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:	***2011.015a-dV***	(to be completed by ICTV officers)

Short title: create a new genus named *Aquamavirus* in the family *Picornaviridae*
(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:
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	***2011.015aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Aquamavirus*** (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:**
Aquamavirus A	EU142040

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 complete genome of a seal picornavirus (HO.02.21), isolated from Arctic ringed seals (*Phoca hispida*) in Canada, has been reported (EU142040; Kapoor et al., 2008). A second related genome sequence has also been reported from a virus isolated from harbour (common) seals (*Phoca vitulina*) in the North Sea (Knowles and Wadsworth, 2010). This virus was isolated from the lungs of 20 animals during the seal plaque epidemic in 1988 (Osterhaus, 1988). Both seal viruses grow in Vero cells and showing a CPE.

The genome layout of both viruses is identical and generally typical for a picornavirus, however, both viruses are predicted to possess two VPg coding regions (Fig. 1):

VPg+5'UTR$^{\text{IRES-IV}}$[1AB-1C-1D-2A$^{\text{npgp}}$/2A-2B-2C/3A-3B1$^{\text{VPg1}}$-3B2$^{\text{VPg2}}$-3C$^{\text{pro}}$-3D$^{\text{pol}}$]3'UTR-poly(A)

This is the only picornavirus (apart from foot-and-mouth disease virus) so far found which potentially has multiple genome-linked proteins.

The two seal picornaviruses are related across the whole genome (Fig. 2). Their 3D$^{\text{pol}}$ regions shared 87.2% nt and 98.6% amino acid (aa) identity while their VP1 regions shared 81.2% nt and 99.6% aa identity. This suggests that, not only do both seal picornaviruses belong to the same virus species, but also to the same antigenic type. The harbour seal's range is limited to temperate and Arctic marine coastlines of the Northern hemisphere. They are found in coastal waters of the northern Atlantic and Pacific Oceans as well as those of the Baltic and North Seas, making them the most wide-ranging of the pinnipeds. The range of ringed seal's is throughout the Arctic Ocean including the Baltic Sea, the Bering Sea and the Hudson Bay. The ranges of the two seal species overlap in the coastal waters of Scandinavia. The close relationship between these two viruses suggests picornaviruses may circulate between different seal species.

The seal picornaviruses are phylogenetically distinct from all other picornaviruses (Figs. 3 and 4).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2011.015bV***	(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	***2011.015cV***	(assigned by ICTV officers)

To name the new genus: *Aquamavirus*

Assigning the type species and other species to a new genus

Code	***2011.015dV***	(assigned by ICTV officers)

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

Aquamavirus 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

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 the seal picornavirus and other picornaviruses are all lower than 30% (Table 1). The seal picornavirus is uniquely predicted to possess two VPg's.

The seal picornaviruses are phylogenetically distinct from all other picornaviruses in homologous genome regions (Figs. 3 and 4).

Origin of the new genus name:

Aquamavirus from Aquatic mammal virus

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.

Only a single species has been found.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Kapoor, A., Victoria, J., Simmonds, P., Wang, C., Shafer, R.W., Nims, R., Nielsen, O. and Delwart, E. (2008). A highly divergent picornavirus in a marine mammal. J. Virol. 82: 311-320.

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.

Knowles, N.J. and Wadsworth, J. (2010). The complete genome sequence of a picornavirus isolated from a harbour (common) seal (*Phoca vitulina*). EUROPIC 2010: XVI Meeting of the European Study Group on the Molecular Biology of Picornaviruses, St. Andrews, Scotland, 11-16 September 2010. Abstract H16, p. 148.

Osterhaus, A.D.M.E. (1988). Seal death. Nature, Lond. 334: 301-302.

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. Pairwise amino acid sequence identities between SePV-1 and other picornavirus genera in the P1 and 3D regions[a]

