host range

The characterized members of the proposed new species have unique features in their genome organization and/or distinct host as summarized in Table 1. The genomic layouts of the representatives of the proposed new virus species are shown in Fig. 2.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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. 125-41.

Marek A, Ballmann MZ, Kosiol C, Harrach B, Schlötterer C, Hess M (2014a) Whole-genome sequences of two turkey adenovirus types reveal the existence of two unknown lineages that merit the establishment of novel species within the genus *Aviadenovirus*. J Gen Virol 95: 156-70.

Marek A, Kaján GL, Kosiol C, Harrach B, Schlötterer C, Hess M (2014b) Complete genome sequences of pigeon adenovirus 1 and duck adenovirus 2 extend the number of species within the genus *Aviadenovirus*. Virology 462-463: 107-14.

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 proposed virus species

Proposed species names	*Duck aviadenovirus B*	*Pigeon aviadenovirus A*	*Turkey aviadenovirus C*	*Turkey aviadenovirus D*
Virus types classified into the species	duck adenovirus 2	pigeon adenovirus 1	turkey adenovirus 4	turkey adenovirus 5
Representative strains	GR	IDA4	TNI1	1277BT
Host species	Muscovy duck (*Cairina moschata*)	pigeon (*Columba livia domestica*)	turkey (*Meleagris gallopavo*)	turkey (*Meleagris gallopavo*)
Number of fiber genes	1	2	1	2
Unique open reading frames	55A, 63–67	58, 58A, 59–62	-	fusion of 14 + 14A
Identity with the closest established species*	73.64%	64.99%	81.90%	81.86%
Closest established species and type	*Goose aviadenovirus A*, goose adenovirus 4	*Turkey aviadenovirus B*, turkey adenovirus 1	*Fowl aviadenovirus D*, fowl adenovirus 9	*Fowl aviadenovirus A*, fowl adenovirus 1

* Based on the amino acid sequence deduced from the complete DNA polymerase gene.

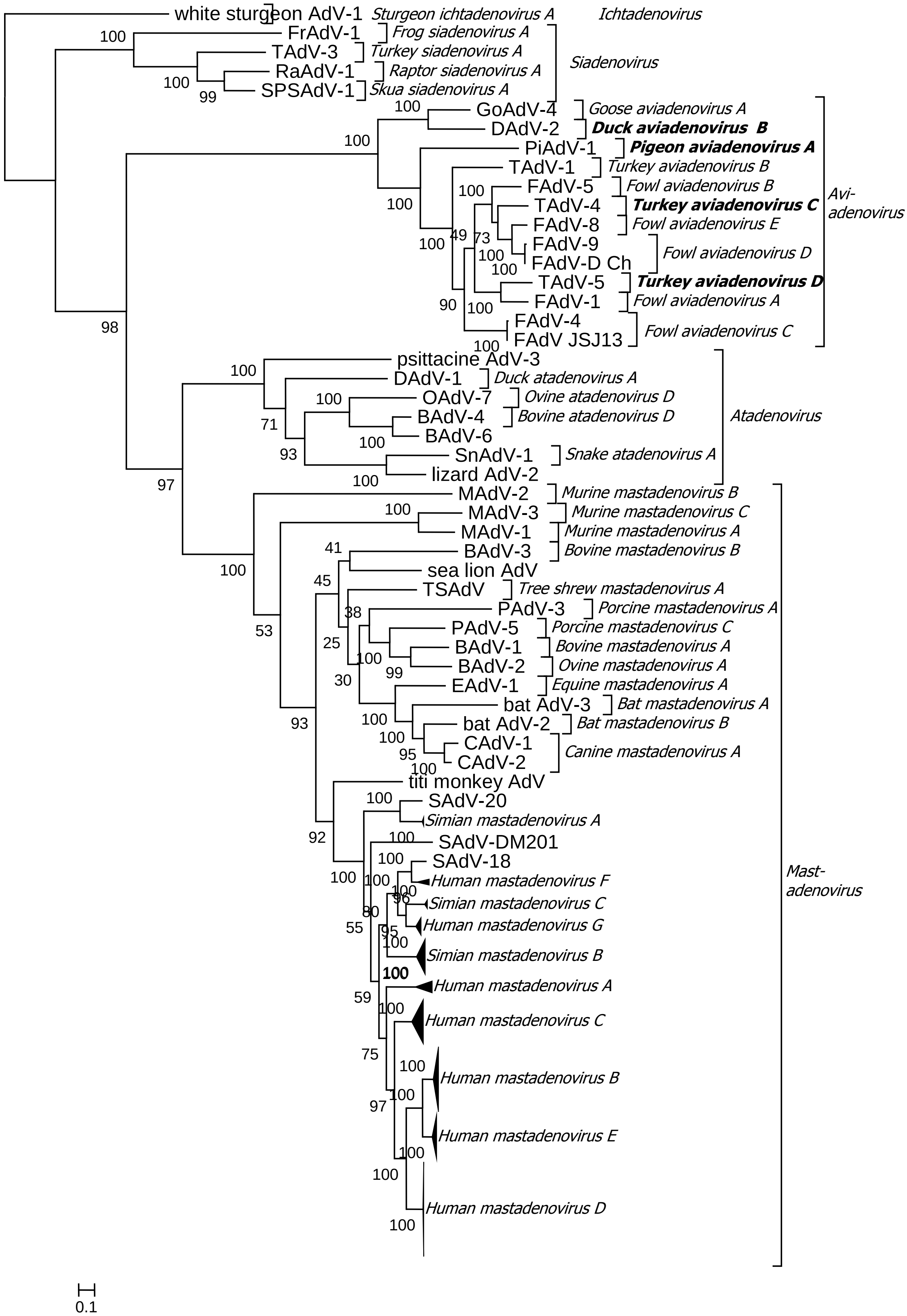
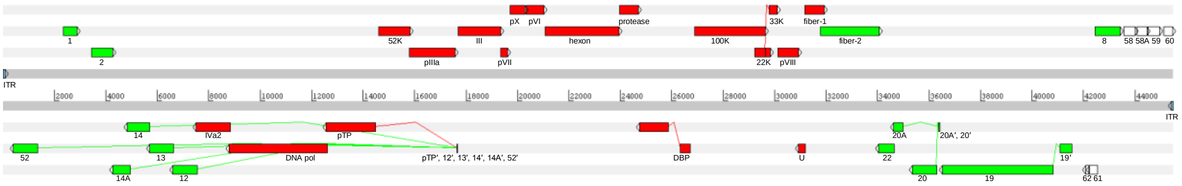


