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:	***2011.020aV***	(to be completed by ICTV officers)

Short title: create species *Aichivirus C* in the genus *Kobuvirus*, 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:

The ICTV EC (at EC43) asked that the originally proposed species name (*Porcine kobuvirus*) be reconsidered to remove reference to the host.

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	***2011.020aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Kobuvirus***
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:**
Aichivirus C	EU787450

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 *Aichivirus C* would contain a single virus commonly called porcine kobuvirus 1 (PKV-1) (Reuter et al., 2008, 2009; Yu et al., 2009, 2011). PKV-1 has, so far, only been found in pigs although related 3Dpol sequences have been found in Korean black goats (Lee et al., 2012).

The genome organization of PKV-1 is:

$\text{VPg+5'UTR}^{\text{IRES-IV}}\text{[L/VP0-VP3-VP1/2A}^{\text{H-Box/NC}}\text{-2B-2C/3A-3B}^{\text{VPg}}\text{-3C}^{\text{pro}}\text{-3D}^{\text{pol}}\text{]3'UTR-poly(A)}$

Porcine kobuvirus 1 is most closely related to, but distinct from bovine kobuvirus 1 (Figs. 1-3).

There are two major differences in genome organization between PKV-1 and the other kobuviruses; 1) PKV-1 possesses a type IV IRES (Hellen and de Breyne, 2007; Reuter et al., 2009), while Aichi virus 1 and bovine kobuvirus 1 have a type V IRES (Yu et al., 2011; Sweeney et al., 2012); 2) within the 2B region, PKV-1 encodes two copies of a 30-amino-acid (90-nucleotide)-long motif, AANRVAESIETTAS(/T)V(/A)VREADLARSTLNISM, one after the other (in tandem), which extends the 2B region (to 585 instead of 495 nucleotide in bovine kobuvirus or Aichi virus).

Species criteria

According to the 9th ICTV Report, members of kobuvirus species share:

greater than 70% aa identity in the polyprotein
greater than 70% aa identity in P1
greater than 80% aa identity in 2C + 3CD
share a common genome organization

Genetic distances between PKV-1 and other two kobuvirus species (*Aichi virus* and *Bovine kobuvirus* are: polyprotein, 56% and 64%; P1 capsid, 54.9% and 63.1%; 2C, 68% and 77%; 3C, 53% and 63%; and 3D, 70% and 81% (each respectively), thus meeting the above criteria.

A separate taxonomic proposal has been submitted to rename the species *Aichi virus* and *Bovine kobuvirus* as *Aichivirus A* and *Aichivirus B*, respectively, to remove host names and make the naming of kobuvirus species more consistent.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Hellen, C.U. and de Breyne, S. (2007). A distinct group of hepacivirus/pestivirus-like internal ribosomal entry sites in members of diverse picornavirus genera: evidence for modular exchange of functional noncoding RNA elements by recombination. J Virol. 81: 5850-5863.

Lee, M.H., Jeoung, H.Y., Lim, J.A., Song, J.Y., Song, D.S. and An, D.J. (2012). Kobuvirus in South Korean black goats. Virus Genes. 2012 Apr 12. [Epub ahead of print]

Park, S.J., Kim, H.K., Moon, H.J., Song, D.S., Rho, S.M., Han, J.Y., Nguyen, V.G. and Park, B.K. (2010). Molecular detection of porcine kobuviruses in pigs in Korea and their association with diarrhea. Arch. Virol. 155: 1803-1811.

Reuter, G., Boldizsár, Á., Kiss, I. and Pankovics, P. (2008). Candidate new species of kobuvirus in porcine hosts [letter]. Emerg. Infect. Dis. 14: 1968-1970. doi: 10.3201/eid1412.080797.

Reuter, G., Boldizsár, A. and Pankovics, P. (2009). Complete nucleotide and amino acid sequences and genetic organization of porcine kobuvirus, a member of a new species in the genus *Kobuvirus*, family *Picornaviridae*. Arch Virol. 154: 101-108. 2008 Dec 19. [Epub ahead of print]; doi: 10.1007/s00705-008-0288-2.

