



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:	2011.017a-dV	(to be completed by ICTV officers)			
Short title: create a new genus named <i>Cosavirus</i> in the family <i>Picornaviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input checked="" type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

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	2011.017aV	(assigned by ICTV officers)
To create one new species within:		
Genus:	<i>Cosavirus</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:	n/a	
Family:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Cosavirus A</i>		FJ438902 to 6, GU968209

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

Cosavirus is a newly described candidate picornavirus genus consisting of viruses originally identified in the stools of south Asian children (Kapoor et al., 2008). The authors suggest, by comparison with human enteroviruses, that there may be four distinct human cosavirus (HCoSV) species, which they name HCoSV-A to -D. Cosaviruses are most closely related to members of the *Cardiovirus* and *Senecavirus* genera, but they lack a leader polypeptide. They possess a 2A NPG↓P motif, which may or may not be cleaved from VP1. An unusually long (1,164 nt) 5' UTR contains a type II IRES (similar to cardioviruses and aphthoviruses). A fifth candidate human cosavirus species (designated HCoSV-E) has recently been described (Holtz et al., 2008).

Cosaviruses share a common genome layout:

VPg+5'UTR^{IRES-II}[VP4-VP2-VP3-VP1-2A^{np9p}/2B-2C/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3'UTR-poly(A)

The other cosaviruses which have been suggested to be distinct species (HCoSV-B to E) will be designated as unassigned viruses in the genus until suitable species-defining criteria have been established.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	2011.017bV	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	n/a	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:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	

naming a new genus

Code	2011.017cV	(assigned by ICTV officers)
To name the new genus: <i>Cosavirus</i>		

Assigning the type species and other species to a new genus

Code	2011.017dV	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Cosavirus 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:		
<i>1</i>		

Reasons to justify the creation of a new genus:

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

Cosaviruses form a monophyletic group distinct from other picornaviruses (Figs. 1 and 2) and differ from closely related viruses (*Cardiovirus* and *Senecavirus*) principally by genetic distance and the lack of a leader polypeptide.

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 cosaviruses and other picornaviruses are all lower than 35% in P1 and lower than 50% in 3D (Table 1).

Origin of the new genus name:

Cosavirus is from common stool-associated picornavirus.

Reasons to justify the choice of type species:

Only a single species is being designated at this stage.

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.

Demarcation criteria are being considered by the *Picornaviridae* Study Group and therefore only a single species is being designated in this proposal.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Blinkova, O., Rosario, K., Li, L., Kapoor, A., Slikas, B., Bernardin, F., Breitbart, M. and Delwart, E. (2009). Frequent detection of highly diverse variants of cardiovirus, cosavirus, bocavirus, and circovirus in sewage samples collected in the United States. *J. Clin. Microbiol.* 47: 3507-3513.

Dai, X.Q., Hua, X.G., Shan, T.L., Delwart, E. and Zhao, W. (2010). Human cosavirus infections in children in China. *J. Clin. Virol.* 48: 228-229.

Holtz, L.R., Finkbeiner, S.R., Kirkwood, C.D. and Wang, D. (2008). Identification of a novel picornavirus related to cosaviruses in a child with acute diarrhea. *Virology Journal* 5: 159; doi:10.1186/1743-422X-5-159.

Kapoor, A., Victoria, J., Simmonds, P., Slikas, E., Chieochansin, T., Naeem, A., Shaukat, S., Sharif, S., Masroor Alam, M., Angez, M., Wang, C., Shafer, R.W., Zaidi, S. and Delwart, E. (2008). A highly prevalent and genetically diversified Picornaviridae genus in South Asian children. *Proc. Natl. Acad. Sci., USA* 105: 20482-20487. doi 10.1073 pnas.0807979105.

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. Amino acid identity between and within *Picornaviridae* genera (from Kapoor et al., 2008).

P1 Region

Cosavirus	55.3%															
Cardiovirus	32.7%	68.7%														
Teschovirus	20.6%	24.7%	76.8%													
Aphthovirus	22.1%	26.1%	23.2%	55.5%												
Erbovirus	23.3%	28.5%	22.6%	30.7%	72.5%											
SVV	28.8%	35.0%	22.2%	25.0%	26.1%	---										
Enterovirus	18.2%	20.6%	17.4%	17.6%	18.8%	19.0%	46.3%									
Sapelovirus	10.0%	10.7%	10.3%	10.6%	10.6%	10.6%	11.0%	46.6%								
Parechovirus	21.3%	23.2%	18.6%	20.3%	20.7%	21.2%	33.3%	11.5%	49.2%							
DHV	10.9%	12.8%	11.8%	11.0%	12.1%	10.2%	12.1%	28.9%	13.1%	78.8%						
SePV-1	12.9%	10.5%	9.6%	11.4%	12.2%	11.3%	12.3%	23.8%	12.8%	22.0%	---					
Hepatovirus	13.9%	15.5%	12.2%	14.2%	13.0%	14.4%	15.1%	12.9%	15.5%	10.9%	12.7%	63.4%				
Kobuvirus	16.3%	17.3%	14.5%	15.5%	17.3%	16.7%	15.8%	10.6%	16.1%	10.5%	11.9%	12.8%	63.4%			
	Cosavirus	Cardiovirus	Teschovirus	Aphthovirus	Erbovirus	SVV	Enterovirus	Sapelovirus	Parechovirus	DHV	SePV-1	Hepatovirus	Kobuvirus			

