



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:	2010.011.aV	(to be completed by ICTV officers)			
Short title: Create species named Bat adenovirus A in genus Mastadenovirus, family Adenoviridae (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:

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:

June 3, 2010

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.

Code	<i>2010.011.aV</i>	(assigned by ICTV officers)
To create one new species within:		
Genus:	<i>Mastadenovirus</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:		
Family:	<i>Adenoviridae</i>	
Order:		
And name the new species:		
<i>Bat adenovirus A</i>		

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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. • Provide accession numbers for genomic sequences • Further material in support of this proposal may be presented in the Appendix, Module 9 <p>The proposed species contains an adenovirus type that shows adequate phylogenetic distance (based on hexon and DNA polymerase proteins) from the members of all other accepted adenovirus species to merit the establishment of new species. This novel AdV has been described to occur in bat (<i>Myotis ricketti</i>); this is presently the only bat adenovirus with a published full genome sequence. The phylogenetic distance and the special host point to an evolutionary distance that seems to justify the creation of this species. Accession number of the genomic sequence: GU226970.</p>

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Li Y, Ge X, Zhang H, Zhou P, Zhu Y, Zhang Y, Yuan J, Wang LF, Shi Z (2010) Host range, prevalence and genetic diversity of adenoviruses in bats. *Journal of Virology* 84, 3889–3897.

Maeda K, Hondo E, Terakawa J, Kiso Y, Nakaichi N, Endoh D, Sakai K, Morikawa S, Mizutani T (2008) Isolation of novel adenovirus from fruit bat (*Pteropus dasymallus yaeyamae*). *Emerging Infectious Diseases* 14, 347–349.

Sonntag M, Mühldorfer K, Speck S, Wibbelt G, Kurth A (2009) New adenovirus in bats, Germany. *Emerging Infectious Diseases* 15, 2052–2055.

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.

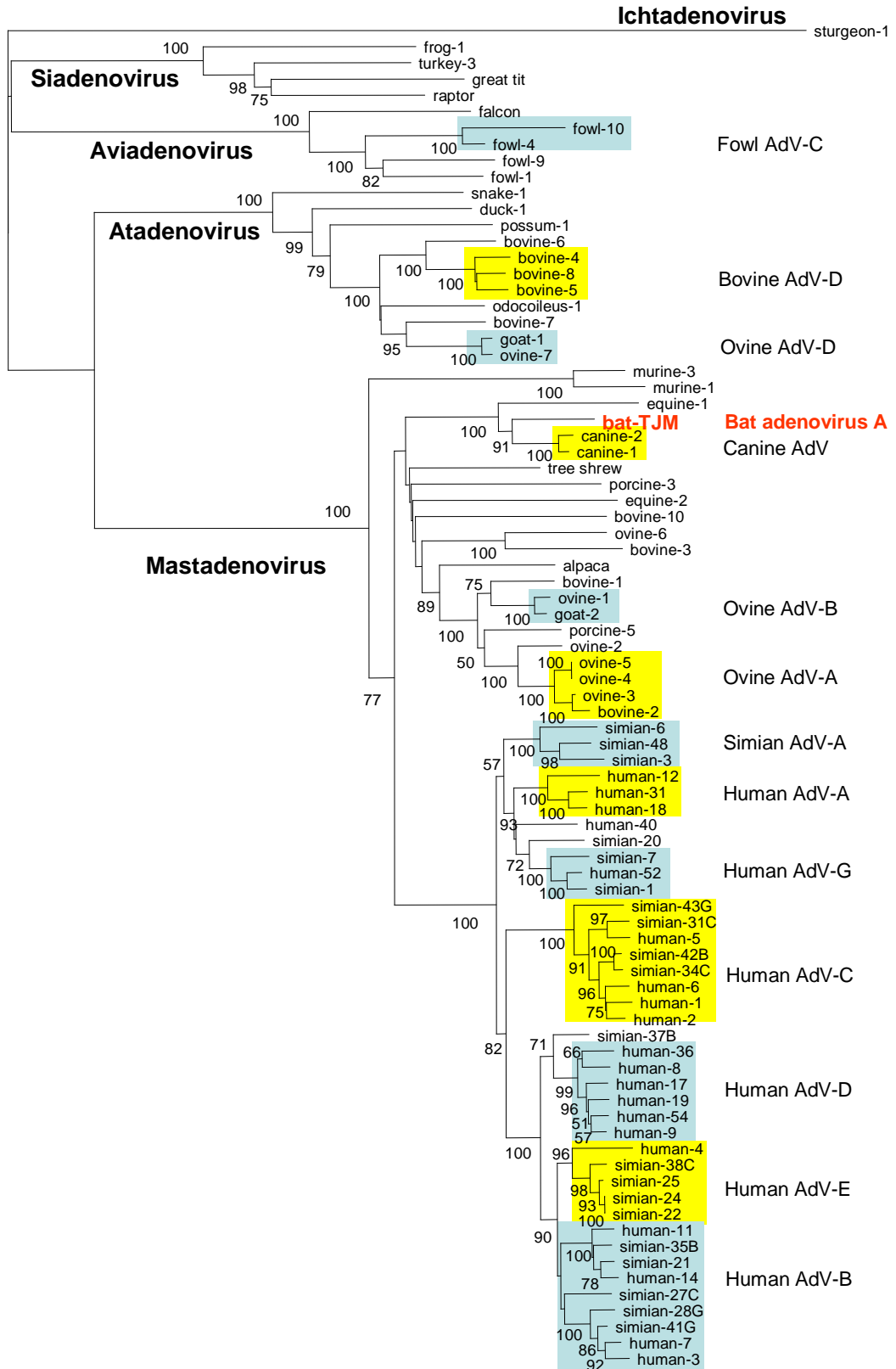
The isolation and genome analysis of a bat adenovirus (BtAdV) originating from Rickett's big-footed bat (*Myotis ricketti*) have been described in China (Li et al., 2010). As this is the first bat adenoviruses with fully sequenced genome, it seems to be important and possible to tackle its official taxonomical status. Based on the very specific host (no adenovirus species has yet been created for any bat adenovirus) and the adequate phylogenetic distance of this type (Fig. 1 and 2), this virus should be seen as the first member of a novel adenovirus species. The name of the species presently proposed to be established should reflect the name of the host thus the proposed name is Bat adenovirus A.

