



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:	2016.007a-dS	(to be completed by ICTV officers)
Short title: Create 1 new species (<i>Ampivirus A</i>) in a new genus (<i>Ampivirus</i>) (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	2 <input checked="" type="checkbox"/> 3 <input checked="" type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/> 11 <input checked="" type="checkbox"/>	

Author(s):

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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 Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

15/06/2016

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	2016.007aS	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Ampivirus</i> (new)	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.
Subfamily:		
Family:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Ampivirus A</i>	newt picornavirus [newt/2013/HUN]	KP770140

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 11

A novel picornavirus was detected in faecal samples of the smooth newt (*Lissotriton vulgaris*) in Hungary. Virus isolates are not available. The sequence exhibits significant similarity to picornaviruses and a 3-3-4 picornavirus genome layout (compare Figure 1):

VPg+5'UTR[1AB-1C-1D/2A-2B-2C^{Hel}/3A-3B^{VPg}-3C^{Prot}-3D^{Pol}]3'UTR-poly(A)

Ampivirus proteins P1, 2C and 3CD show only very low amino acid similarities with the orthologous proteins of other picornaviruses.

Alignments reveal amino acid identities ranging from:

P1: 11.1-16.0%,

2C^{Hel}: 15.2-22.0%,

3D^{Pol}: 17.0-24.4%.

Further typical picornavirus features of the ampivirus polyprotein sequence are:

- two rhv-like domains (Pfam database) corresponding to VP0, VP3
- NTP-binding motif of 2C^{Hel} (**G₁₄₄₇DSQCGKT**, Walker A motif, and a **D₁₄₉₉DLLQ** motif)
- putative 3C proteinase catalytic triad (**H₁₉₆₁, D₂₀₂₅, D₂₀₈₉ICG**)
- RNA-dependent RNA polymerase motifs (**K₂₃₅₁DEL**R, **G₂₄₉₄LPSG**, **L₂₅₃₉GDD**, **F₂₅₉₈LKS**)

Phylogenetic trees comprising reference sequences of the order *Picornavirales* indicate that ampivirus clusters at the root of the picornavirus branch (compare Figure 2; Appendix). Figures 3, 4 (Appendix) show phylogenetic trees of the picornavirus P1 and 3CD proteins.

MODULE 3: NEW GENUS

creating a new genus

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

Code	2016.007bS	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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
Family:	Picornaviridae	
Order:	Picornavirales	

naming a new genus

Code	2016.007cS	(assigned by ICTV officers)
To name the new genus: <i>Ampivirus</i>		

Assigning the type species and other species to a new genus

Code	2016.007dS	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Ampivirus A</i>		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 11

Ampivirus is the most divergent picornavirus presently known (Figures 2, 4; Appendix). It has only little sequence similarity to the other picornaviruses. It is the first picornavirus with a capsid protein (VP1) that has similarity to the CRPV capsid superfamily (Pfam database) of the dicistroviruses, iflaviruses, marnaviruses and some diatom viruses (labrynavirus, bacillarnavirus) (Figure 1; Appendix). Other unique features of *Ampivirus* are rather large 3C^{Pro} and 3D^{Pol} proteins.

Origin of the new genus name:

Ampivirus: from amphibian picornavirus

Reasons to justify the choice of type species:

only a single species

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

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Reuter G, Boros A, Toth Z, Phan TG, Delwart E, Pankovics P. 2015. A highly divergent picornavirus in an amphibian, the smooth newt (*Lissotriton vulgaris*). J Gen Virol 96:2607-2613.

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.

Genome organization:

Fig. 1 *Ampivirus A1* (KP770140)

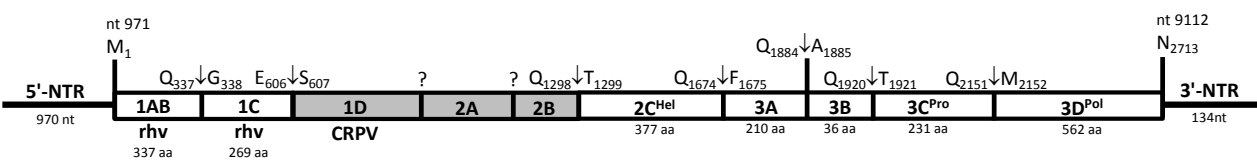


Figure 1: Schematic depiction of the *Ampivirus* genome organization. The open reading frames are indicated by boxes. Positions of putative aa cleavage sites and the lengths of the deduced proteins are shown as proposed by Reuter et al. (2015). Arrows (↓) indicate the putative 3C^{pro} processing sites, whereas question marks (?) hint at two unknown cleavage sites. The sizes of the respective proteins (shaded gray) is unclear. Rhv and CRPV domains proposed by the Pfam database are also indicated

