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:	***2011.024aV***	(to be completed by ICTV officers)

Short title: Create two species, *Bat adenovirus B* and *Murine adenovirus B*, in the genus *Mastadenovirus*, family *Adenoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

proposal for *Bat adenovirus B:*
Claudia Kohl (kohlc@rki.de)
Márton Z. Vidovszky (vidovszky@vmri.hu)
Andreas Kurth (kurtha@rki.de)
proposal for *Murine adenovirus B*
Márton Z. Vidovszky (vidovszky@vmri.hu)
Silvio Hemmi (silvio.hemmi@imls.uzh.ch)
Urs F. Greber (urs.greber@imls.uzh.ch)
on behalf of the Study Group:
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:	To SG chair: August 03, 2011 To Vertebrate Virus Subcommittee chair (A. J. Davison): Aug 12, 2011
Date of this revision (if different to above):	August 18, 2011

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	***2011.024aV***	(assigned by ICTV officers)

To create two 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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Bat adenovirus B	JN252129
Murine adenovirus B	HM049560

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

The proposed novel species *Bat adenovirus B* within the genus *Mastadenovirus* would contain an adenovirus type that shows adequate phylogenetic distances (based on three large non-structural and three large structural proteins: DNA polymerase, pTP, pIIIa, penton base, hexon, 100K) from the member of proposed species *Bat adenovirus A* and members of all established adenovirus species. The viruses in the proposed species *Bat adenovirus A* and *Bat adenovirus B* originate from bats of different genera and are appreciably different in G+C content. The phylogenetic relationships and the specific hosts reflect an evolutionary distance that justifies the creation of this species.

The proposed novel species *Murine adenovirus B* contains an adenovirus type that shows adequate phylogenetic distances (>15% based on three large non-structural and three large structural proteins: DNA polymerase, pTP, pIIIa, penton base, hexon, 100K) from the members of accepted species *Murine adenovirus A* and *Murine adenovirus C* and members of all accepted adenovirus species. The phylogenetic relationships, differences in genome organization from the two other murine adenovirus types and distinct G+C content (63.35% compared to 47.78 and 47.22%) justify the creation of this species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Drexler, J.F., V.M. Corman, T. Wegner, A.F. Tateno, R.M. Zerbinati, F. Gloza-Rausch, A. Seebens, M.A. Müller and C. Drosten, 2011: Amplification of emerging viruses in a bat colony. Emerg. Infect. Dis. 17, 449–456

Hartley J.W. and W.P. Rowe, 1960: A new mouse virus apparently related to the adenovirus group. Virology 11, 645–647.

Hashimoto, K., T. Sugiyama and S. Sasaki, 1966: An adenovirus isolated from feces of mice. I. Isolation and identification, Jpn. J. Microbiol. 10, 115–125.

Hemmi, S., M.Z., Vidovszky, J. Ruminska, S. Ramelli, W. Decurtins, U. Greber and B. Harrach, 2011: Genomic and phylogenetic analyses of murine adenovirus 2. Virus Res (in press) 2011 Jun 12. [Epub ahead of print] doi:10.1016/j.virusres.2011.05.023

Klempa, B., D.H. Krüger, B. Auste, M. Stanko, A. Krawczyk, K.F. Nickel, K. Überla and A. Stang, 2009: A novel cardiotropic murine adenovirus representing a distinct species of mastadenoviruses. J. Virol. 83, 5749–5759.

Jánoska, M., M. Vidovszky, V. Molnár, M. Liptovszky, B. Harrach and M. Benkő, 2011: Novel adenoviruses and herpesviruses detected in bats. Vet. J. 189, 118–121.

Kohl, C., M. Z. Vidovszky, K. Mühldorfer, P.W. Dabrowski, A. Radonic, A. Nitsche, G. Wibbelt, A. Kurth and B. Harrach, 2011: Genome analysis of bat adenovirus 2 PPV1: indications for ancient interspecies transmission. In submission.

