



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:	2010.018a-cV	(to be completed by ICTV officers)			
Short title: in the genus <i>Mamastrovirus</i> , family <i>Astroviridae</i> , create 14 species, abolish one species and rename 5 species (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 checked="" 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:

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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)	<i>Astroviridae</i> Study Group
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ICTV-EC or Study Group comments and response of the proposer:

This proposal describing a new species classification within the genus *Mamastrovirus* has been prepared, supervised and accepted by all members of the *Astroviridae* Study Group during preparation of the 9th ICTV Report.

Date first submitted to ICTV: 06.06.2010
Date of this revision (if different to above): 08.06.2011

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	2010.018aV	(assigned by ICTV officers)
To create 14 new species within:		
Genus:	<i>Mamastrovirus</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>Astroviridae</i>	
Order:		
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Mamastrovirus 4</i>		FJ890352
<i>Mamastrovirus 5</i>		FM213330, FM213331, FM213332
<i>Mamastrovirus 6</i>		FJ402983, FJ222451
<i>Mamastrovirus 7</i>		FJ890355
<i>Mamastrovirus 8</i>		NC_013443, GQ502193
<i>Mamastrovirus 9</i>		GQ415661, GQ415662, FJ973620
<i>Mamastrovirus 11</i>		FJ890351
<i>Mamastrovirus 12</i>		FJ571067
<i>Mamastrovirus 14</i>		EU847144
<i>Mamastrovirus 15</i>		FJ571066
<i>Mamastrovirus 16</i>		EU847145
<i>Mamastrovirus 17</i>		FJ571074, FJ571068
<i>Mamastrovirus 18</i>		EU847155
<i>Mamastrovirus 19</i>		FJ571065, FJ571069, FJ571070, FJ571071, FJ571072, FJ571073

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

This proposal is the result of the work done in agreement by all members of the ***Astroviridae* Study Group** during the preparation of the 9th ICTV Report. During recent years, a high amount of literature has been published to describe several new astrovirus strains infecting mammalian species (see references 1-8). These new data need to be incorporated in the ICTV database. In the 8th ICTV Report, astrovirus isolates were classified into species within the *Mamastrovirus* genus based only on the basis of host of origin, but some of the new findings denote that this criterion needs to be redefined and updated. Several examples include:

- Although the two recently identified groups MLB and VA/HMO astroviruses (refs. 3, 4, 5) infect

humans, they are extremely genetically divergent from the classical human astroviruses included in the *Human astrovirus* (HAstV) species. These new strains are even closer to some other animal astroviruses such as mink or sheep rather than to HAstV, and thus must be considered as different *Mamastrovirus* species infecting the same host.

- New recently identified astroviruses that infect cheetahs are genetically strongly related to feline astroviruses (ref. 1). Although these viruses infect different animal species, they may actually represent the same astrovirus species.
- The recently identified group of astroviruses infecting bats is formed by a highly genetically diverse group of viruses and some of them can infect more than one species (refs.2 and 8).

Based on these new data, the ***Astroviridae* Study Group** states that a classification based on genetic criteria is more appropriate. A phylogenetic analysis of mamastroviruses based on the amino acid sequence of the full length ORF2, which encodes the capsid polyprotein, results in 19 groups or species. Mean amino acid genetic distances (p-dist) range between 0.378-0.750, and 0.006-0.312 between and within groups, respectively. All groups are supported by a high bootstrap value (see Figure 1 in supporting material module 9). Astroviruses for which only partial sequences are available, or no sequences at all are deposited in Genbank should be listed as “Related viruses which may be members of the *Mamastrovirus* genus but have not been approved as species” (Table 1).

Table 1

Name of tentative species	Accession number(s)
Bovine astrovirus	
California sea lion astrovirus 1	FJ890351
California sea lion astrovirus 3	FJ890353
Cheetah astrovirus	EU650331, EU650332
Human astrovirus MLB2	GQ502192
Steller sea lion astrovirus 1	FJ890354

In summary, compared to the list of species of the 8th Report, this new classification establishes 14 new species within the genus, and renames 5 of the 6 previously demarked species (Table 2). Due to the lack of sequences available for bovine astroviruses, the *Bovine astrovirus* species is now listed as a related virus (see Table 1).