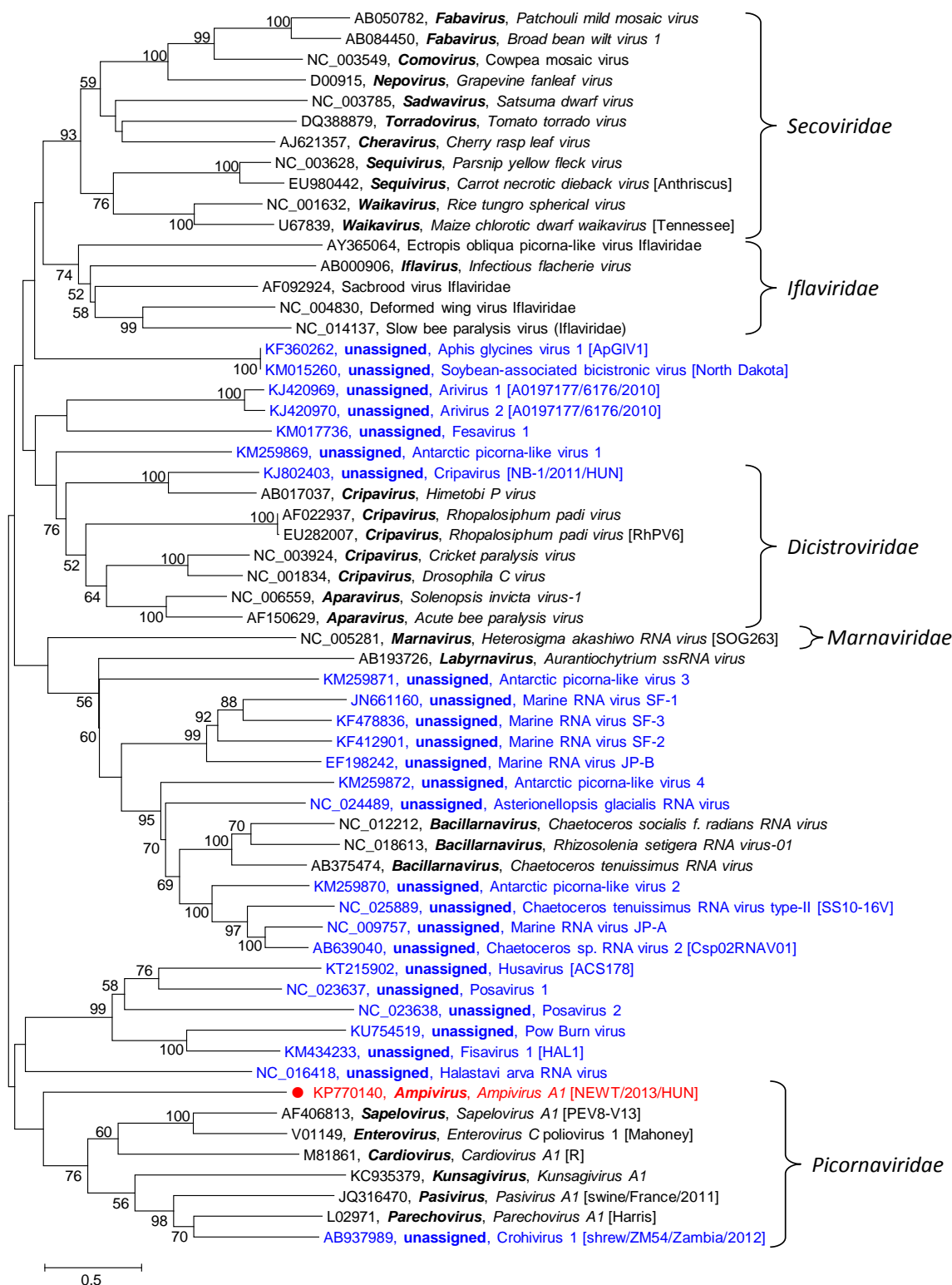


Figure 2: Phylogenetic analyses of the 3CD protein of representative members of the *Picornavirales* using maximum likelihood tree inference (MEGA 5.2). 60 sequences were retrieved from GenBank. Presented are GenBank accession numbers, **genus names**, *species names* and *types*. If available, designations of isolates [in square brackets] are given. Yet unassigned viruses are printed in blue. Proposed *Ampivirus* is printed in red and indicated by a dot (●). Numbers at nodes indicate bootstrap values obtained after 200 replications. The optimal substitution model (GTR+G+I) was determined with MEGA 5.2. The scale indicates substitutions/site.

