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:	***2013.009a-dV***	(to be completed by ICTV officers)

Short title: Create a new species, *Avisivirus A*, in a new genus, *Avisivirus*, within the family *Picornaviridae* (order *Picornavirales*)
(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:

Nick Knowles (nick.knowles@pirbright.ac.uk) on behalf of the *Picornaviridae* Study Group

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)	*Picornaviridae* Study Group

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

Date first submitted to ICTV: 25/06/2013
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. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.009aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Avisivirus* (new)**
Subfamily:	**n/a**
Family:	***Picornaviridae***
Order:	***Picornavirales***

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:**
Avisivirus A	KC465954, KC614703

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

Virus discovery

Avisiviruses have been detected in a metagenomic analyses of turkeys (*Meleagris gallopavo*) in Hungary (stunting syndrome and/or poultry enteritis) and the USA (fatigue and increased mortality was observed in 3- to 5-week-old domestic turkey poults) and complete genome sequences have been determined for both using conventional RT-PCR and sequencing techniques (Boros et al., 2013; Ng et al., 2013).

Growth in cell cultures

None has been cultivated in cell cultures.

Untranslated regions

The avisivirus 5′ untranslated region (UTR), which is 609 nt long, is predicted to contain a type II internal ribosome entry site (IRES). The 5′ UTR (predicted to contain a type IV IRES) of DHAV is 623-653 nt long and shares only 42-44% nt identity with the avisiviruses. The 3′ UTR is very long at 264-266 nt (e.g. that of poliovirus is 68 nt), although it is shorter than the 3′ UTR of DHAVs (314 to 367 nt) with which it shares only 45% nt identity.

Genome organization/proteins

Avisivirus genome layout:

VPg+5'UTR$^{\text{IRES-II}}$[1AB-1C-1D?2A$^{\text{npgp}}$/(2A$^{\text{npgp}}$)/2A$^{\text{AIG1-like}}$-2A$^{\text{H-Box/NC}}$-2B-2C/3A-3B$^{\text{VPg}}$-3C$^{\text{pro}}$-3D$^{\text{pol}}$]3'UTR-poly(A)

DHAV genome layout:

VPg+5'UTR$^{IRES\text{-}IV}$[1AB-1C-1D?2A^{npgp}/2A$^{AIG1\text{-}like}$-2A$^{H\text{-}Box/NC}$-2B-2C/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3'UTR-poly(A)

?, indicates that it is unclear if a cleavage occurs between 1D and the short 2A-like peptide.
(), indicates that this predicted polypeptide is not present in TuASV-USA-IN1 or in DHAV.
[], defines the long ORF encoding the polyprotein.
/, Indicates primary polyprotein cleavages.
-, indicates secondary cleavages mainly performed by the 3C^{pro} polypeptide.

VP0 (1AB) is uncleaved and has no canonical myristoylation signal (GxxxT/S) at its amino-terminus. The first 2A motif (NPG↓P) may be part of VP1 and be used to separate P1 from P2 (as is suspected with DHAV). The Hungarian virus, but not the American virus (or DHAV), possesses an extra 2A polypeptide (2A1; 76 aa long) between the first VP1-linked NPG↓P motif and an AIG1-motif-containing 2A (2A2; which is present in both viruses and is 140 aa long). The final 2A (2A3; 123 aa long) contains an H-box/NC motif.

Genetic relationships

The two avisiviruses share 83.5% nt identity over the polyprotein-coding region. They differ in that 2A1 is present in the Hungarian virus, but not in the American virus. They are genetically different from the currently known picornaviruses of turkey origin (megriviruses and galliviruses), and show a distant phylogenetic relationship and common genomic features (e.g. uncleaved VP0 and three predicted and unrelated 2A polypeptides) to duck hepatitis A virus (DHAV; genus *Avihepatovirus*). The relationships between avisiviruses and DHAV in the P1, P2 and P3 polypeptides are 37.8%, 35.7% and 38.4%, respectively. Individual polypeptide relationships between avisiviruses and DHAV are shown in Table 1. Figures 1 and 2 show the phylogenetic relationship of avisiviruses to other picornaviruses for the P1 capsid and 3D^{pol} polypeptides.

Table 1. Percentage nucleotide identities between avisivirus and DHAV for each of the virus polypeptides.