Table 2

Previous species name	Proposed species name	Accession number(s)
<i>Feline astrovirus</i>	<i>Mamastrovirus 2</i>	AF056197
<i>Human astrovirus</i>	<i>Mamastrovirus 1</i>	L23513
<i>Mink astrovirus</i>	<i>Mamastrovirus 10</i>	AY179509
<i>Ovine astrovirus</i>	<i>Mamastrovirus 13</i>	NC_002469
<i>Porcine astrovirus</i>	<i>Mamastrovirus 3</i>	Y15938, AB037272

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	2010.018bV	(assigned by ICTV officers)
To remove the following taxon from its present position:		
<i>Bovine astrovirus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:	<i>Mamastrovirus</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Astroviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

According to the list of species within the *Mamastrovirus* genus that results from the use of the new criteria defined by the **Astrovirus Study Group** during preparation of the 9th ICTV Report, the species Bovine astrovirus should be listed as a "Related virus which may be members of the *Mamastrovirus* genus but has not been approved as species" due to the lack of sequences available in Genbank.

Part (b) re-assign to a higher taxon

Code		(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
Genus:		Fill in all that apply. • If the higher taxon has yet to be created write " (new) " after its proposed name and complete relevant module to create it. If no genus is specified, enter " unassigned " in the genus box.
Subfamily:		
Family:		
Order:		

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

MODULE 8: NON-STANDARD

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	2010.018cV	(assigned by ICTV officers)
Title of proposal: Change the names of five species in the genus <i>Mamastrovirus</i>		

Text of proposal:

Change the names of five species in the genus *Mamastrovirus* as follows

existing species name	proposed new name
<i>Feline astrovirus</i>	<i>Mamastrovirus 2</i>
<i>Human astrovirus</i>	<i>Mamastrovirus 1</i>
<i>Mink astrovirus</i>	<i>Mamastrovirus 10</i>
<i>Ovine astrovirus</i>	<i>Mamastrovirus 13</i>
<i>Porcine astrovirus</i>	<i>Mamastrovirus 3</i>

Reasons to justify the change of names:

Explain why the taxa should be renamed

According to the list of species within the *Mamastrovirus* genus that results from the use of the new criteria defined by the **Astrovirus Study Group** during preparation of the 9th ICTV Report, 5 of the 6 previously demarked species should be renamed (see Table 2 in Module 2).

additional material in support of this proposal

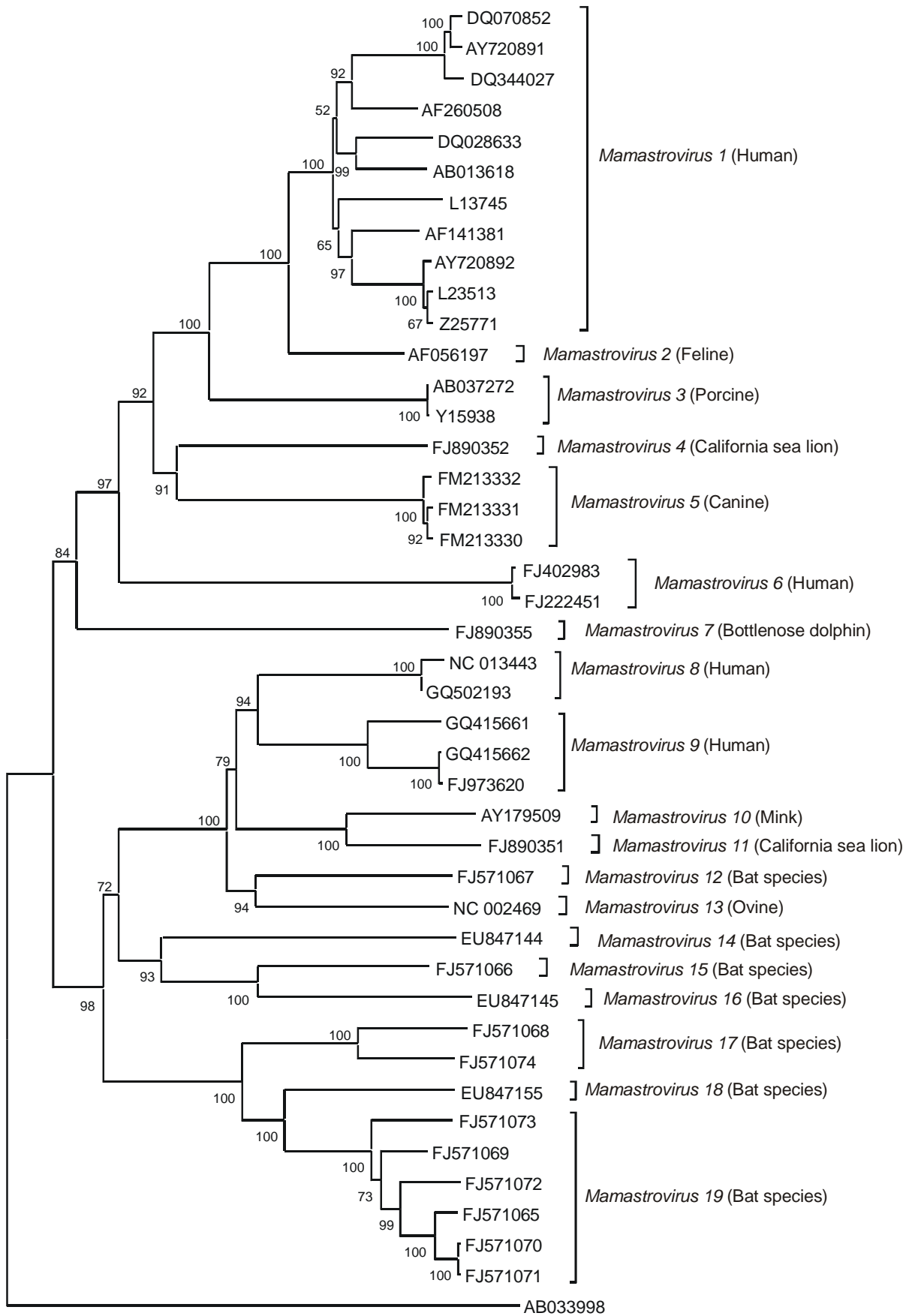
References:

