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:	***2016.002aD***	(to be completed by ICTV officers)

Short title: 2 new species in the genus *Atadenovirus*
(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** ☐

Author(s):

Mónika Z. Ballmann, sibilatrix@gmail.com
Balázs Harrach, harrach.balazs@agrar.mta.hu

Corresponding author with e-mail address:

Mónika Z. Ballmann, sibilatrix@gmail.com

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 21, 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

Code	***2016.002aD***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Atadenovirus***
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)**
Lizard atadenovirus A	lizard adenovirus 2	KJ156523
Psittacine atadenovirus A	psittacine adenovirus 3	KJ675568

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

Lizard adenovirus 2 (LiAdV-2) and psittacine adenovirus 3 (PsAdV-3) were fully sequenced and their genome organization and some further biological properties described (Pénzes et al., 2014; To et al., 2014). According to phylogenetic calculations and genome organization, both LiAdV-2 and PsAdV-3 belong to the genus *Atadenovirus*. Within the genus *Atadenovirus,* we propose the establishment of two new species; *Lizard atadenovirus A* for LiAdV-2 and *Psittacine atadenovirus A* for PsAdV-3. LiAdV-2 and PsAdV-3 possess several properties that clearly separate them from the phylogenetically closest species. One of the species demarcation criteria in the family *Adenoviridae* is a 5-15% phylogenetic distance in the amino acid sequence of the DNA-dependent DNA polymerase. The distances of LiAdV-2 and PsAdV-3 are more than 15% from their closest relatives belonging to accepted species, i.e. from snake adenovirus 1 (SnAdV-1) and duck adenovirus 1 (DAdV-1), respectively (Figure 1). LiAdV-2 is monophyletic with SnAdV-1, the other adenovirus of squamate origin, yet they show a clear phylogenetic distance from each other. However, PsAdV-3 does not even compose a monophyletic lineage with its closest relative, DAdV-1 (Figure 1). Another species demarcation criterion is the host. No species have been accepted for any lizard or psittacine AdVs. Additional species demarcation criteria are the differences in the G+C content and in the genome organization)e.g. the number of fibre genes). As shown in Table 1, these characteristics also differentiate the members of the presently proposed two species from their phylogenetically closest relatives. The genome of both PsAdV-3 and LiAdV-2 contain 2 fibre genes, which is a unique trait in the genus *Atadenovirus*. Furthermore, PsAdV-3 lacks the LH3 gene. This distinguishes it from all other viruses in the *Atadenovirus* genus. The right end of the LiAdV-2 genome harbors four unique ORFs without homology to any genes described in other AdVs to date. Regarding the virion structure, on the surface of the LiAdV-2 particles, alternating triple or single fibre projections per vertex have been observed by electron microscopy. This is a unique feature not only in the genus *Atadenovirus*, but also in the family *Adenoviridae*.

The proposed species names are in-line with the earlier naming policy in the family, including the incorporation of the genus designation.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Pénzes, J.J., Menéndez-Conejero, R., Condezo, G.N., Ball, I., Papp, T., Doszpoly, A., Paradela, A., Pérez-Berná, A.J., López-Sanz, M., Nguyen, T.H., van Raaij, M.J., Marschang, R.E., Harrach, B.., Benkő, M., San Martín, C. (2014). Molecular characterization of a lizard adenovirus reveals the first atadenovirus with two fiber genes and the first adenovirus with either one short or three long fibers per penton. J. Virol. **88** (19) 11304-11314 doi: 10.1128/JVI.00306-14.

To, K.K., Tse, H., Chan, W.M., Choi, G.K., Zhang, A.J., Sridhar, S., Wong, S.C., Chan, J.F., Chan, A.S., Woo, P.C., Lau, S.K., Lo, J.Y., Chan, K.H., Cheng, V.C., Yuen, K.Y. (2014). A novel psittacine adenovirus identified during an outbreak of avian chlamydiosis and human psittacosis: zoonosis associated with virus-bacterium coinfection in birds. PLoS Negl. Trop. Dis. **8** (12):e3318.doi: 10.1371/journal.pntd.0003318.