The first published bat AdV (designated as FBV1 as being from fruit bat) was isolated in Japan during attempts to establish a specific cell line from a Ryukyu flying fox (*Pteropus dasymallus yaeyamae*) for the isolation of other viruses of this megachiropteran host (Maeda et al., 2008). Isolation of the second bat AdV, which is the first AdV from a microchiropteran bat, the common pipistrelle (*Pipistrellus pipistrellus*) has been reported from Germany: strain PPV1 (Sonntag et al., 2009). They named this virus bat adenovirus 2. Thus we could call the first AdV (from fruit bat) as bat adenovirus 1, and the third isolate (the fully sequenced strain TJM) bat adenovirus 3. While it is not the task of ICTV to deal with taxons below the level of species, we need a member (and its name) to establish a new species. That is why we propose to use a classical type name for strain TJM: bat adenovirus 3.

Li et al. detected also 19 further adenoviruses from different microchiropteran bats living in China. The detection of these viruses was performed by applying PCR. Similarly, two novel adenoviruses from a common noctule (*Nyctalus noctula*) and a lesser horseshoe bat (*Rhinolophus hipposideros*) were detected by PCR in Hungary (submitted). While there are only very short genome fragment of these later bat AdVs, it can be seen that they show quite a remarkable diversity. Presently, it seems to be wise not dare to engage either in the further type numbering or

in the official taxonomic classification of any other BtAdV than type 3 until further genome sequencing is performed with those viruses.

Fig. 1. (next page) Phylogenetic tree constructed by distance matrix analysis from aa sequence alignment of the main capsid protein hexon. Non-rooted calculation. White sturgeon adenovirus selected as outgroup. Bat adenovirus 3 (strain TJM) is shown in bold and with red letters. Type members of the different species are shown by changing background colouring whenever there are more than one members are shown. Numbers at the nodes refer to the level of confidence as determined by bootstrap analysis (when they confirmed the initial phylogenetic calculation). Scale bar indicates an evolutionary distance of 0.1 aa substitution per position in the sequence.



