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:	***2013.008a-dV***	(to be completed by ICTV officers)

Short title: Create a new species, *Hunnivirus A*, in a new genus, *Hunnivirus*, 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:

EC comment: Provide a different genus name.

Date first submitted to ICTV: 25/06/2013
Date of this revision (if different to above): 30/07/2013

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	***2013.008aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Hunnivirus* (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:**
Hunnivirus A	JQ941880, HM153767

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

The complete genome sequences of three genotypes of hunniviruses have been determined (Reuter et al., 2012; Boros et al., unpublished). The first two genotypes were found in cattle and sheep in Hungary and are commonly known as bovine hungarovirus 1 (BHuV-1) and ovine hungarovirus 1 (OHuV-1) (this name will be modified to hunnivirus). The third genotype (whose complete genome has recently been sequenced) was originally isolated in cell cultures from sheep in Northern Ireland in 1965 (McFerran et al., 1969). Subsequently the virus was characterized by electron microscopy and shown to be a picorna-like virus with a diameter of 28±3 nm (McFerran et al., 1971). Further biochemical characterization was undertaken by Adair et al. (1987). Confirmation that this was a novel picornavirus was later obtained by RT-PCR and sequencing of the ~450 nt at the 3′ end of the genome (Knowles, 2005).

Growth in cell cultures

Neither of the Hungarian genotypes has been cultivated in cell cultures, although attempts have been made to grow them in secondary calf and lamb kidney cells. The Northern Ireland virus (four isolates) grows in lamb kidney cell cultures and shows an obvious CPE.

Untranslated regions

The 5′ UTRs of hunniviruses (715-732 nt) are predicted to contain a type II internal ribosome entry site (IRES) (Boros et al., 2012). The 3′ UTRs are 114-119 nt long and are predicted to have a long double-stranded hairpin stem. They have no primary nt identity to other picornaviruses.

Genome organization/proteins

VPg+5′UTR$^{IRES\text{-}II}$[L/1A-1B-1C-1D-2A^{npgp}/2B-2C/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3′UTR-poly(A)

[ ], defines the long ORF encoding the polyprotein.
/, Indicates primary polyprotein cleavages.
-, indicates secondary cleavages mainly performed by the 3C^{pro} polypeptide.

A leader polypeptide of 83 aa precedes the capsid; it has no sequence identity with other picornaviruses. VP0 (1AB) is predicted to be cleaved to VP4 and VP2 and a myristoylation motif (GxxxT/S as GPGQS) is present at the amino-terminus of VP0/VP4. The 2A is short (21 aa) and ends in NPG↓P like aphthoviruses, teschoviruses, erboviruses, etc.

Genetic relationships

The genomes of the three hunnivirus genotypes are related to each other by ~80% nt identity. The hunniviruses are distantly related to all other picornaviruses. In the P1, P2 and P3 polypeptides the closest relationships are 32.7% (*Equine rhinitis B virus*), 33.7% (*Porcine teschovirus*) and 41.0% (*Porcine teschovirus*), respectively.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.008bV***	(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	***2013.008cV***	(assigned by ICTV officers)

To name the new genus: *Hunnivirus*

Assigning the type species and other species to a new genus

Code	***2013.008dV***	(assigned by ICTV officers)

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

Hunnivirus 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 hunniviruses and other picornaviruses in the P1, P2 and P3 polypeptides are 32.7% (*Equine rhinitis B virus*), 33.7% (*Porcine teschovirus*) and 41.0% (*Porcine teschovirus*), 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 *Hunnivirus A* is placed in a new genus named *Hunnivirus*.

Origin of the new genus name:

Hunnivirus: from **Hun**gary and **N**orthern **I**reland where samples for the first three complete genome sequences were collected.

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

additional material in support of this proposal

References:

Adair, B.M., Kennedy, S., McKillop, E.R., McNulty, M.S. and McFerran, J.B. (1987). Bovine, porcine and ovine picornaviruses: identification of viruses with properties similar to human coxsackieviruses. Arch Virol. 97: 49-59.

Knowles, N.J. (2005). A pan-picornavirus RT-PCR: identification of novel picornavirus species. EUROPIC 2005: XIIIth Meeting of the European Study Group on the Molecular Biology of Picornaviruses, Lunteren, The Netherlands, 23-29th May 2005. Abstract A06.