P1

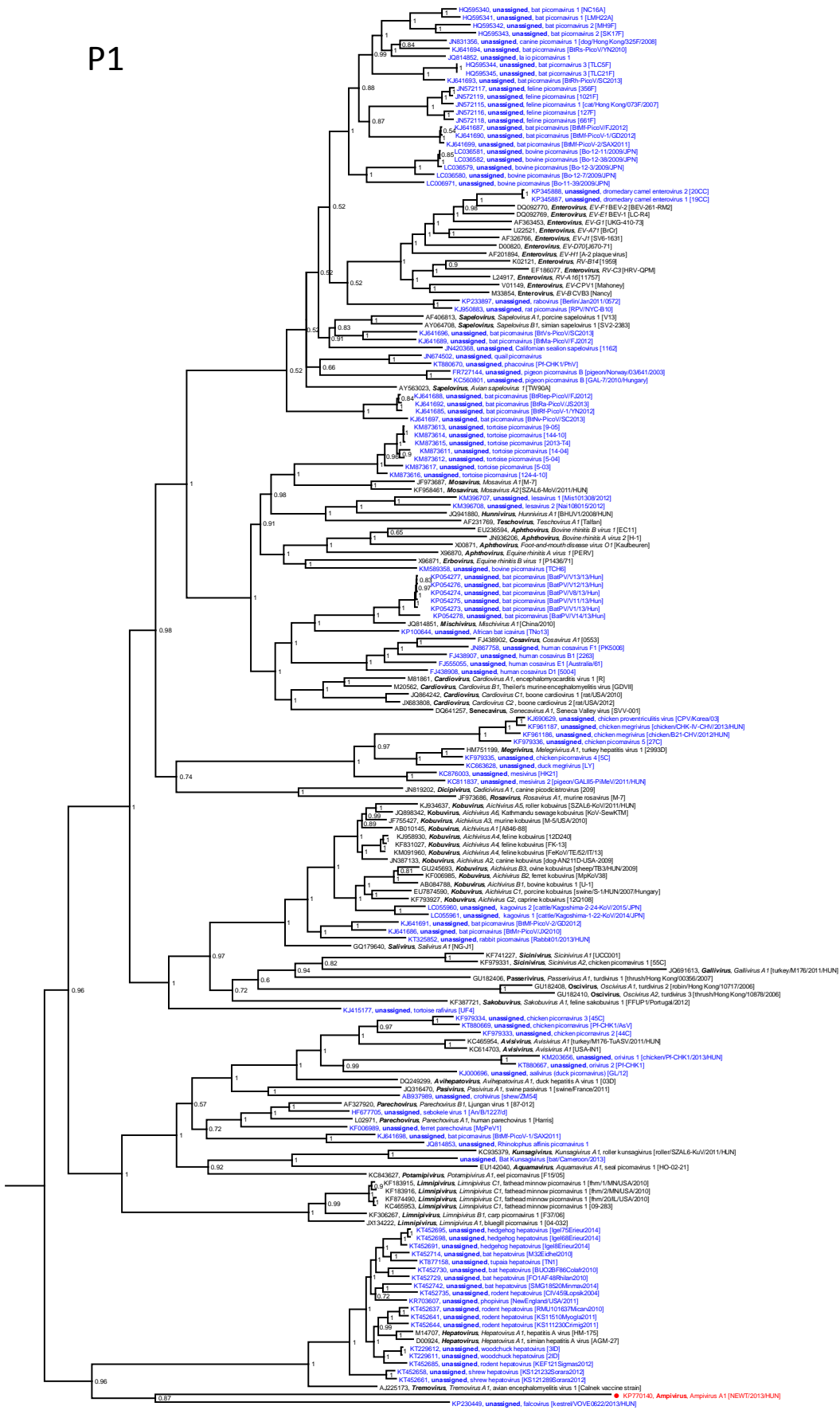


Figure 3 (previous page): Phylogenetic analyses of picornavirus P1 using Bayesian tree inference (MrBayes 3.2). 178 picornavirus sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square brackets] are given. Yet unassigned viruses are printed in blue. Proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 6,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