Li, L., J.G. Victoria, C. Wang, M. Jones, G.M. Fellers, T.H. Kunz and E. Delwart, 2010a: Bat guano virome: predominance of dietary viruses from insects and plants plus novel mammalian viruses. J. Virol. 84, 6955–6965.

Li Y, X. Ge , H. Zhang, P. Zhou, Y. Zhu, Y. Zhang, J. Yuan, L.F. Wang and Z. Shi, 2010b: Host range, prevalence and genetic diversity of adenoviruses in bats. J. Virol. 84, 3889–3897.

Maeda K, E. Hondo, J. Terakawa, Y. Kiso, N. Nakaichi, D. Endoh, K. Sakai, S. Morikawa and T. Mizutani, 2008: Isolation of novel adenovirus from fruit bat (*Pteropus dasymallus yayeyamae*). Emerg. Infect. Dis. 14, 347–349.

Sonntag M, K. Mühldorfer, S. Speck, G. Wibbelt and A. Kurth, 2009: New adenovirus in bats, Germany. Emerg. Infect. Dis. 15, 2052–2055.

Sugiyama, T., K. Hashimoto and S. Saski, 1967: An adenovirus isolated from the feces of mice. II. Experimental infection, Jpn. J. Microbiol. 11, 33–42.

Vidovszky M. Z. and S. Boldogh, 2011: Detection of adenoviruses in the Northern Hungarian bat fauna. Magy. Állatorvos, In submission.

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.

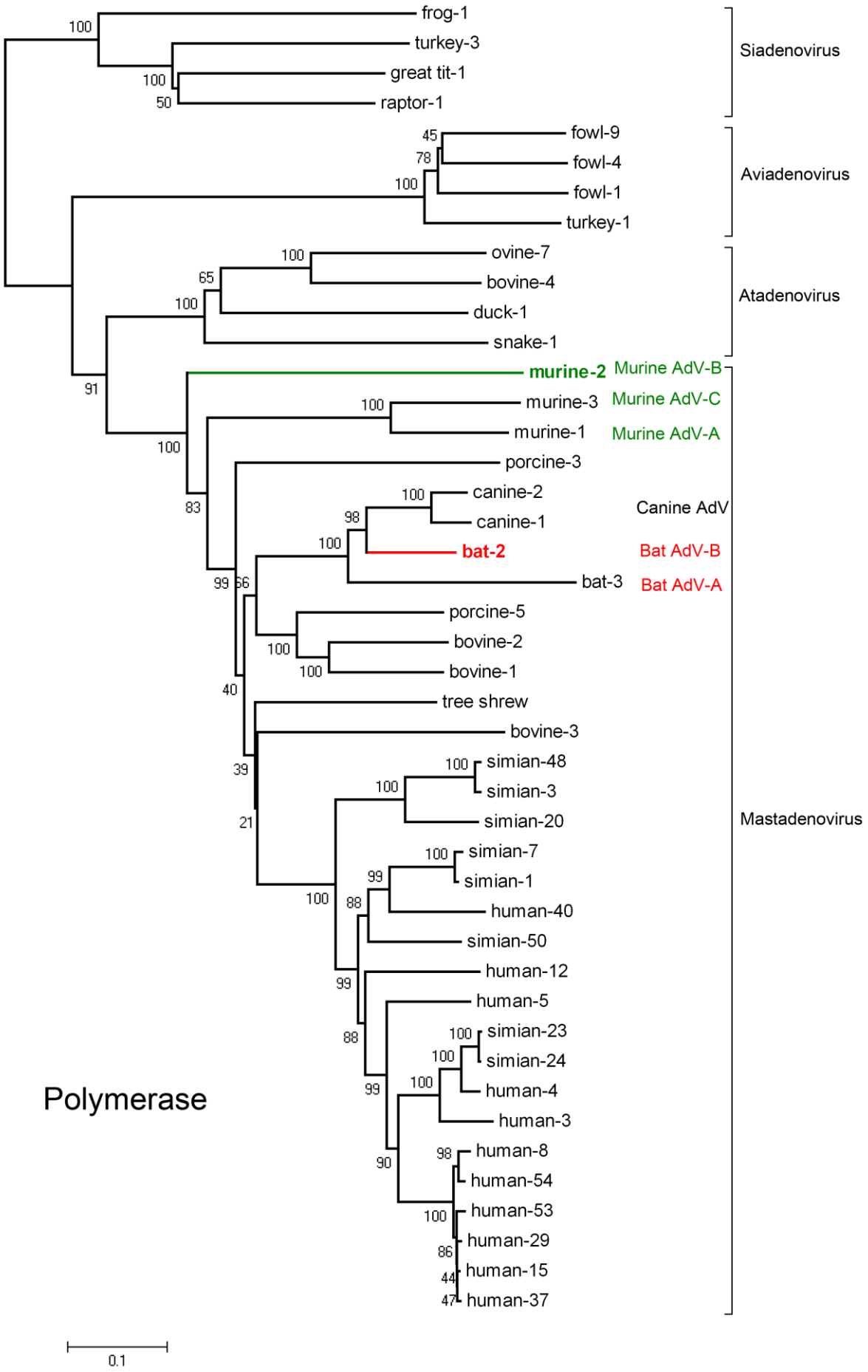
The first bat adenovirus (BtAdV-1) was isolated from a fruit bat of the suborder Megachiroptera [Maeda et al., 2008]. Also in 2008, a novel adenovirus (BtAdV-2 strain PPV1) was isolated from German free-ranging vespertillionid bats (*Pipistrellus pipistrellus*) [Sonntag et al., 2009]. This was the first adenovirus isolated from a microchiropteran bat. In 2010, Li Y. et al. published the isolation and the whole genome sequence of a third bat adenovirus (BtAdV-3, proposed species *Bat adenovirus A*). Meanwhile, the full genome sequence of the isolated BtAdV-2 (strain PPV1) was also determined and analyzed [Kohl et al. 2011].

