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:	***2011.019a-dV***	(to be completed by ICTV officers)

Short title: create genus named *Megrivirus* in 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@iah.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: 22/08/2011
Date of this revision (if different to above): 01/07/2012

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	***2011.019aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Megrivirus*** (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:**
Melegrivirus A	HM751199, HQ189775

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 species, *Melegrivirus A*, would contain a single virus, turkey hepatitis virus (THV). The ~9-kb genome of THV has an organization similar to that of other picornaviruses with conservation of motifs within the P1, P2, and P3 genome regions, but also unique features, including a 1.2-kb sequence of unknown function at the junction of P1 and P2 regions. Real-time PCR confirmed viral RNA in liver, bile, intestine, serum and cloacal swab specimens from diseased turkey poults. Analysis of liver by in situ hybridization with viral probes and immunohistochemical testing of serum demonstrated viral nucleic acid and protein in livers of diseased poults. Molecular, anatomic, and immunologic evidence suggests that TVH is caused by a novel picornavirus, THV. Farkas et al., (2012) has also detected THV-like sequences in chickens. For this reason the originally proposed species name, *Turkey hepatitis virus*, has been changed to *Melegrivirus A*.

The THV genome layout is shown in Fig. 1. THV is distantly related to other picornaviruses (Figs. 2 and 3).

Melegrivirus from the host (turkey) genus name ***Mele**a**gri**s*.

MODULE 3: NEW GENUS

creating a new genus

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

Code	***2011.019bV***	(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	***2011.019cV***	(assigned by ICTV officers)

To name the new genus: *Megrivirus*

Assigning the type species and other species to a new genus

Code	***2011.019dV***	(assigned by ICTV officers)

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

Melegrivirus 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:**

one

Reasons to justify the creation of a new genus:

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

Members of a picornavirus genus should normally share phylogenetically related P1, P2 and P3 genome regions, each sharing >40%, >40% and >50% amino acid identity, respectively.

Sequence (aa) identities between turkey hepatitis virus and other picornaviruses are all lower than the cut-offs shown above. For example, the closest relationships can be found in 3CD (Table 1).

The insertion of approximately 1200 nt between recognizable 2A and 2B regions is a novel feature of this proposed genus.

Origin of the new genus name:

Megrivirus from the host (turkey) genus name ***Me***_lea_***gri***_s_.

Reasons to justify the choice of type species:

Only a single species has so far been identified.

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:

Farkas, T., Fey, B., Hargitt, E. 3rd., Parcells, M., Ladman, B., Murgia, M. and Saif, Y. (2012). Molecular detection of novel picornaviruses in chickens and turkeys. Virus Genes 44: 262-272.

Honkavuori, K.S., Shivaprasad, H.L., Briese, T., Street, C., Hirschberg, D.L, Hutchison, S.K. and Lipkin, W.I. (2011). Novel picornavirus in turkey poults with hepatitis, California, USA. Emerg. Infect. Dis. 17: 480-487.

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.

Table 1. Average percentage amino acid identities for turkey hepatitis virus versus other picornaviruses.

Genus	average aa% (3CD)
Aphthovirus	25.2
Avihepatovirus	22.3
Cardiovirus	28.1
Enterovirus	27.8
Erbovirus	24.9
Hepatovirus	21.7
Kobuvirus	36.4
Parechovirus	21.8
Sapelovirus	28.0
Senecavirus	28.7
Teschovirus	25.8
Tremovirus	20.9
"Aquamavirus"	19.9
"Cosavirus"	27.5
"Salivirus"	33.7