- 1- Atkins, A., Wellehan, J.F.Jr, Childress, A.L., Archer, L.L., Fraser, W.A., Citino, S.B., 2009. Characterization of an outbreak of astroviral diarrhea in a group of cheetahs (*Acinonyx jubatus*). *Vet. Microbiol.* 14, 160-165.
- 2- Chu, D.K.W., Poon, L.L.M., Guan, Y., Peiris, J.S.M., 2008. Novel astroviruses in insectivorous bats. *J. Virol.* 82, 9107-9114.
- 3- Finkbeiner, S.R., Holtz, L.R., Jiang, Y., Rajendran, P., Franz, C.J., Zhao, G., Kang, G., Wang, D., 2009. Human stool contains a previously unrecognized diversity of novel astroviruses. *Virol. J.* 8, 6:161.
- 4- Finkbeiner, S.R., Li, Y., Ruone, S., Conrardy, C., Gregoricus, N., Toney, D., Virgin, H.W., Anderson, L.J., Vinjé, J., Wang, D., Tong, S., 2009. Identification of a novel astrovirus (astrovirus VA1) associated with an outbreak of acute gastroenteritis. *J. Virol.* 20, 10836-10839.
- 5- Kapoor, A., Li, L., Victoria, J., Oderinde, B., Mason, C., Pandey, P., Zaidi, S.Z., Delwart, E., 2009. Multiple novel astrovirus species in human stool. *J Gen Virol.* 90, 2965-2972.
- 6- Rivera, R., Nollens, H.H., Venn-Watson, S., Gulland, F.M., Wellehan, J.F.Jr., 2010. Characterization of phylogenetically diverse astroviruses of marine mammals. *J. Gen. Virol.* 91, 166-173.
- 7- Toffan, A., Jonassen, C.M., De Battisti, C., Schiavon, E., Kofstad, T., Capua, I., Cattoli, G., 2009. Genetic characterization of a new astrovirus detected in dogs suffering from diarrhoea. *Vet. Microbiol.* 139, 147-152.
- 8- Zhu, H.C., Chu, D.K., Liu, W., Dong, B.Q., Zhang, S.Y., Zhang, J.X., Li, L.F., Vijaykrishna, D., Smith, G.J., Chen, H.L., Poon, L.L., Peiris, J.S., Guan, Y., 2009. Detection of diverse astroviruses from bats in China. *J. Gen. Virol.* 90, 883-887.

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.

Figure 1. Phylogenetic tree based on the amino acid sequence of the complete ORF2 of astrovirus infecting mammals available in Genbank and included in the *Mamastrovirus* genus. Name of units correspond to Accession Numbers of astrovirus isolates. The evolutionary history was inferred using the Neighbor-Joining method and the MEGA4 software. The evolutionary distances are computed using the p-dist method and correspond to the number of amino acid substitutions per site (scale bar). All positions containing alignment gaps and missing data were eliminated only in pairwise sequence comparisons (Pairwise deletion option). Numbers at each node of the tree show bootstrap percentages obtained after 100 replicates. An avian astrovirus was used as an outgroup (AB033998). Astrovirus isolates cluster in 19 groups which are indicated and named as species within the genus. Words in brackets beside each species name indicate the species of the host from which they have been isolated.



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