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 those of the phylogenetically closest species (shown below the proposed species)

Species	G+C content (%)	Host species	Fibre genes
Lizard atadenovirus A	44.16	Mexican beaded lizard (*Heloderma horridum*)	2
Snake atadenovirus A	50.22	corn snake (*Pantherophis guttatus*)	1
Psittacine atadenovirus A	53.54	mealy parrot (*Amazona farinosa*)	2
Duck atadenovirus A	43.00	domestic duck (*Anas platyrhynchos domestica*)	1

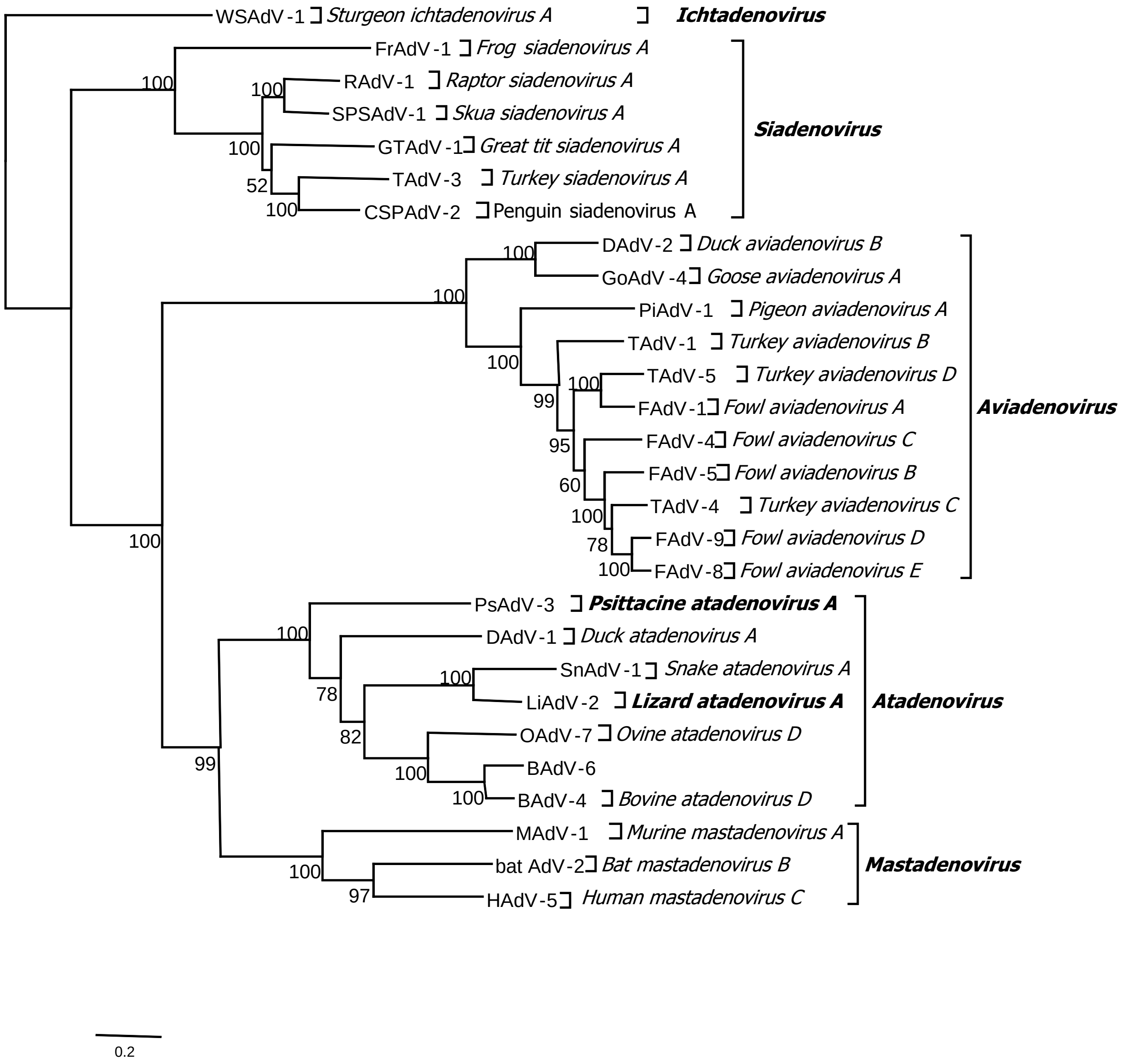

Fig. 1. Maximum likelihood analysis of the complete DNA-dependent DNA polymerase amino acid sequences shows the genetic distance of the two proposed species (highlighted in bold). Only three selected types were included in the calculations from the members of the genus *Mastadenovirus*. According to 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 corresponds to 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.