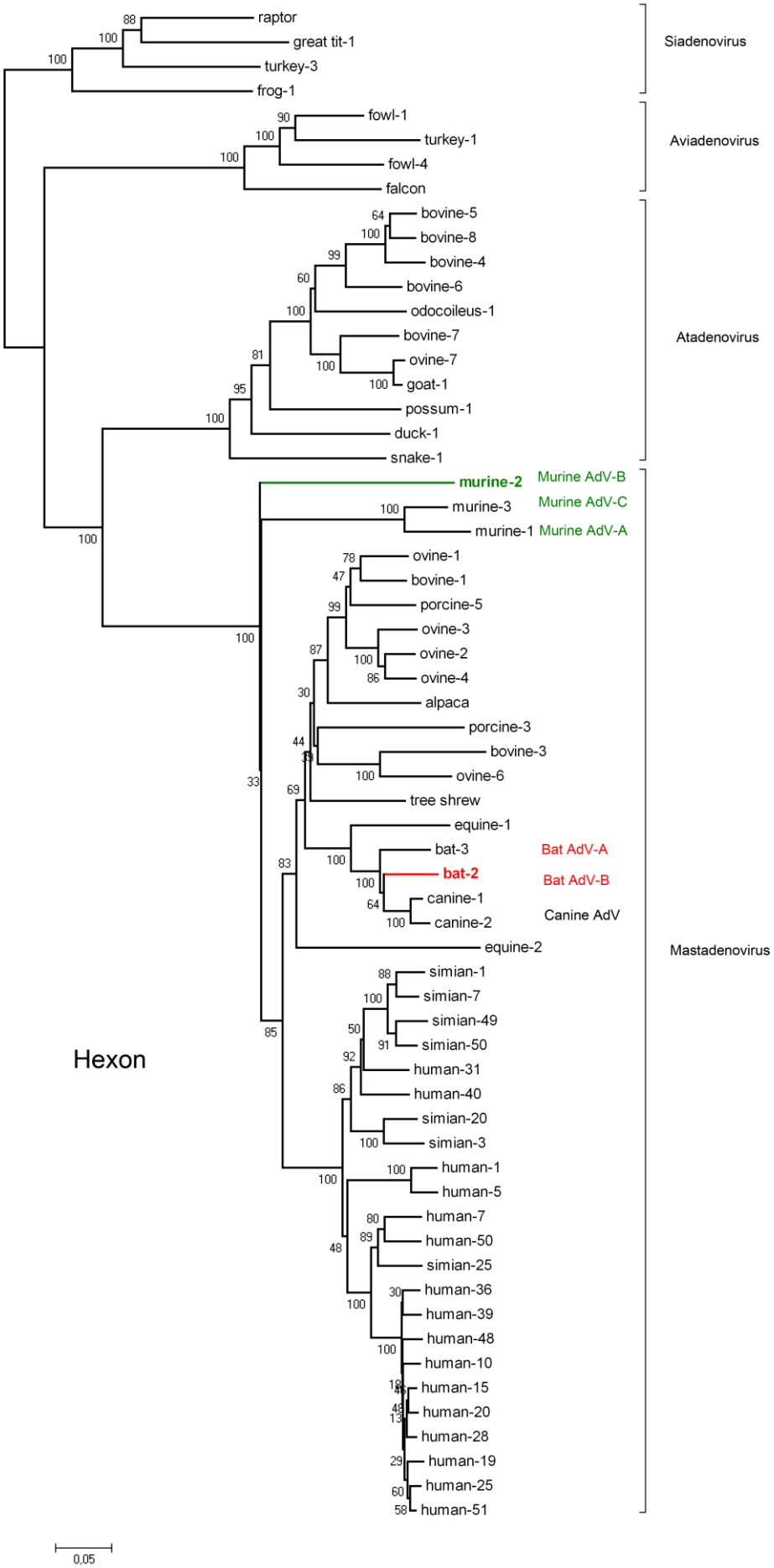
We appreciate and fully agree with the proposal for and the conditional EC approval of the species *Bat adenovirus A*. We now propose the establishment of a second bat adenovirus species named *Bat adenovirus B* for BtAdV-2. This species would contain an adenovirus type (BtAdV-2 strain PPV1) with a sufficient phylogenetic distances from the single member (BtAdV-3) of proposed species *Bat adenovirus A* and all members of established adenovirus species. Bats are the second largest order of mammals, containing more than 1,000 different species. BtAdV-2 and BtAdV-3 originate from bat hosts in different genera. Moreover, the G+C content difference between BtAdV-3 (56.8%) and BtAdV-2 (53.5%) is appreciable.

