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:	***2016.010aD***	(to be completed by ICTV officers)

Short title: 9 new species in the genus *Mastadenovirus*
(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** ☐

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

Date first submitted to ICTV: 05.04.2016.
Date of this revision (if different to above):

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	***2016.010aD***	(assigned by ICTV officers)

To create 9 new species within:

Genus:	***Mastadenovirus***
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)**
Simian mastadenovirus D	simian adenovirus 13	KP329563
Simian mastadenovirus E	simian adenovirus 16	KP329564
Simian mastadenovirus F	simian adenovirus 18	FJ025931
Simian mastadenovirus G	simian adenovirus 20	HQ605912
Simian mastadenovirus H	simian adenovirus DM-2014	KM190146
Platyrrhini mastadenovirus A	titi monkey adenovirus ECC-2011	HQ913600
Skunk mastadenovirus A	skunk adenovirus PB1	KP238322
Sea lion mastadenovirus A	California sea lion adenovirus 1	KJ563221
Dolphin mastadenovirus A	bottlenose dolphin adenovirus 1	KR024710

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 11

Several Old World monkey (OWM) adenoviruses (AdVs), fully sequenced and described recently, were proposed to be members of novel species, *Simian mastadenovirus D* to *Simian mastadenovirus G* (Pantó *et al.*, 2015; Podgorski *et al.*, 2016). An additional fully sequenced OWM AdV (SAdV-DM2014) was proposed to be a member of a novel species *Simian mastadenovirus D* (Malouli *et al.*, 2014), but we propose it to be member of a novel species *Simian mastadenovirus H*, since the serotyped AdV (SAdV-13) would be a sole member of the species *Simian mastadenovirus D* (Pantó *et al.*, 2015*)*. The viruses which belong to the proposed species have several properties which clearly separate them from the species established earlier. Phylogenetic distance analyses (based on DNA-dependent DNA polymerase) prove clear distance of the proposed species from other accepted species (more than 10%; Figure 1). Besides the phylogenetic distance, several other biological properties differentiate them from the phylogenetically closest species, i.e. the host, the number of fibre genes, the haemagglutination properties (Rapoza, 1967), and the G+C content (summarized in Table 1).

We also propose an additional mastadenovirus species for the only fully sequenced New World monkey (NWM) AdV, the titi monkey AdV (Chen *et al.*, 2011). The phylogenetic distance (Figure 1), the host (NWM vs OWM), the pairwise nucleotide identities being less than 56.3%

compared to the other OWM AdVs, and novel genes in the E3 region support the need to establish a novel species for this virus, *Platyrrhini mastadenovirus A*. We think that differentiation of OWM and NWM AdV species names is important, therefore we propose that OWM AdV species continue under the name *Simian mastadenovirus* (followed by the appropriate capital letter), and the NWM AdV species under the name *Platyrrhini mastadenovirus* (followed by the appropriate capital letter).

We propose several additional species within the genus *Mastadenovirus*: *Skunk mastadenovirus A* for skunk adenovirus PB1 (Kozak *et al.*, 2015), *Sea lion mastadenovirus A* for California sea lion adenovirus 1 (Cortés-Hinojosa *et al.*, 2015), and *Dolphin mastadenovirus A* for bottlenose dolphin adenovirus 1 (direct submission, KR024710). All the proposed species are supported by the notable phylogenetic distance (Figure 1) and different host species.

The names of the species, *Simian mastadenovirus D, Simian mastadenovirus E, Simian mastadenovirus F, Simian mastadenovirus G, Simian mastadenovirus H, Platyrrhini mastadenovirus A*, *Skunk mastadenovirus A*, *Sea lion mastadenovirus A* and *Dolphin mastadenovirus A* are in-line with the earlier naming policy in *Adenoviridae* family, and in line with recent proposal to change the species names to incorporate the genus designation.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Chen, E. C., Yagi, S., Kelly, K. R., Mendoza, S. P., Tarara, R. P., Canfield, D. R., Maninger, N., Rosenthal, A., Spinner, A., Bales, K. L., Schnurr, D. P., Lerche, N. W. & Chiu, C. Y. (2011). Cross-species transmission of a novel adenovirus associated with a fulminant pneumonia outbreak in a new world monkey colony. *PLoS Pathog* **7**, e1002155.

Cortés-Hinojosa, G., Gulland, F. M., Goldstein, T., Venn-Watson, S., Rivera, R., Waltzek, T. B., Salemi, M. & Wellehan, J. F. (2015). Phylogenomic characterization of California sea lion adenovirus-1. *Infect Genet Evol* **31**, 270-276.

Kozak, R. A., Ackford, J. G., Slaine, P., Li, A., Carman, S., Campbell, D., Welch, M. K., Kropinski, A. M. & Nagy, É. (2015). Characterization of a novel adenovirus isolated from a skunk. *Virology* **485**, 16-24.

Malouli, D., Howell, G. L., Legasse, A. W., Kahl, C., Axthelm, M. K., Hansen, S. G. & Früh, K. (2014). Full genome sequence analysis of a novel adenovirus of rhesus macaque origin indicates a new simian adenovirus type and species. *Virol Rep* **3-4**, 18-29.

Pantó, L., Podgorski, I. I., Jánoska, M., Márkó, O. & Harrach, B. (2015). Taxonomy proposal for Old World monkey adenoviruses: characterisation of several non-human, non-ape primate adenovirus lineages. *Arch Virol* **160**, 3165-3177.