0.1

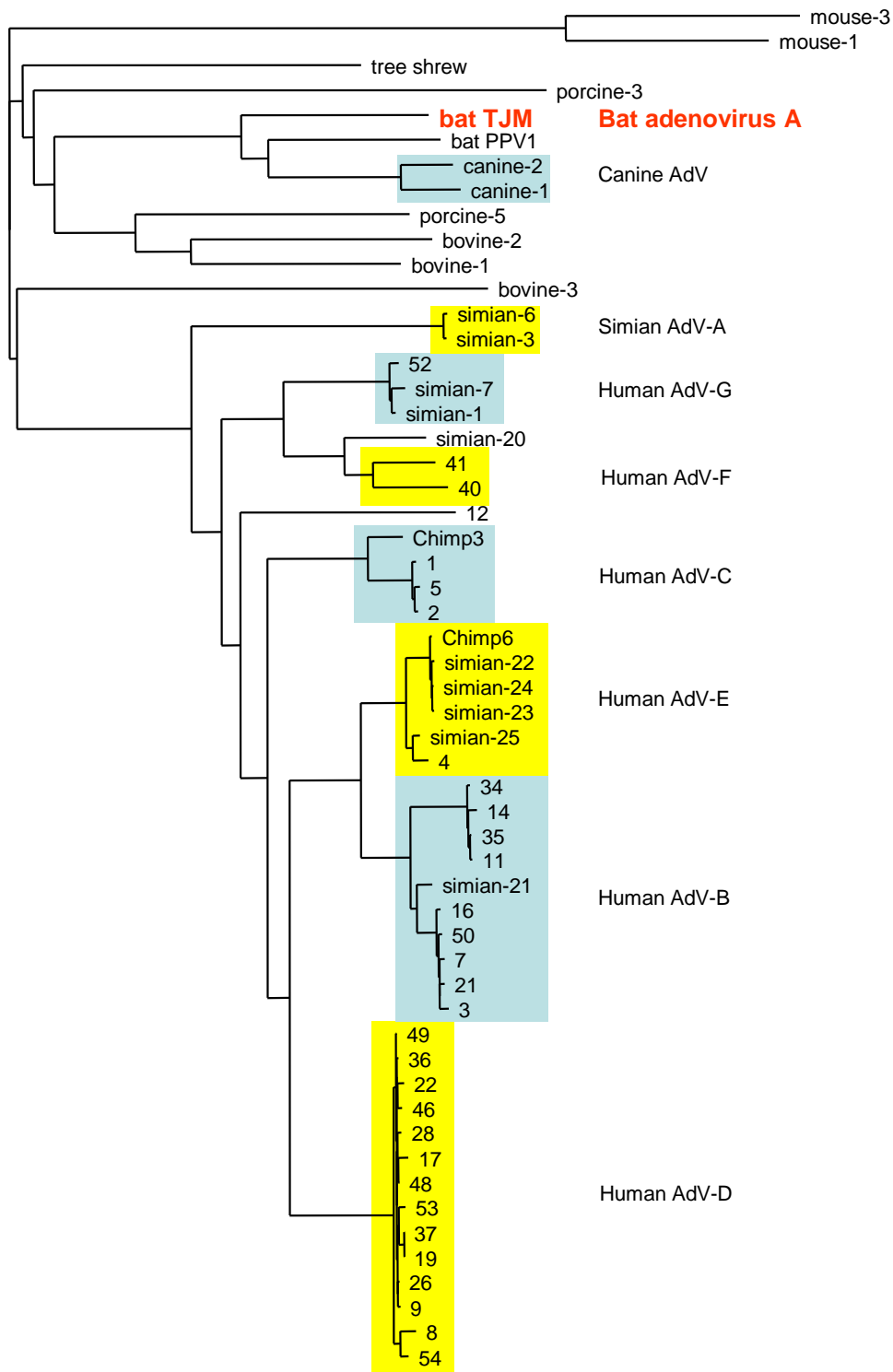


Fig. 1. Phylogenetic tree constructed by distance matrix analysis from aa sequence alignment of the DNA polymerase gene. Murine adenoviruses shown as outgroup.