MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2015.012aD*	(to be completed by ICTV officers)

Short title: 2 new species in the genus *Mastadenovirus*
(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 ☒

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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 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:

Decision: Ac. Provide correct species names in Table 1.
Response: Done

creating and naming one or more new species.

Code	*2015.012aD*		(assigned by ICTV officers)

To create 2 new species within:

		Fill in all that apply.
Genus:	*Mastadenovirus*	
Subfamily:	**Unassigned**	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Family:	*Adenoviridae*	• If no genus is specified, enter
Order:	**Unassigned**	"**unassigned**" in the genus box.

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Simian mastadenovirus B	simian adenovirus 49	HQ241819
Simian mastadenovirus C	baboon adenovirus 3	KC693022

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

Partial or full genome sequence analyses of previously known (simian AdV-1 to -20, -48 to -50) and newly discovered (in rhesus macaque and baboons) Old World monkey AdVs clearly indicated the existence of separate lineages and the need for the establishment of two simian adenovirus species, namely *Simian mastadenovirus B* and *Simian mastadenovirus C* (Roy et al., 2012; Chiu et al., 2013; Podgorski et al., 2013; Pantó et al., 2015).

The species demarcation criteria for mastadenoviruses include more than 15% phylogenetic distance (based on the amino acid sequence of the DNA-dependent DNA polymerase). If this distance is between 5 and 15%, some further separating characteristics, such as different host, G+C percentage, genome organization, cross-neutralisation or haemagglutination properties should be considered (Harrach et al., 2011). Phylogenetic analyses (based on several genes and proteins) prove a clear distance (exceeding 10%) of the two proposed species from each other and the previously approved species (Fig. 1). Members of both of the proposed species possess two fibre genes. Members in species *Simian mastadenovirus A* have only one fibre gene (Table 1). Most members (13 viruses) of candidate species *Simian mastadenovirus B* were found in rhesus or crab-eating macaques, and only one proposed member (baboon AdV-1) originates from olive baboon (Table 1). The previously described candidate members of species *Simian mastadenovirus B* (SAdV-5 and -8) belong to haemagglutination (HA) group III, whereas members of the established species *Simian mastadenovirus A* are classified into HA group II. All members of species *Simian mastadenovirus C* were found in baboons. The genomic G+C content of their members also separates the three species: 52.2−52.6% in *Simian mastadenovirus A*; 54−56% in *Simian mastadenovirus B*, and 63−66% in *Simian mastadenovirus C*.

The names of the species, *Simian mastadenovirus B* and *Simian mastadenovirus C* are in-line with earlier naming practice in the *Adenoviridae* family, and in line with recent policy to incorporate the genus designation.

References:

Chiu CY, Yagi S, Lu X, Yu G, Chen EC, Liu M, Dick EJ, Carey KD, Erdman DD, Leland MM, Patterson JL (2013) A novel adenovirus species associated with an acute respiratory outbreak in a baboon colony and evidence of coincident human infection. MBio 4:e00084

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. 125-141

Pantó L, Podgorski II, 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, Pantó L, Harrach B, Benkő M (2013) Genomic and bioinformatics analysis of simian adenovirus 19 confirm the need to establish a new adenovirus species. Acta Microbiol Immunol 60(Suppl):216-217

Roy S, Sandhu A, Medina A, Clawson DS, Wilson JM (2012) Adenoviruses in fecal samples from asymptomatic rhesus macaques, United States. Emerg Infect Dis 18:1081-1088

Annex:

Table 1. Properties of the viruses according to the species they belong to

Adenovirus	Existing/ Proposed species	Host species	HAG	Fiber genes	G+C content
SAdV-1	*Human mastadenovirus G*	Crab-eating macaque	III	2	55.2
SAdV-7		Rhesus macaque		2	56.3
HAdV-52		Human		2	55.1
SAdV-3	*Simian mastadenovirus A*	Rhesus macaque	II	1	55.3
SAdV-6		Macaque		1	55.8
SAdV-48		Crab-eating macaque		1	54.4
SAdV-5	*Simian mastadenovirus B*	Rhesus macaque	III	2	(65.3)[c]
SAdV-8					60.3
SAdV-49		Crab-eating macaque			62.8
SAdV-50					62.6
BaAdV-1		Olive baboon			62.7
A1139[a]					62.6
A1163[a]					62.0
A1173[a]					61.1
A1258[a]		Rhesus macaque			60.1
A1285[a]					61.0
A1296[a]					62.6
A1312[a]					62.6
A1327[a]					62.9
A1335[a]					62.8
SAdV-19[b]	*Simian mastadenovirus C*	Yellow baboon		2[b]	52.2[b]
BaAdV-2[a]		Olive baboon		2	52.6
BaAdV-3[a]					52.3