Several further BtAdVs have been detected by PCR in China, Hungary and Germany [Li et al., 2010b; Drexler et al., 2011; Jánoska et al., 2011; Vidovszky and Boldogh, 2011], and by metagenomic study of guano from American bats [Li et al, 2010a]. This increasing number of novel BtAdVs reflects a large genetic diversity among their hosts, and will require the establishment of further viral species in future.

Two AdV serotypes have been isolated from house mice (*Mus musculus*): murine adenovirus 1 (MAdV-1) strain FL [Hartley and Rowe, 1960] and murine adenovirus 2 (MAdV-2) strain K87 [Hashimoto et al., 1966; Sugiyama et al., 1967]. The third MAdV type isolated recently from a striped field mouse (*Apodemus agrarius*) was named murine adenovirus 3 (MAdV-3) and the analysis of its genome accomplished [Klempa et al., 2009]. MAdV-1 and MAdV-3 are classified into the species *Murine adenovirus A* and *Murine adenovirus C*. The name *Murine adenovirus B* was retained for MAdV-2 until its genome sequencing and publication were completed.

Fig. 1 (following two pages). Phylogenetic analysis of BtAdV-2 and MAdV-2 using amino acid sequences of DNA polymerase and hexon proteins of the four adenovirus genera having multiple adenovirus species. The phylogenetic trees were made by Neighbour-joining calculations and bootstrap analysis with 1,000 replications (MEGA4; http://www.megasoftware.net). Bootstrap values are shown as percentage. BtAdV-2 is shown in red and bold. MAdV-2 is shown in green and bold. The scale bar shows the evolutionary distance of 0.1aa substitution (polymerase) or 0.05 aa substitution (hexon) per position.


frog-1
turkey-3
great tit-1
raptor-1
Siadenovirus
fowl-9
fowl-4
fowl-1
turkey-1
Aviadenovirus
ovine-7
bovine-4
duck-1
snake-1
Atadenovirus
murine-2
murine-3
murine-1
Murine AdV-B
Murine AdV-C
Murine AdV-A
porcine-3
canine-2
canine-1
Canine AdV
bat-2
bat-3
Bat AdV-B
Bat AdV-A
porcine-5
bovine-2
bovine-1
tree shrew
bovine-3
simian-48
simian-3
simian-20
simian-7
simian-1
human-40
simian-50
human-12
human-5
simian-23
simian-24
human-4
human-3
human-8
human-54
human-53
human-29
human-15
human-37
Mastadenovirus
Polymerase
0.1


raptor
great tit-1
turkey-3
frog-1
Siadenovirus
fowl-1
turkey-1
fowl-4
falcon
Aviadenovirus
bovine-5
bovine-8
bovine-4
bovine-6
odocoileus-1
bovine-7
ovine-7
goat-1
possum-1
duck-1
snake-1
Atadenovirus
murine-2
murine-3
murine-1
Murine AdV-B
Murine AdV-C
Murine AdV-A
ovine-1
bovine-1
porcine-5
ovine-3
ovine-2
ovine-4
alpaca
porcine-3
bovine-3
ovine-6
tree shrew
equine-1
bat-3
bat-2
canine-1
canine-2
Bat AdV-A
Bat AdV-B
Canine AdV
equine-2
simian-1
simian-7
simian-49
simian-50
human-31
human-40
simian-20
simian-3
human-1
human-5
human-7
human-50
simian-25
human-36
human-39
human-48
human-10
human-15
human-20
human-28
human-19
human-25
human-51
Mastadenovirus
Hexon
0,05

The MAdV-2 genome has a length of 35,203 bp and a G+C content of 63.35% [Hemmi et al., 2011]. Both values are considerably higher than those for MAdV-1 and MAdV-3 (30,944 and 30,570 bp, 47.78 and 47.22%). The genome maps of the three MAdV types demonstrate that almost every gene of MAdV-2 is larger than its counterpart in MAdV-1 and MAdV-3. Furthermore, there are important differences in the genome organization (Fig. 2). The E3 region in MAdV-2 is different from that in MAdV-1 and MAdV-3. MAdV-2 E3 contains two genes, whereas MAdV-1 and MAdV-3 E3 contains a single gene. Also, whereas almost all mastadenoviruses (including MAdV-2) contain a 12.5K homologue in the E3 region, both MAdV-1 and MAdV-3 lack it. The second E3 gene of MAdV-2 is unique and does not show any similarity to any known gene. In the E4 region, in addition to the 34K gene homologue, which is present in all three MAdVs (and almost all other mastadenoviruses), the four MAdV-3 ORFs have homologues in four of the five MAdV-1 ORFs. In MAdV-2 E4 , there are only two ORFs in addition to the 34K gene homologue, and they are not homologous with any E4 ORFs of MAdV-1 or MAdV-3 (or any other known gene). Overall, MAdV-1 and MAdV-3 (which are members of different species) are much more similar to each other than is either to MAdV-2.

Phylogenetic calculations show that MAdV-1 and MAdV-3 are more closely related to each other than MAdV-2 [Hemmi et al., 2011]. The calculated phylogenetic distance between MAdV-2 and MAdV-1 or MAdV-3 or any other AdV consistently exceeds that required (5-15%) in the species demarcation criteria (Fig. 1; the six phylogenetic trees in the original publication).