Sweeney, T.R., Dhote, V., Yu, Y. and Hellen, C.U. (2012). A distinct class of internal ribosomal entry site in members of the *Kobuvirus* and proposed Salivirus and Paraturdivirus genera of the *Picornaviridae*. J. Virol. 86: 1468-1486.

Yu, J.-M., Jin, M., Zhang, Q., Li, H.-Y., Li, D.-D., Xu, Z.-Q., Li, J.-S., Cui, S.-X., Yang, S.-H., Liu, N. and Duan, Z.-J. (2009). Candidate porcine kobuvirus, China. Emerg. Infect. Dis. 15: 823-825.

Yu, J.-M., Xu, Z.-Q., Li, B.W., Zhang, Q., Cui, S.-X., Jin, M. and Duan, Z.-J. (2011). Analysis and characterization of the complete genome of a member of a new species of kobuvirus associated with swine. Arch Virol. 156: 747-751. 2011 Jan 28. [Epub ahead of print].

Yu, Y., Sweeney, T.R,, Kafasla, P., Jackson, R.J., Pestova, T.V, and Hellen, C.U. (2011). The mechanism of translation initiation on Aichivirus RNA mediated by a novel type of picornavirus IRES. EMBO J. 30: 4423-4436.

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.

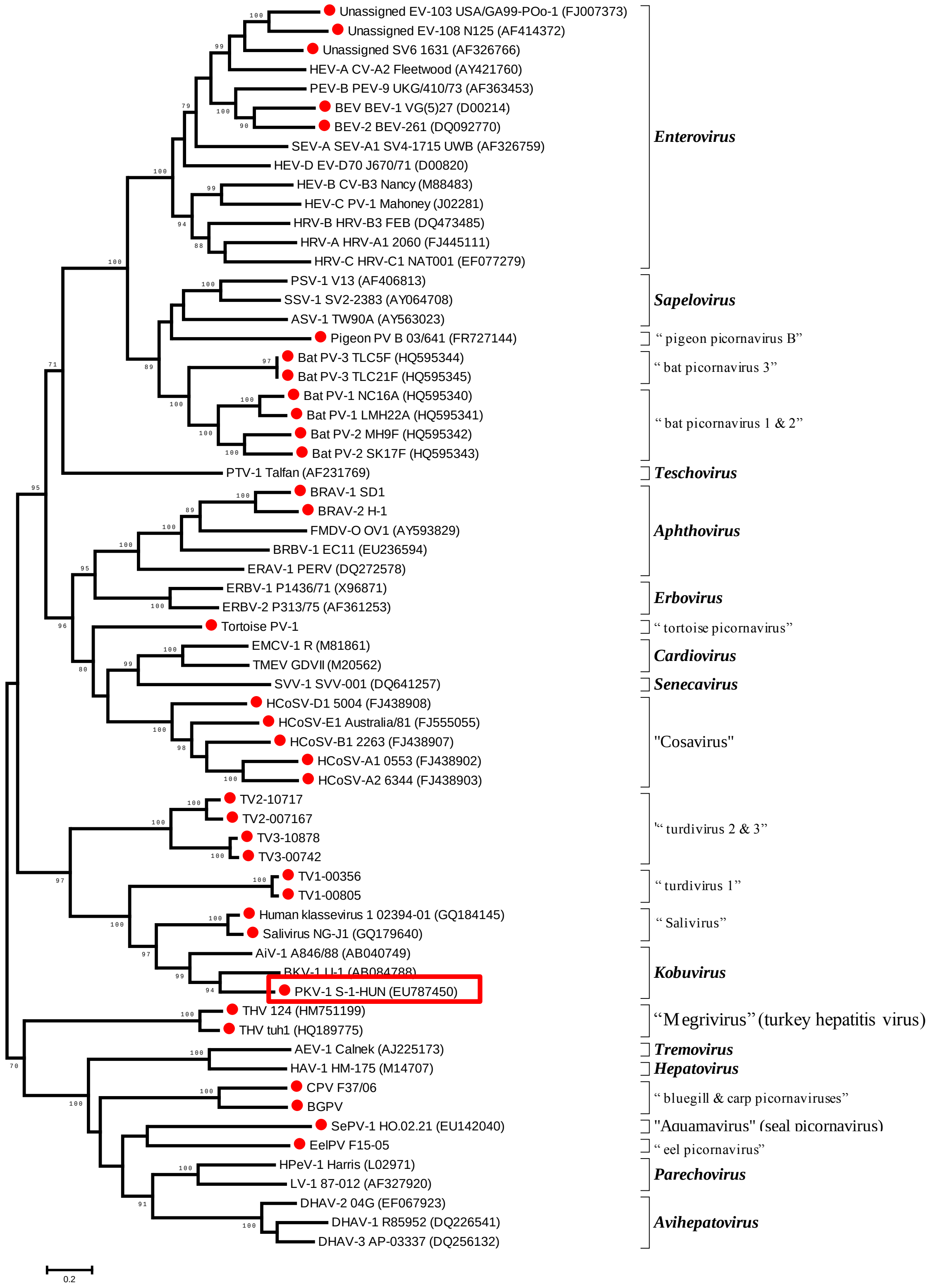


Fig. 1. Phylogenetic tree of the P1 capsids of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