	% Sequence identity with:											
Virus	SePV-1	*Parechovirus*	*Avihepatovirus*	*Aphthovirus*	*Cardiovirus*	*Erbovirus*	*Teschovirus*	*Senecavirus*	*Enterovirus*	*Sapelovirus*	*Hepatovirus*	*Kobuvirus*
P1 region												
Parechovirus	**25.6**	*61.1*										
Avihepatovirus	**24.3**	28.9	*78.3*									
Aphthovirus	**11.6**	12.1	12.4	*61.8*								
Cardiovirus	**9.3**	12.2	12.5	25.9	*70.7*							
Erbovirus	**10.3**	12.3	12.6	30.2	31.5	*73.5*						
Teschovirus	**9.4**	11.5	11.8	20	23.4	21.6	*79.6*					
Senecavirus	**10.6**	11.8	10.7	25.2	31.9	29.4	20.2	*NA*				
Enterovirus	**11**	10.9	12.3	18.9	20.1	21	17.6	19.8	*54.2*			
Sapelovirus	**10.5**	11.5	12.4	19.8	21.2	22.3	18.7	21.1	34.8	*49.1*		
Hepatovirus	**12.4**	12.2	11	13.9	14.2	14.1	13	13.4	15.5	13.4	*69.9*	
Kobuvirus	**12**	12.7	12.5	15.5	18	18.4	14.8	17.6	16.9	16.1	12.8	*63.7*
3D region												
Parechovirus	**29.3**	*64.2*										
Avihepatovirus	**30**	35.2	*97.9*									
Aphthovirus	**20.5**	20.5	20.3	*83*								
Cardiovirus	**21.6**	21.6	20.3	40.5	*72.6*							
Erbovirus	**19.7**	21.4	18.7	35.2	39.8	*96.3*						
Teschovirus	**19.7**	21.5	23.5	33.8	36.1	36.5	*97.2*					
Senecavirus	**23.4**	22.3	21.7	43.6	55.7	37.6	38.1	*NA*				
Enterovirus	**21.5**	23.8	22.9	27.7	28.7	28.3	30.5	28.7	*73.1*			
Sapelovirus	**22.1**	24.2	23.8	29.2	28.7	29	32.5	29	53.5	*61*		
Hepatovirus	**19.3**	21.6	20.1	20.8	22	19.5	22.2	22.2	23.8	24.5	*62.4*	
Kobuvirus	**20.1**	22.2	18.7	31.8	31.2	30.3	28.2	29.8	32	33.8	22.7	*80.7*

[a] Boldface type, averages of pairwise amino acid sequence identities between SePV-1 and members of different picornavius genera. Italics, averages of pairwise amino acid sequence identities between members of the same picornavirus genus. NA, not applicable. (From Kapoor et al., 2008).

```
RSPV (VPg-1)  SAYEGCSTRKTARQLARSVVG-E-
HSPV (VPg-1)  SAYEGTAARRTARQLARSAVG-E-
RSPV (VPg-2)  GAYDGNVKRTTARELARKAIPSEQ
HSPV (VPg-2)  SAYSGEIKRTTARELARRAVPTEQ
```

Fig. 1. Predicted amino acid sequences of the two putative VPg's. Black background, conserved residues between both viruses and both VPg's. Grey background, conserved residues between both viruses for each VPg. RSPV = ringed seal picornavirus, HSPV = harbour seal

