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:	***2010.017a-cV***	(to be completed by ICTV officers)

Short title: reorganize the taxonomy of the genus *Avastrovirus* (family *Astroviridae*) into 3 three newly defined species
(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:

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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)	Astroviridae Study Group

ICTV-EC or Study Group comments and response of the proposer:

This proposal describing a new species classification within the genus Avastrovirus 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):	05/01/2012

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	***2010.017aV***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Avastrovirus***
Subfamily:	
Family:	***Astroviridae***
Order:	

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:**
Avastrovirus 1	Y15936
Avastrovirus 2	AB0333998, AB046864
Avastrovirus 3	AF206663, EU143843 FJ434664

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. Since the last version of the ICTV Report, a complete sequence of a duck astrovirus has been published (ref. 3). In addition, avian astrovirus isolates where classified into species within the *Avastrovirus* 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:

- Some *Turkey astrovirus* isolates have been shown to infect other avian species such as guinea fowl (ref. 2)
- Some avian nephritis viruses (ANV), previously classified as *Chicken astrovirus*, can also infect turkeys (ref. 4).
- New chicken astroviruses have been identified (ref. 1) although only partial sequences are available.

Based on these new data, the ***Astroviridae* Study Group** states that a classification based on genetic criteria is more appropriate. A phylogenetic analysis of avastroviruses based on the amino acid sequence of the full length ORF2, which encodes the capsid polyprotein, results in 3 group or species. Mean amino acid genetic distances (p-dist) range between 0.576-0.742, and 0.204-0.284 between and within groups, respectively. All groups are supported by a high bootstrap value (see Figure 1 in supporting material module 9).

Compared with the list of species of the 8th Report, this new classification establishes 3 new species within the genus:

- *Avastrovirus* 1: including Turkey astrovirus 1
- *Avastrovirus* 2: including Avian nephritis virus 1 and 2
- *Avastrovirus* 3: including Turkey astrovirus 2 and Duck astrovirus

Some chicken astroviruses for which only partial sequences are available (Chicken astrovirus 2, DQ324850), or no sequences at all are deposited in Genbank (Chicken astrovirus 3) should be listed as “Related viruses which may be members of the *Avastrovirus* genus but have not been approved as species”.

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	***2010.017bV***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Chicken astrovirus
Duck astrovirus
Turkey astrovirus

The present taxonomic position of these taxon/taxa:

Genus:	***Avastrovirus***	Fill in all that apply.
Subfamily:		
Family:	***Astroviridae***	
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

These species need to be removed due to new criteria for species demarcation accepted by all members of the ***Astroviridae*** **Study Group** during preparation of the 9th ICTV Report, which are based on genetic analysis of the complete ORF2 capsid sequence.

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:		

MODULE 8: **NON-STANDARD**

Code	***2010.017cV***	(assigned by ICTV officers)

To re-designate the following as the type species of the genus

Avastrovirus 1	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Reasons to justify the designation of a new type species:

With the removal of the existing type species, *Turkey astrovirus*, from the genus *Avastrovirus* (see 2010.017bV, above), it becomes necessary to designate a new type species.

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 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1- Baxendale, W. and Mebatsion, T., 2004. The isolation and characterization of astroviruses from chickens. Avian Pathol. 33, 364-370.

2- Cattoli, G., De Battisti, C., Toffan, A., Salviato, A., Lavazza, A., Cerioli, M., and Capua, I., 2007. Co-circulation of distinct genetic lineages of astroviruses in turkeys and guinea fowl. Arch Virol. 152(3):595-602.

3- Fu, Y., Pan, M., Wang, X., Xu, Y., Xie, X., Knowles, N.J., Yang, H., Zhang, D., 2009. Complete sequence of a duck astrovirus associated with fatal hepatitis in ducklings. J. Gen. Virol. 90, 1104-1108.

4- Pantin-Jackwook, M.J., Spackman, E., and Woolcock, P.R. 2006. Molecular characterization and typing of chicken and turkey astroviruses circulating in the United States: implications for diagnostics. Avian Dis. 50(3):397-404.

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 avian species available in Genbank and included in the *Avastrovirus* 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. A mammalian astrovirus was used as an outgroup (L23513). Astrovirus isolates cluster in 3 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.