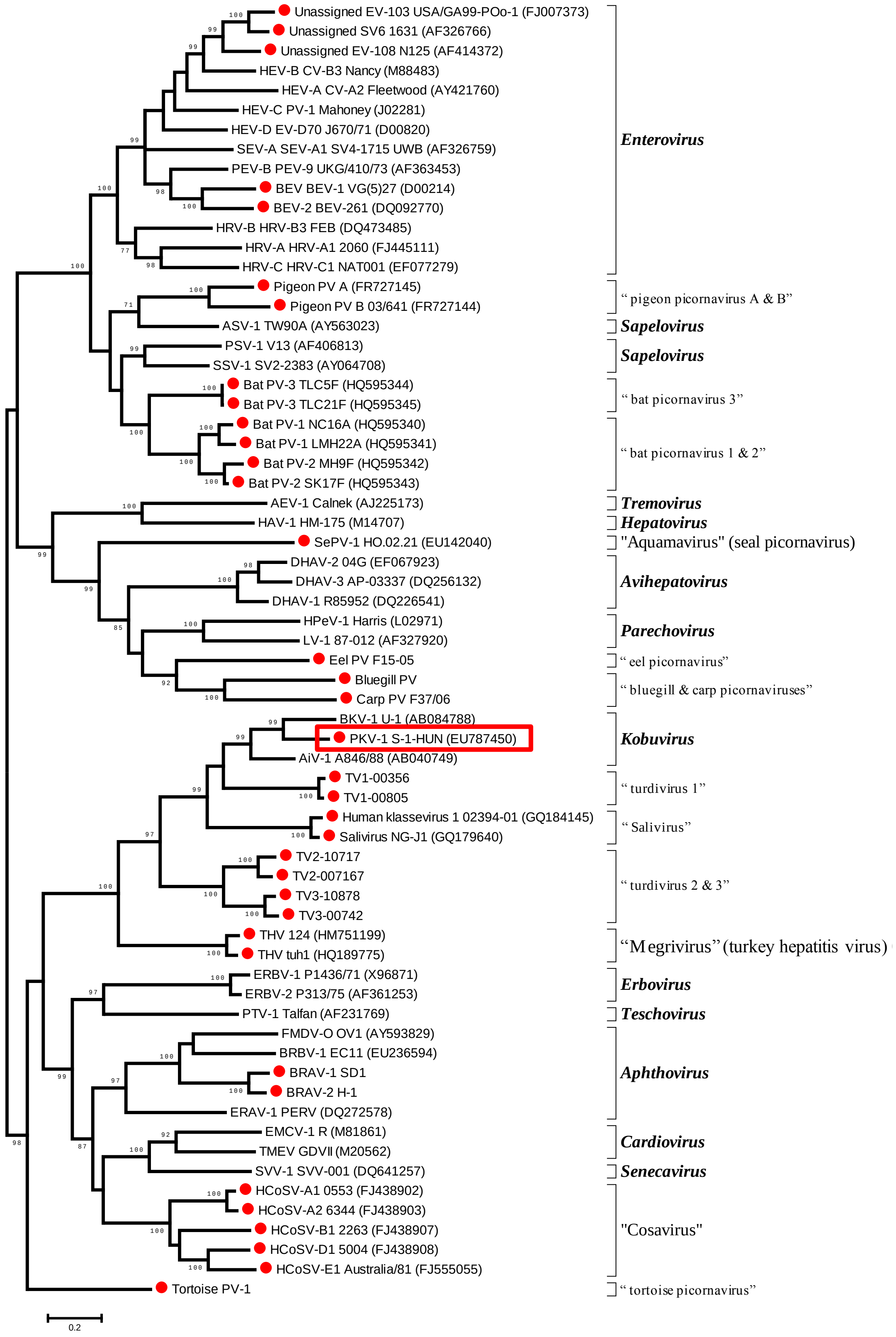
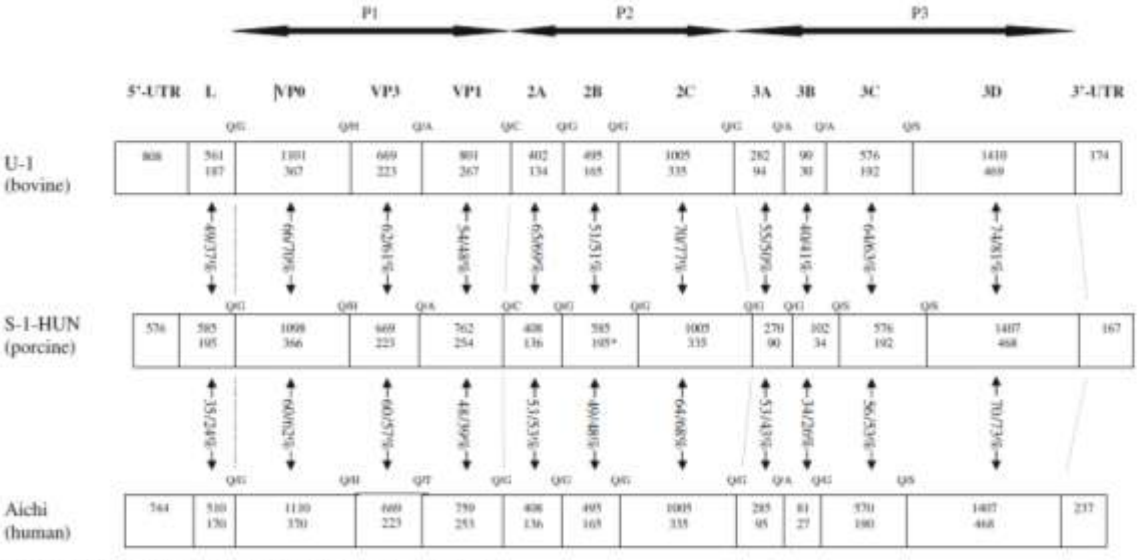


Fig. 2. Phylogenetic tree of the 3CD polypeptides of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.



* two copies of a 30-amino-acid (90 nucleotides) long tandem repeat in 2B region

Fig. 3 Genome organization of porcine kobuvirus S-1-HUN and comparison of the structure among human (Aichi) and bovine (U-1) kobuviruses. P1 represents viral structural proteins and P2 and P3 represent nonstructural proteins. Nucleotide (upper number) and amino acid (lower number) lengths are indicated in each gene box. Nucleotide and amino acid identity between S-1-HUN and members of the two other species of kobuviruses are indicated in percentage (nucleotide/amino acid %) in each gene. Predicted N-terminal cleavage sites are indicated at the top of the border in each gene box. (From Reuter et al., 2009).