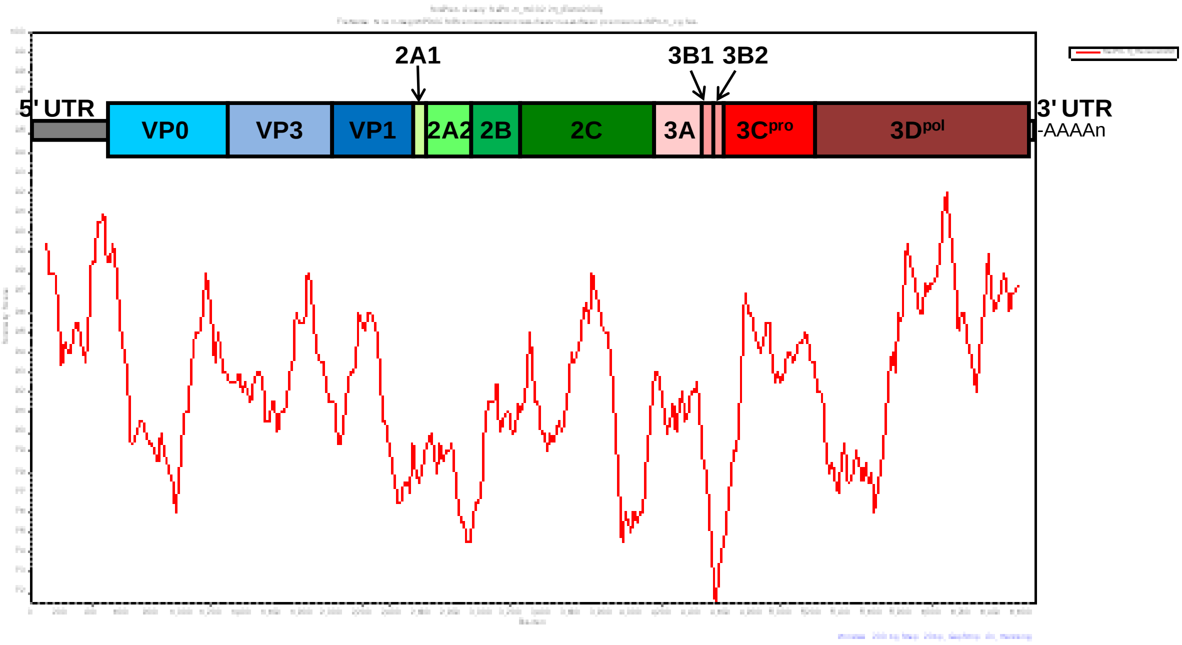

Fig. 2. SimPlot comparison between the complete genome sequences of the two seal picornaviruses. The genome layout is also shown.

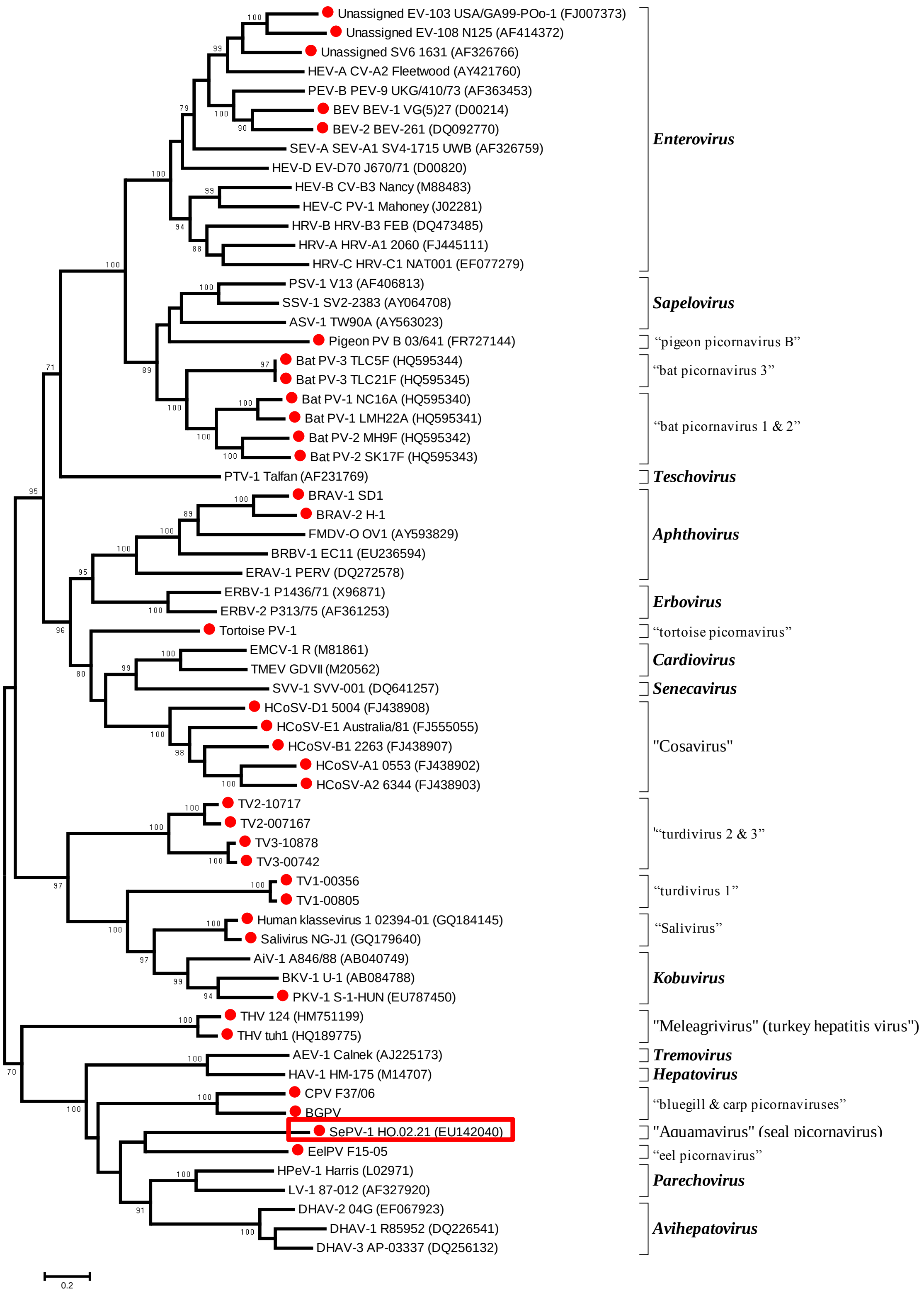

Figure 3. Phylogenetic tree of the P1 capsids of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