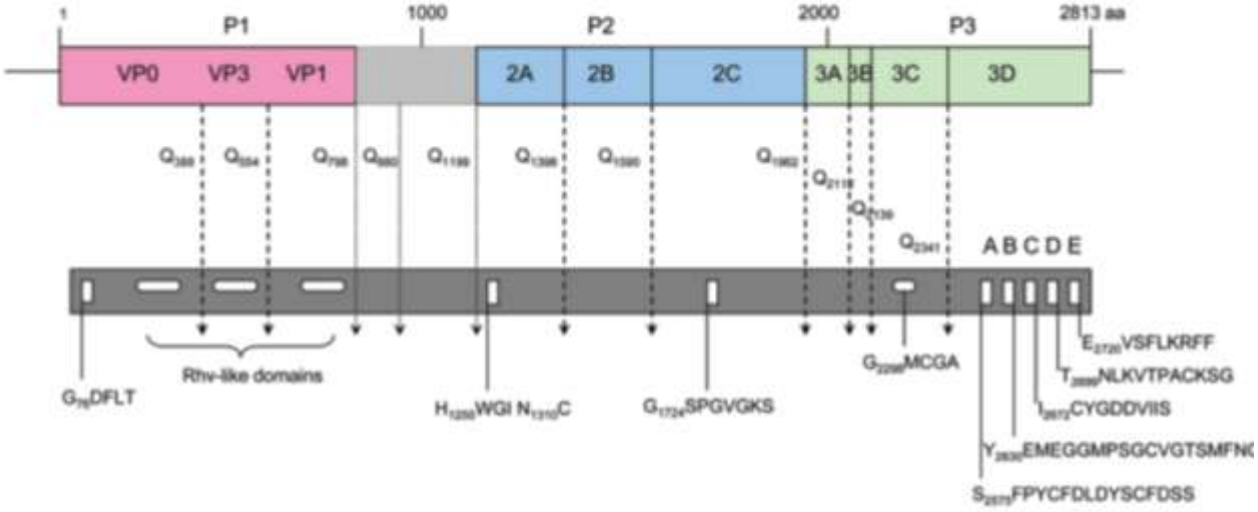

Fig. 1. Predicted turkey hepatitis virus (THV) genome organization based on sequence comparison to known picornaviruses. Conserved picornaviral motifs and predicted potential cleavage sites along the coding region are indicated in the bar below. Adapted from Honkavuori et al., 2011.

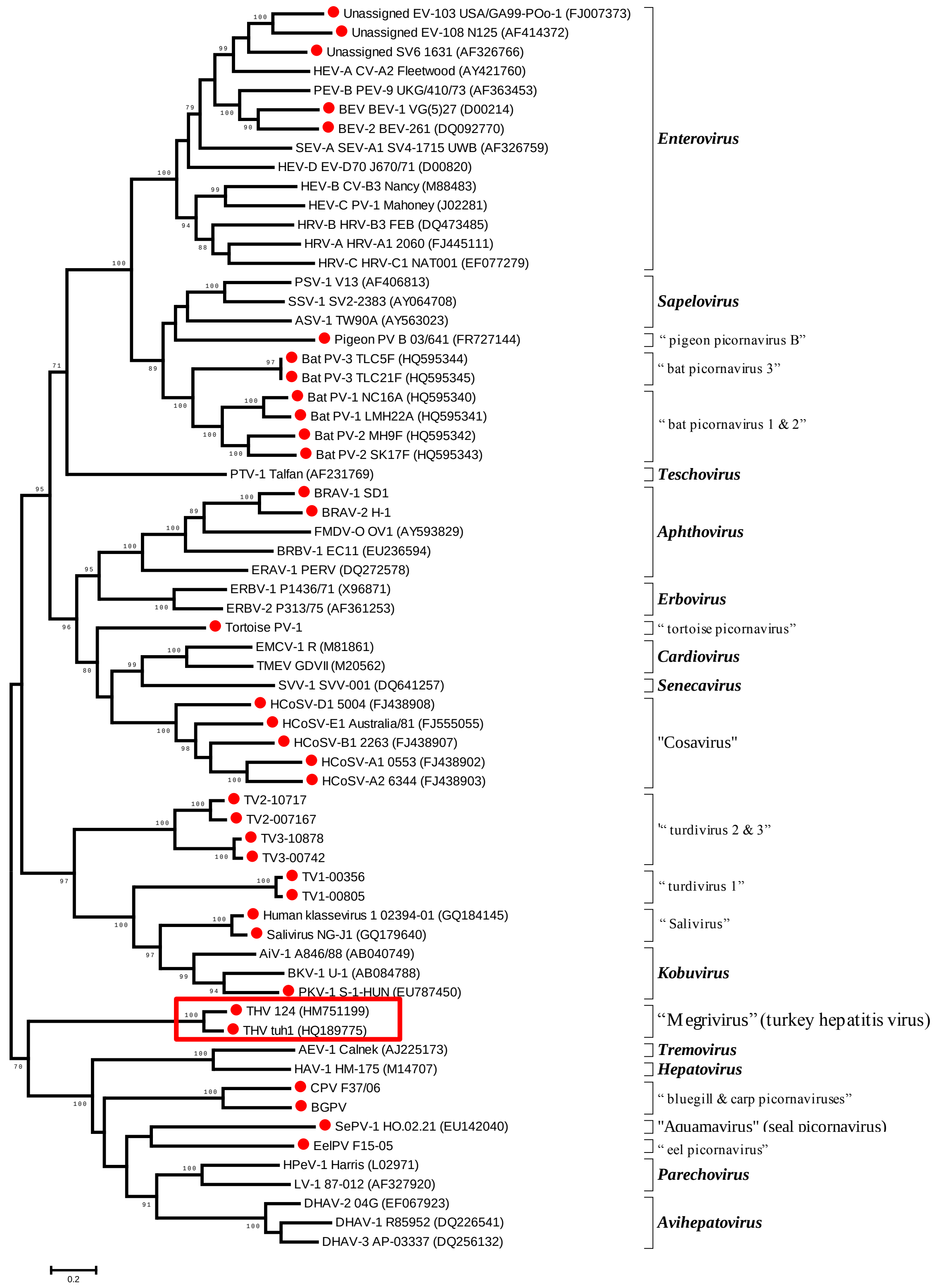

Fig. 2. Phylogenetic tree of the P1 capsids of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