Polypeptide	VP0	VP3	VP1	2A1	2A2	2A3	2B	2C	3A	3B	3C	3D
% aa identity	32	44	26	10	25	32	28	42	21	11	36	38

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.009bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	**n/a**
Family:	***Picornaviridae***
Order:	***Picornavirales***

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.009cV***	(assigned by ICTV officers)

To name the new genus: *Avisivirus*

Assigning the type species and other species to a new genus

Code	***2013.009dV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The relationships between avisiviruses and DHAV in the P1, P2 and P3 polypeptides are 37.8%, 35.7% and 38.4%, respectively. The *Picornaviridae* Study Group (PSG) guidelines state that members of different genera share less that 40%, 40% and 50% amino acid difference in P1, P2 and P3, respectively. We therefore suggest that the proposed species *Avisivirus A* is placed in a new genus named *Avisivirus*.

Origin of the new genus name:

Avihepato **si**ster-clade virus

Reasons to justify the choice of type species:

Only a single species has been described.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

n/a

MODULE 9: **APPENDIX**: supporting material

References:

Boros, Á., Nemes, C., Pankovics, P., Kapusinszky, B., Delwart, E. and Reuter, G. (2013). Genetic characterization of a novel picornavirus in turkeys (*Meleagris gallopavo*) distinct from turkey galliviruses and megriviruses and distantly related to the members of the genus *Avihepatovirus*. J. Gen. Virol. 94: 1496-1509. [Epub ahead of print 2013 Apr 4].

Ng, T.F.F., Cheung, A.K., Wong, W., Lager, K.M., Kondov, N.O., Cha, Y., Murphy, D.A., Pogranichniy, R.M. and Delwart, E. (2013). Divergent picornavirus from a Turkey with gastrointestinal disease. Genome Announcements 1 (3), e00134-13.

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.