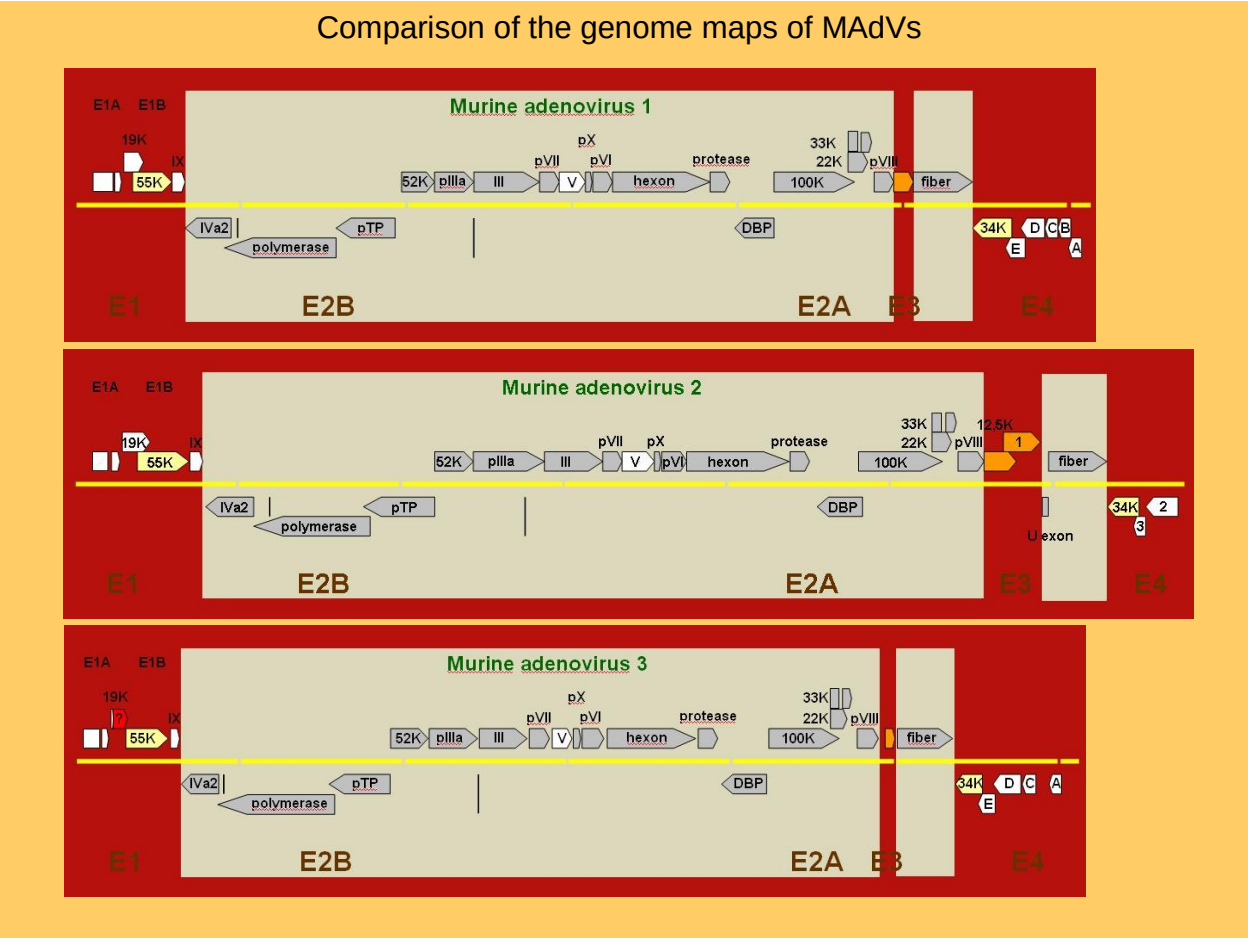


Fig. 2. The genome organizations of the three MAdV types demonstrate characteristic differences that justify their ordering in different viral species.