Fig. 1. Maximum likelihood (PhyML) analysis of the complete amino acid sequences of the DNA-dependent DNA polymerase. Tree topology was tested by bootstrapping (100 datasets). The

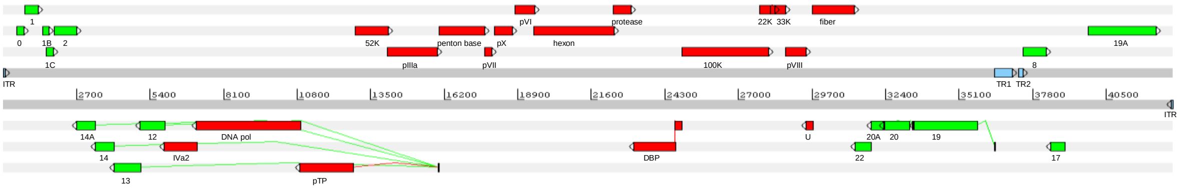
scale bar shows the evolutionary distance of 0.1 aa substitution per site. The proposed new species names are in bold. Abbreviations: AdV: adenovirus; FrAdV: frog AdV; TAdV: turkey AdV; RaAdV: raptor AdV; SPSAdV: South Polar skua AdV; GoAdV: goose AdV; DAdV: duck AdV; PiAdV: pigeon AdV; FAdV: fowl AdV; FAdV-D Ch: a Chinese strain of *Fowl aviadenovirus D* (GenBank Accession No: KM096546); FAdV JSJ13: *Fowl aviadenovirus C* isolate JSJ13 (KM096544); OAdV: ovine AdV; BAdV: bovine AdV; SnAdV: snake AdV; MAdV: murine AdV; TSAdV: tree shrew AdV; PAdV: porcine AdV; EAdV: equine AdV; CAdV: canine AdV; SAdV: simian AdV.

a) *Duck aviadenovirus B*, duck adenovirus 2

b) *Pigeon aviadenovirus A*, pigeon adenovirus 1



c) *Turkey aviadenovirus C*, turkey adenovirus 4



d) *Turkey aviadenovirus D*, turkey adenovirus 5

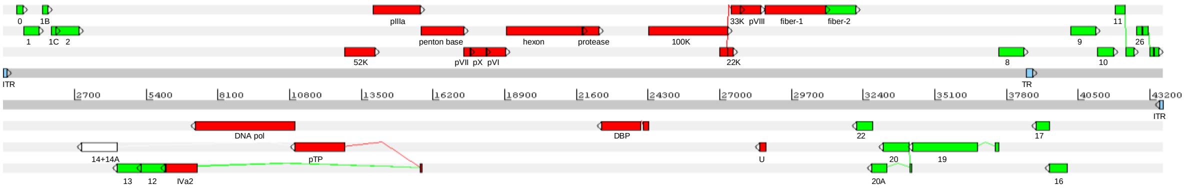


Fig. 2. Genomic layouts of representatives of the proposed virus species. The rightward and leftward strands of the genomes are shown in dark gray with nucleotide positions indicated. The three rightward and three leftward reading frames are shown in light gray above and below the genome, respectively. Protein-encoding regions are depicted as colored arrows and bars (the ORF prefix omitted). Those colored red are conserved in every adenovirus sequenced to date, those colored green have orthologues only in other aviadenoviruses, and those shaded white are unique to the respective species. Repeat regions are colored blue. Splicing between protein-encoding regions is indicated by diagonal lines. DBP, DNA-binding protein; DNA pol, DNA polymerase; ITR, inverted terminal repeat; pTP, terminal protein precursor; TR, tandem repeat.