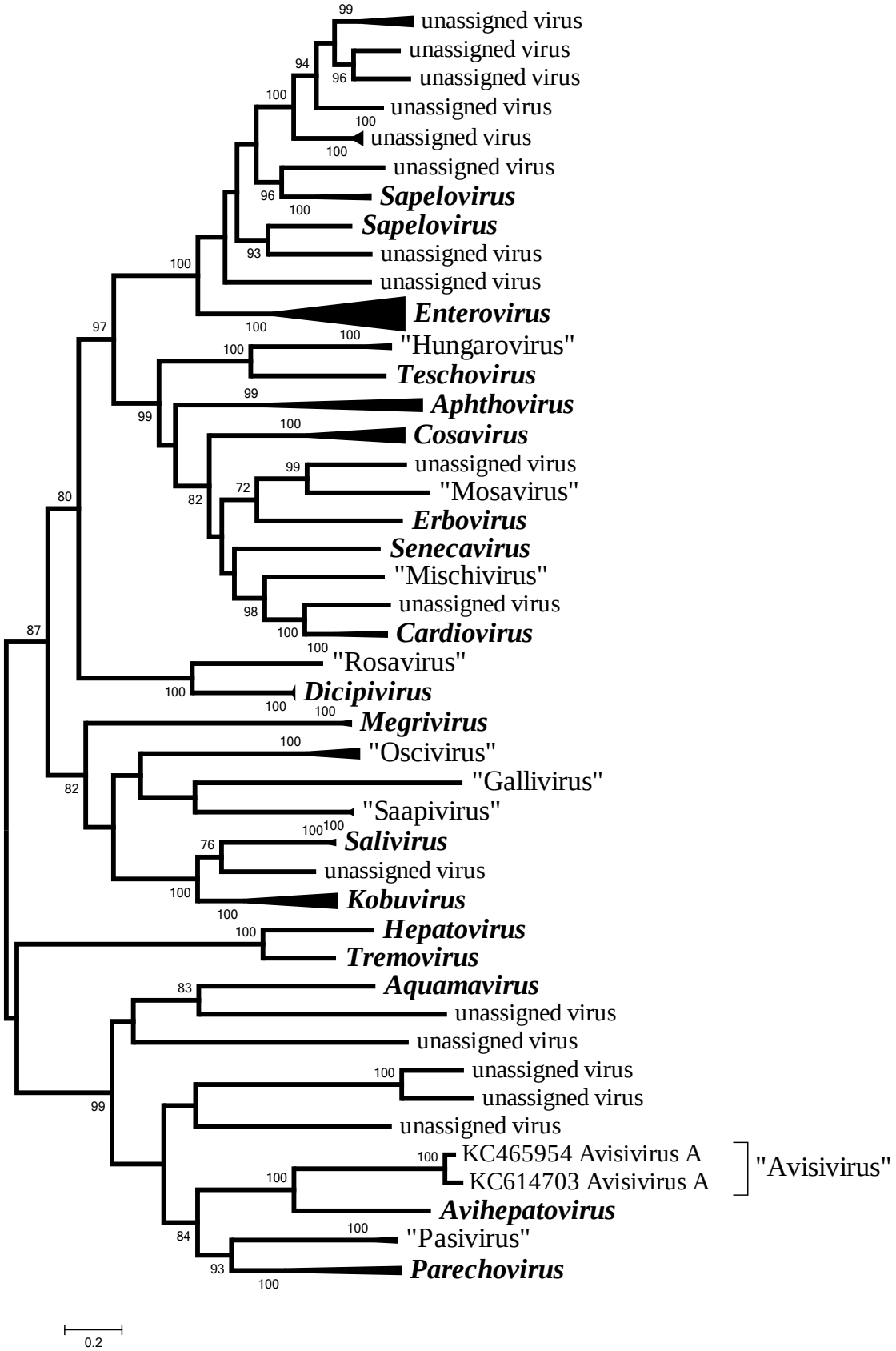

Figure 1. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

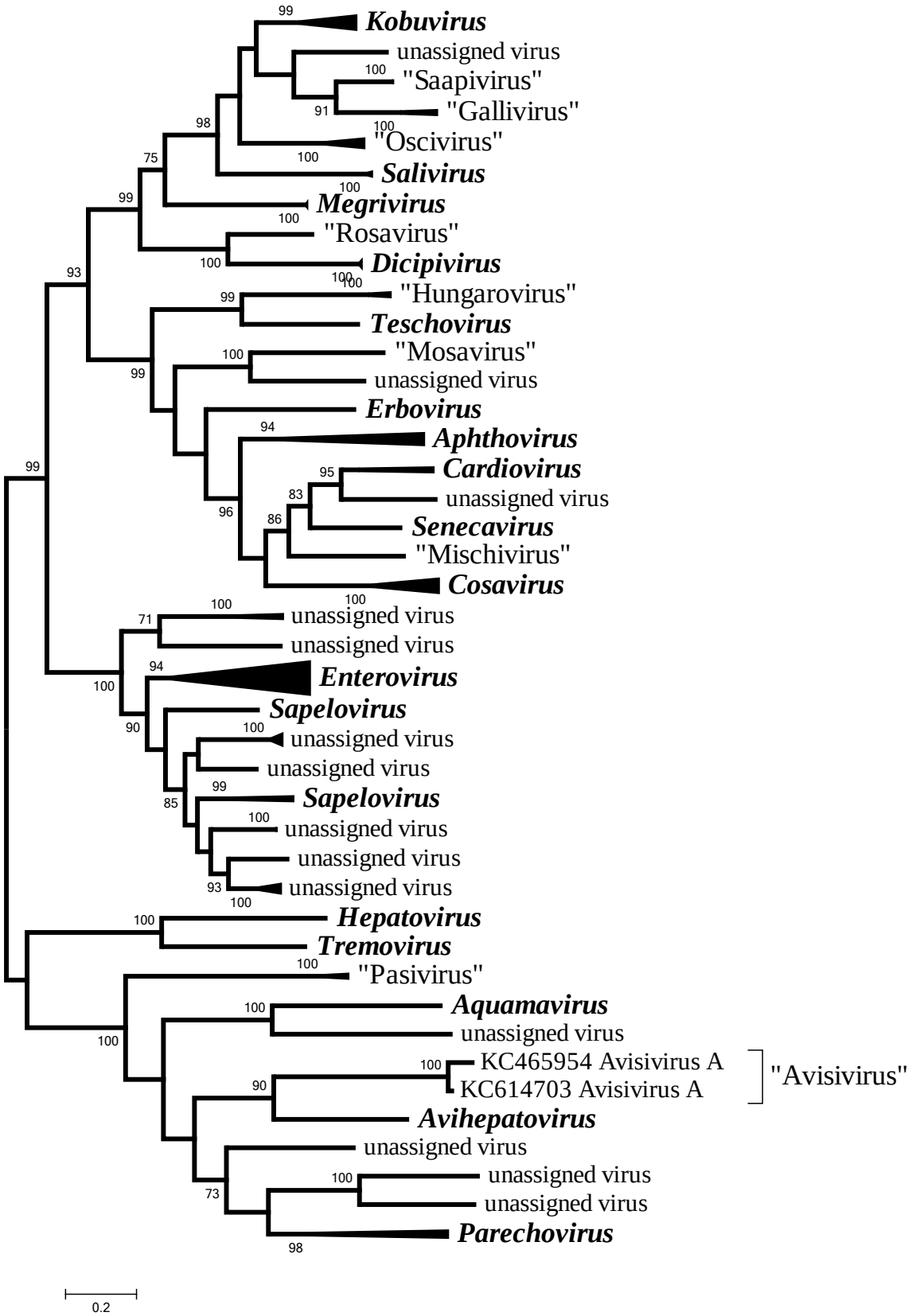

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.