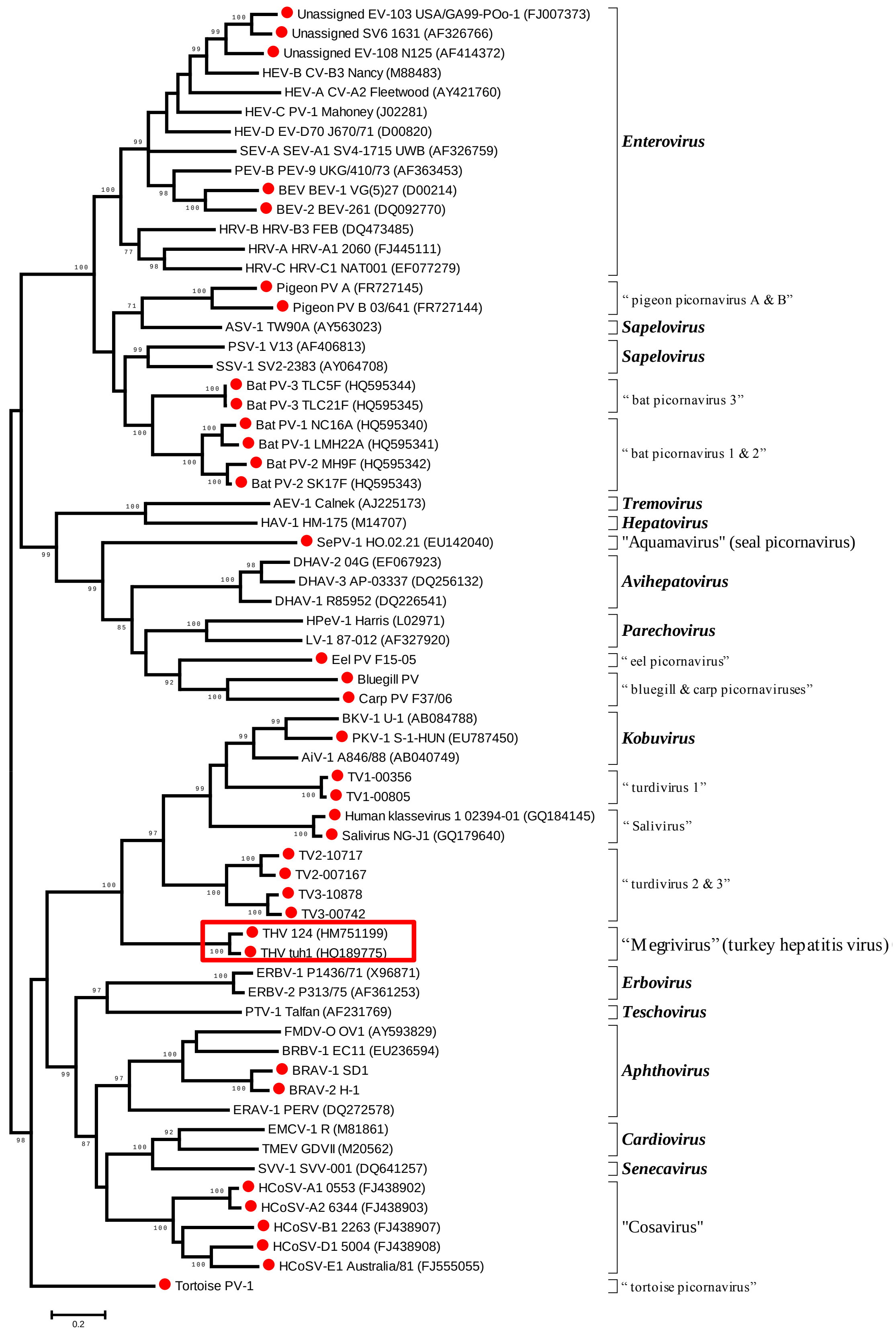

Fig. 3. Phylogenetic tree of the 3CD polypeptides of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.