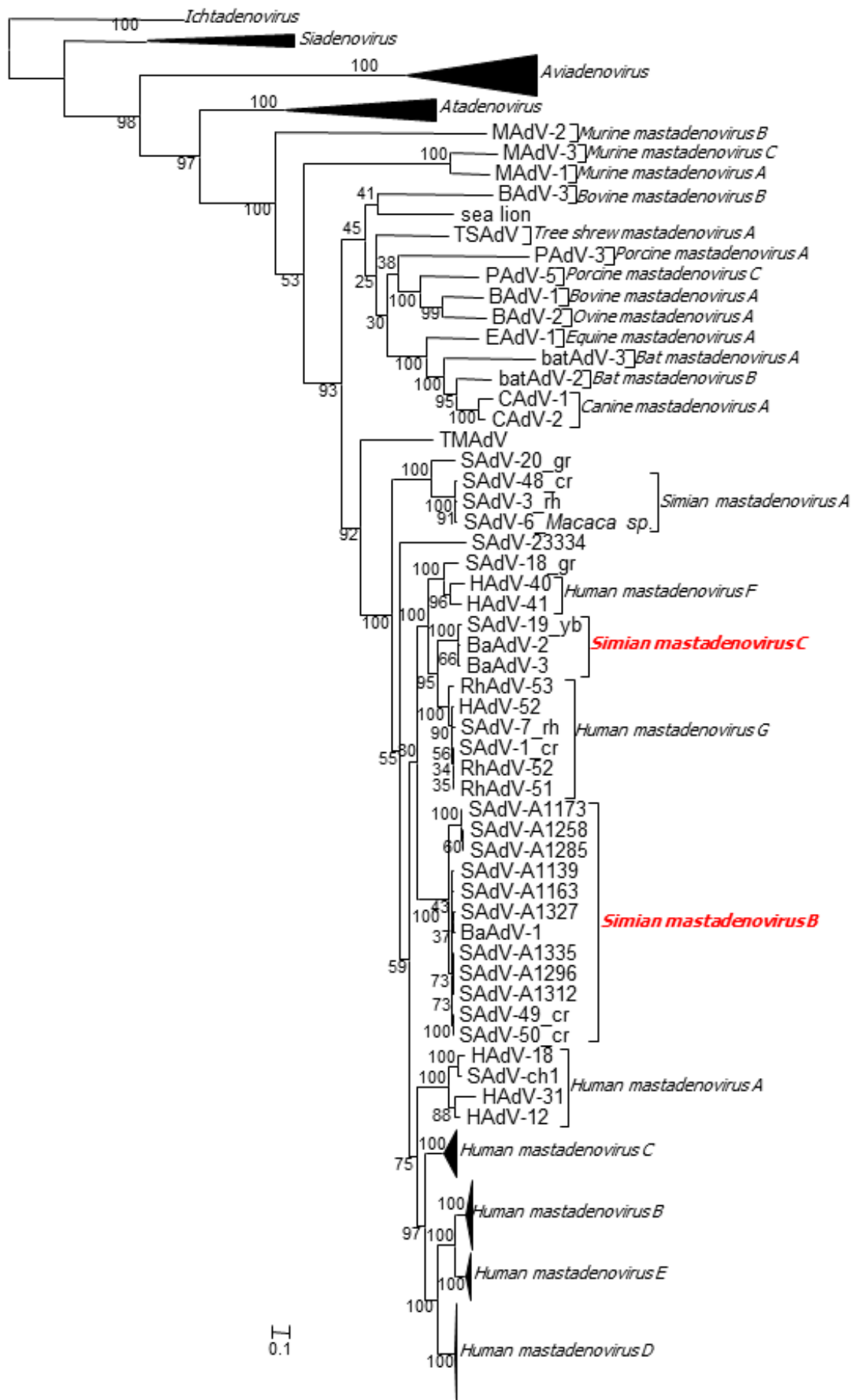[a]strain name; [b]unpublished; [c]partial sequence

Fig. 1. Maximum likelihood analysis of the full DNA-dependent DNA polymerase amino acid sequences shows the genetic distance of the two proposed species *Simian mastadenovirus B* and *Simian mastadenovirus C*. 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. The abbreviated names of the proposed new species are shown by bold red letters. Abbreviations: AdV: adenovirus; MAdV: murine AdV; BAdV: bovine AdV; TSAdV: tree shrew AdV; PAdV: porcine AdV; OAdV: ovine AdV; EAdV: equine AdV; CAdV: canine AdV; TMAdV: titi monkey AdV; SAdV: simian AdV; HAdV: human AdV; gr: grivet; cr: crab eating macaque; rh: rhesus macaque; yb-yellow baboon; BaAdV: baboon AdV; RhAdV: rhesus AdV.