3CD

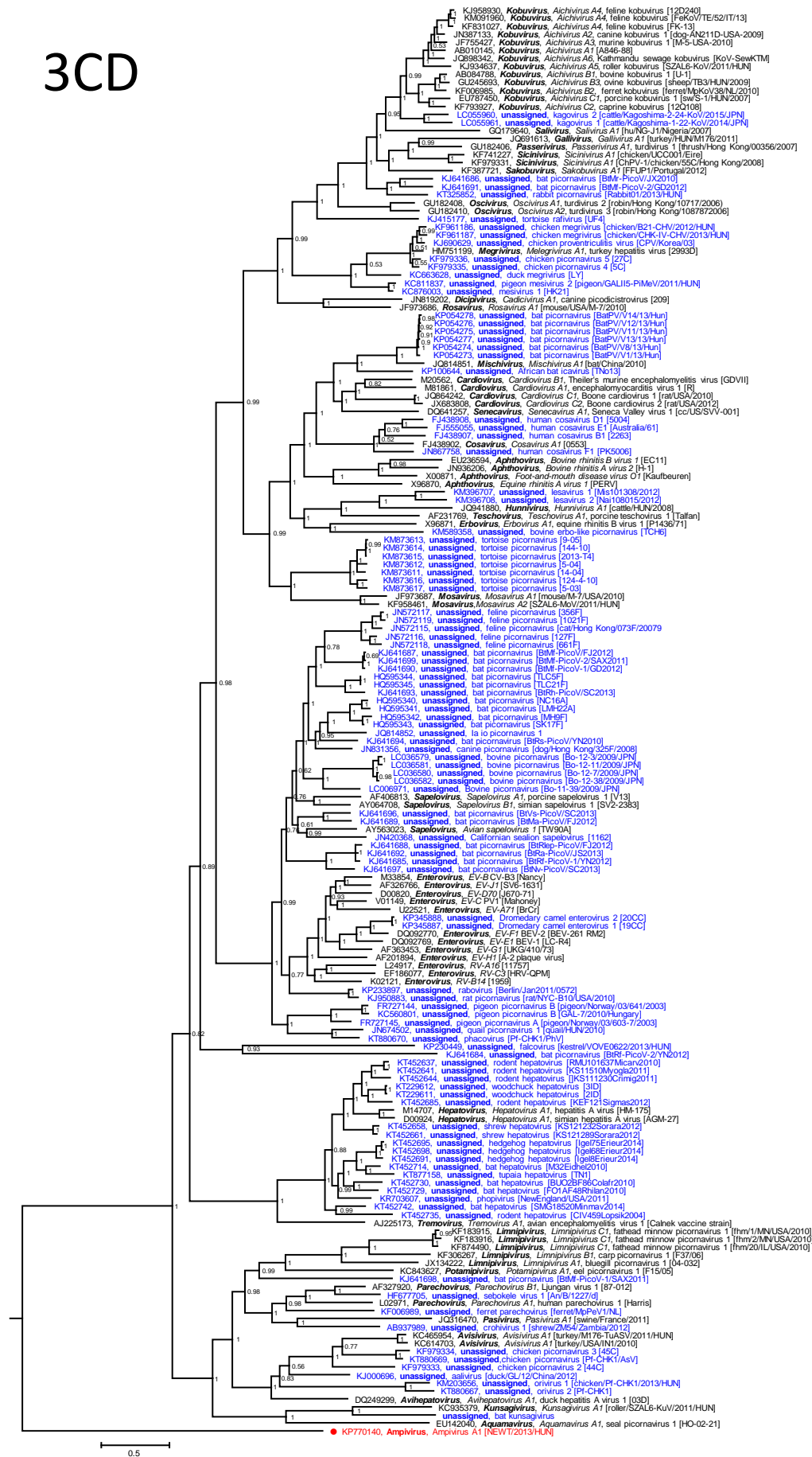


Figure 4 (previous page): Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square brackets] are given. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,750,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.