McFerran, J.B., Nelson, R., McCracken, J.M. and Ross, J.G. (1969). Viruses isolated from sheep. Nature, London 221: 194.

McFerran, J.B., Clarke, J.K. and Connor, T.J. (1971). The size of some mammalian picornaviruses. J. Gen. Virol. 10:279-284.

Reuter, G., Pankovics, P., Knowles, N.J. and Boros, Á. (2012). Two closely related novel picornaviruses in cattle and sheep in Hungary from 2008 to 2009, proposed as members of a new genus in the family *Picornaviridae*. J. Virol. 86: 13295-13302. Epub 2012 Sep 26.

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.

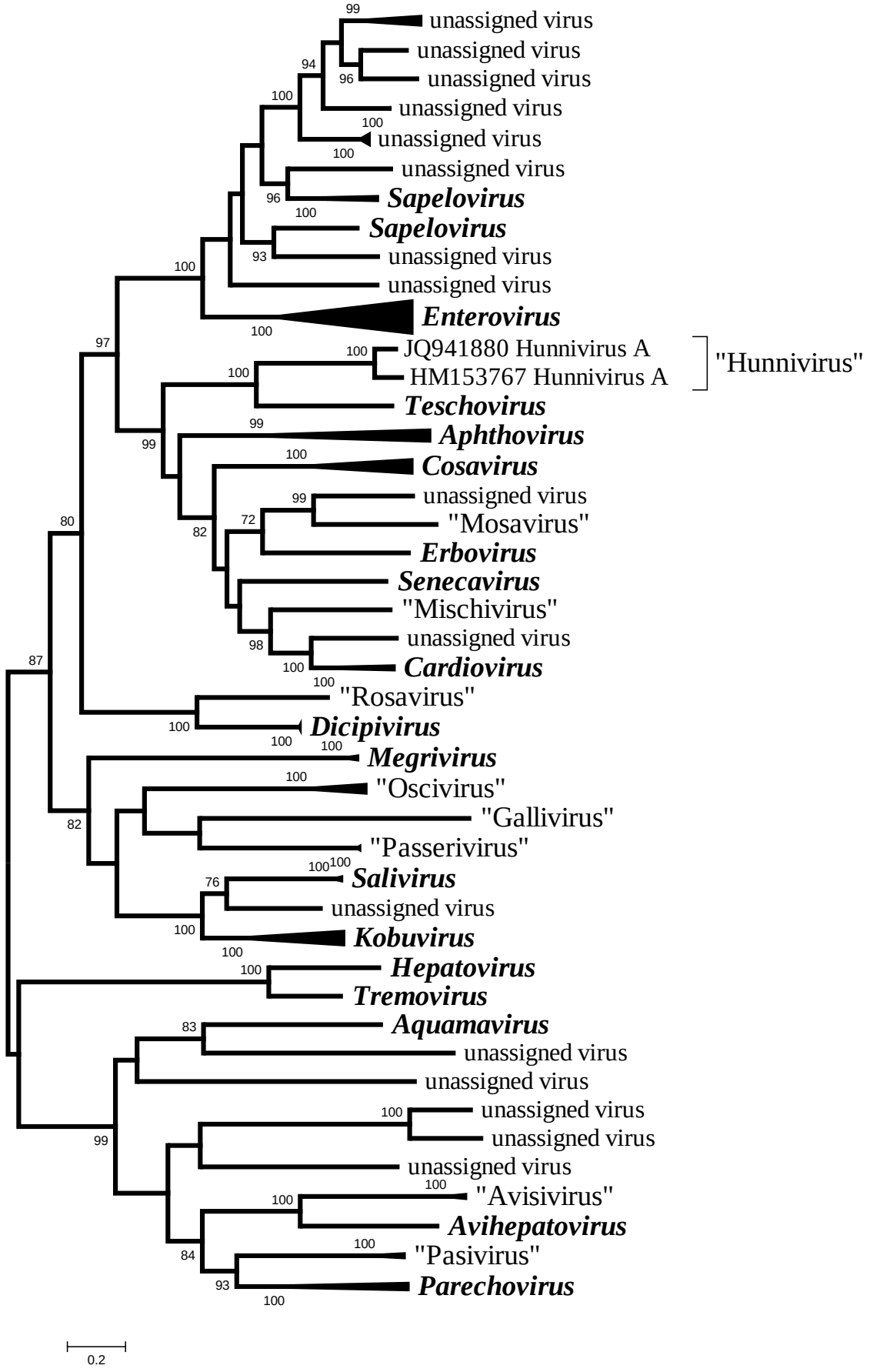

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

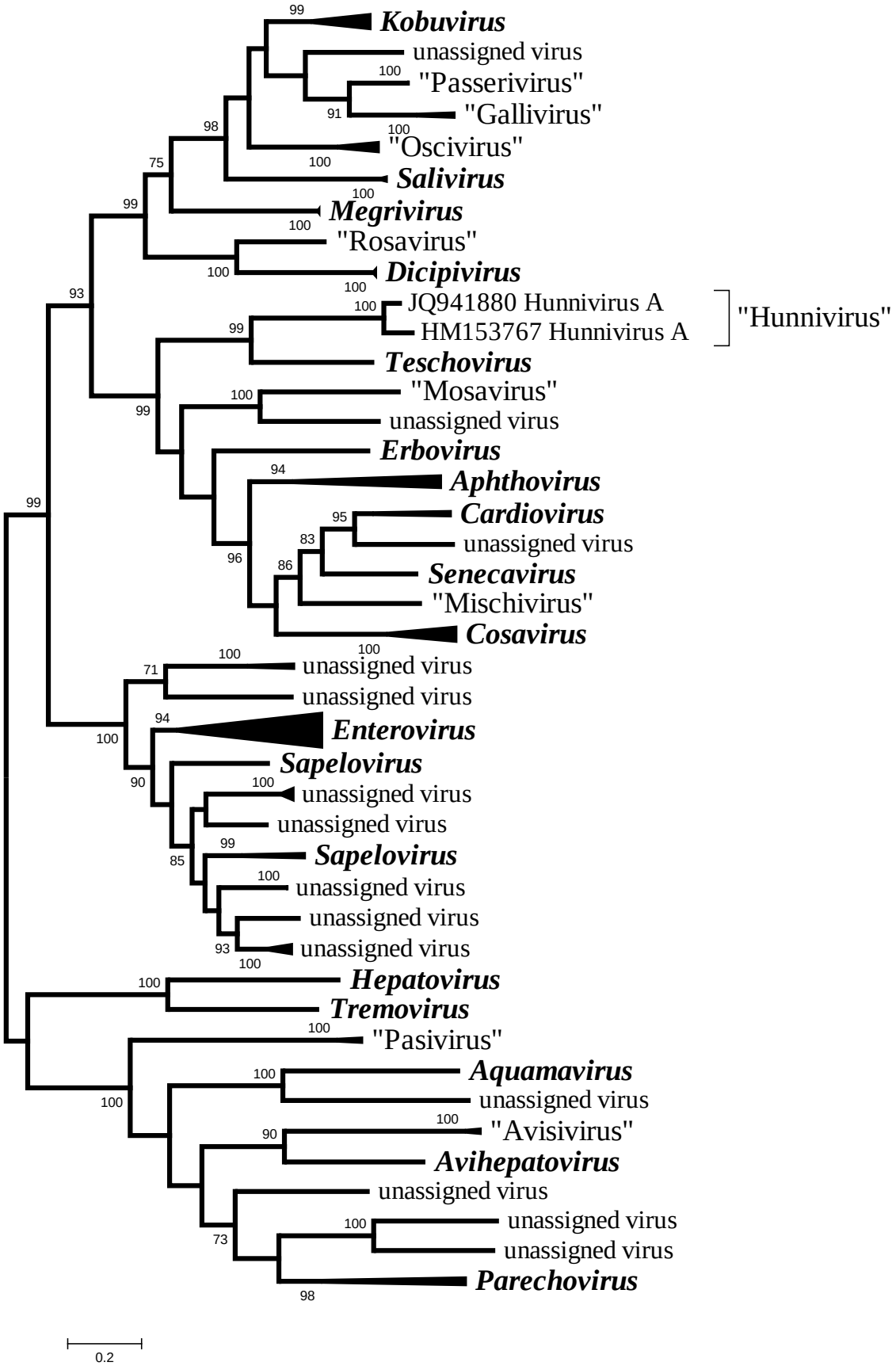

Figure 3. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.