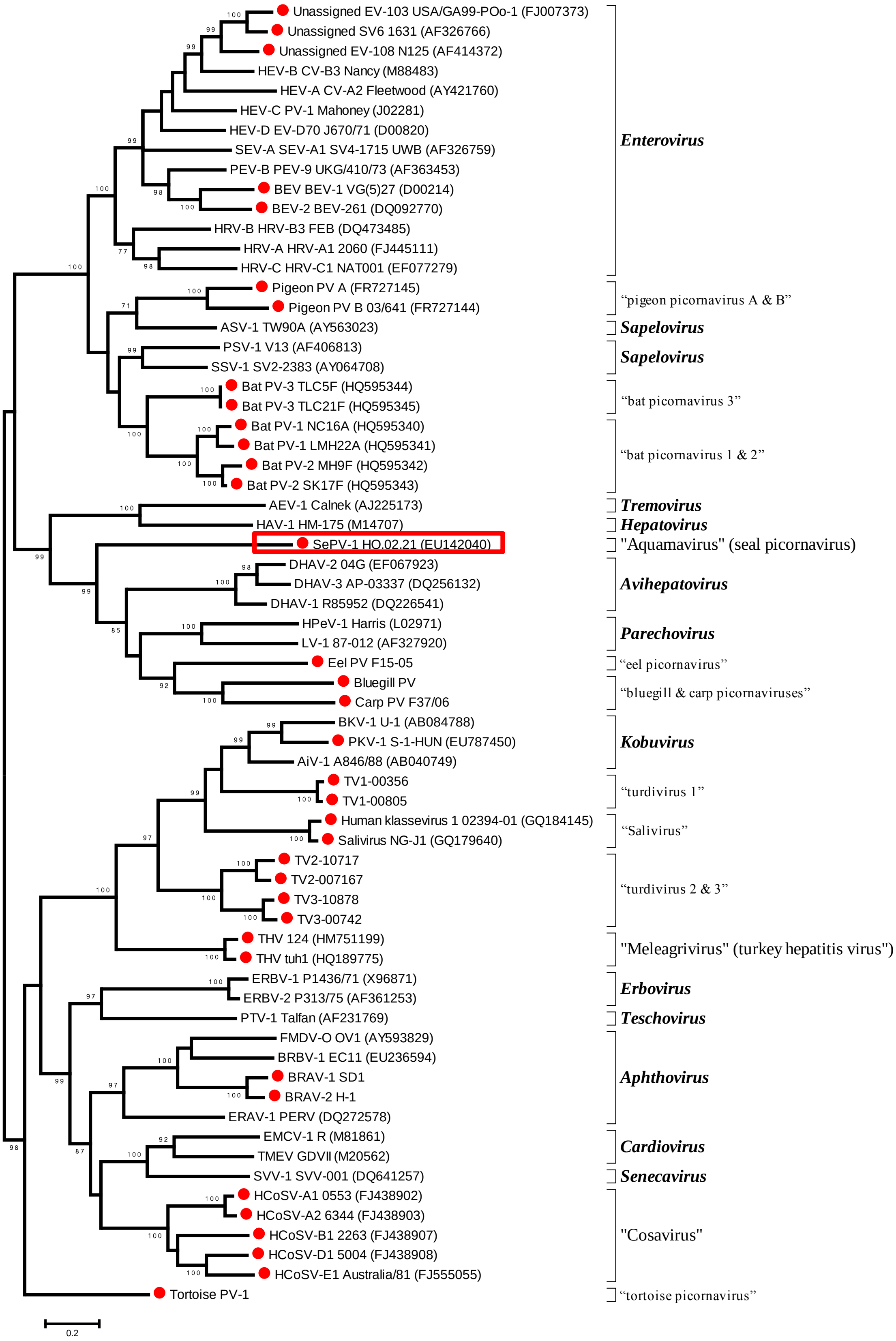

Figure 4. Phylogenetic tree of the 3CD polypeptides of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.