Podgorski, I. I., Pantó, L., Papp, T., Harrach, B. & Benkő, M. (2016). Genome analysis of four Old World monkey adenoviruses supports the proposed species classification of primate adenoviruses and reveals signs of possible homologous recombination. *J Gen Virol*. Published Online: 24/03/2016 doi: 10.1099/jgv.0.000465

Rapoza, N. P. (1967). A classification of simian adenoviruses based on hemagglutination. *Am J Epidemiol* **86**, 736-745.

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 OWM AdV species (highlighted with bold) compared to those of the phylogenetically closest species

Species	G+C content (%)	Host species	Fibre genes	HAG
Simian mastadenovirus D	49.9	macaque	1	I
Simian mastadenovirus H	46.7			
Simian mastadenovirus E	57.9	grivet	2	IV
Simian mastadenovirus B	~62	macaque, baboon		III
Simian mastadenovirus F	61.4	grivet	1	
Human mastadenovirus F	~51.2	human	2	
Simian mastadenovirus G	47.8	grivet	1	
Simian mastadenovirus A	~55	macaque		II

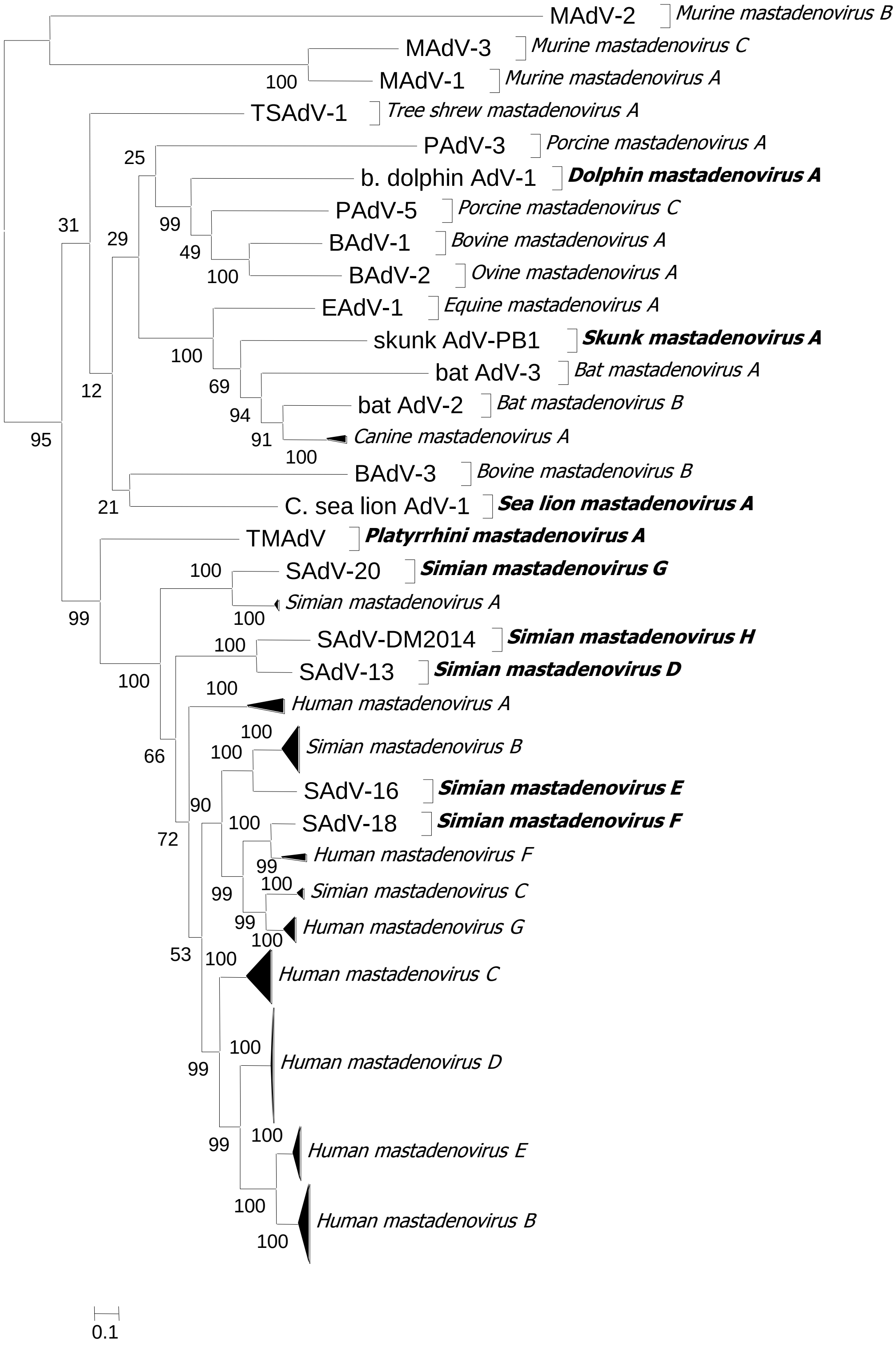

Fig. 1. Maximum likelihood analysis of the complete DNA-dependent DNA polymerase amino-acid sequences shows the genetic distance of the nine proposed species (highlighted with bold). Bootstrap analysis with 100 replicates was used, and the values are shown as percentage. The scale bar shows the evolutionary distance of 0.1 aa substitution per position. Abbreviations: SAdV – simian adenovirus; TMAdV – titi monkey adenovirus; BAdV – bovine adenovirus; EAdV – equine adenovirus; PAdV – porcine adenovirus; TSAdV – tree shrew adenovirus; MAdV – murine adenovirus; b. dolphin – bottlenose dolphin; C. sea lion – California sea lion.