3D Region

Cosavirus	76.6%															
Cardiovirus	46.0%	74.3%														
Teschovirus	37.7%	37.9%	98.2%													
Aphthovirus	44.1%	43.4%	38.0%	77.1%												
Erbovirus	35.2%	42.0%	39.4%	39.0%	96.5%											
SVV	48.7%	57.2%	40.3%	46.4%	40.4%	---										
Enterovirus	30.7%	30.4%	34.3%	31.1%	33.6%	31.2%	65.1%									
Sapelovirus	22.1%	23.5%	21.4%	22.1%	23.8%	23.1%	25.9%	50.8%								
Parechovirus	30.6%	30.9%	36.3%	31.7%	34.9%	31.4%	54.9%	26.1%	63.0%							
DHV	24.0%	24.1%	25.5%	22.3%	21.9%	23.1%	25.9%	39.0%	26.4%	89.4%						
SePV-1	21.5%	22.4%	21.1%	21.7%	23.5%	23.2%	23.2%	29.6%	23.1%	30.3%	---					
Hepatovirus	23.6%	25.0%	26.3%	22.7%	23.0%	24.5%	26.2%	24.0%	27.9%	25.1%	22.2%	56.1%				
Kobuvirus	31.8%	32.4%	30.6%	33.1%	34.2%	31.4%	32.6%	24.8%	33.7%	21.3%	21.6%	25.2%	82.5%			
	Cosavirus	Cardiovirus	Teschovirus	Aphthovirus	Erbovirus	SVV	Enterovirus	Sapelovirus	Parechovirus	DHV	SePV-1	Hepatovirus	Kobuvirus			

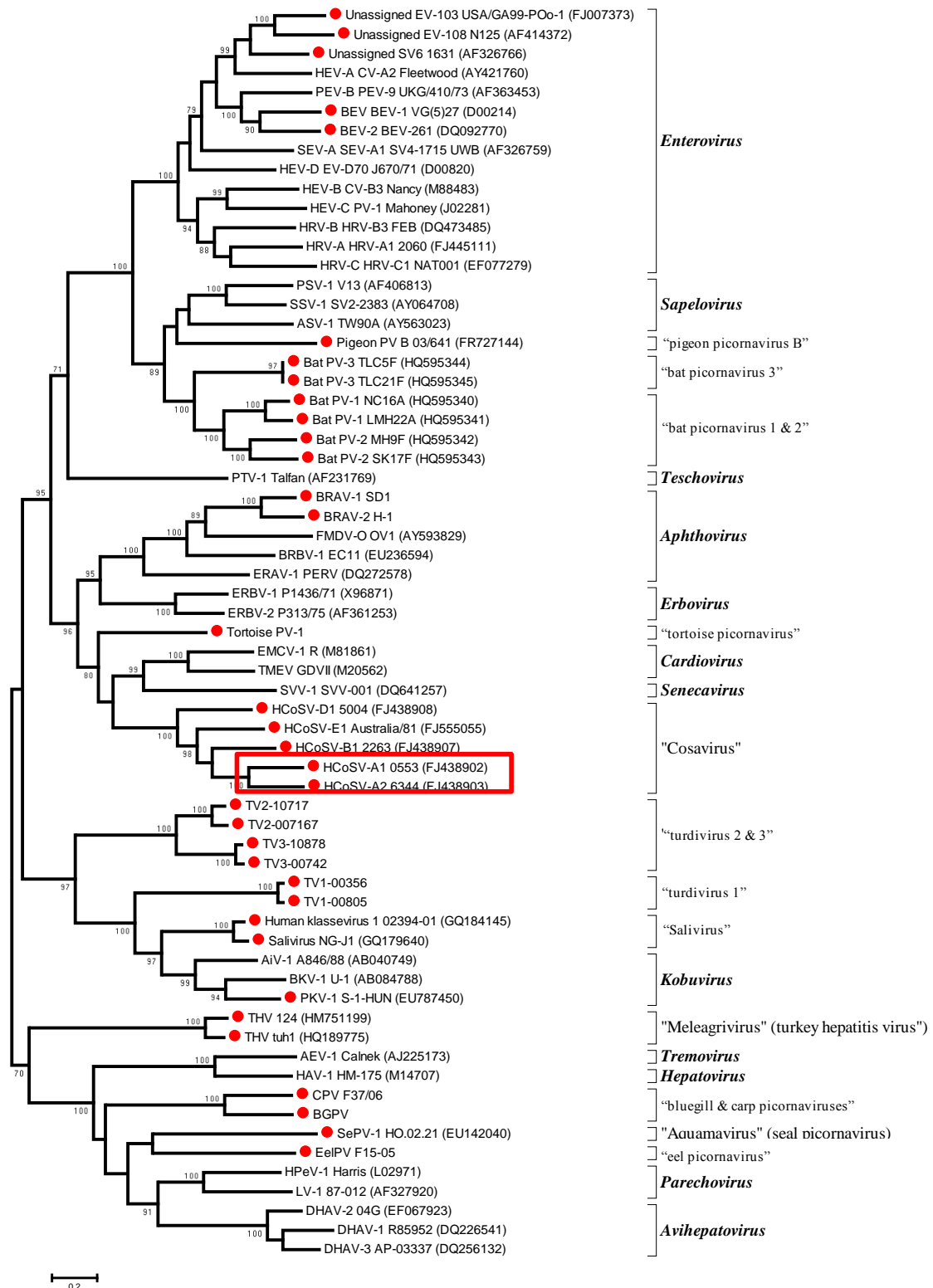


Fig. 1. Phylogenetic tree of the P1 capsids of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

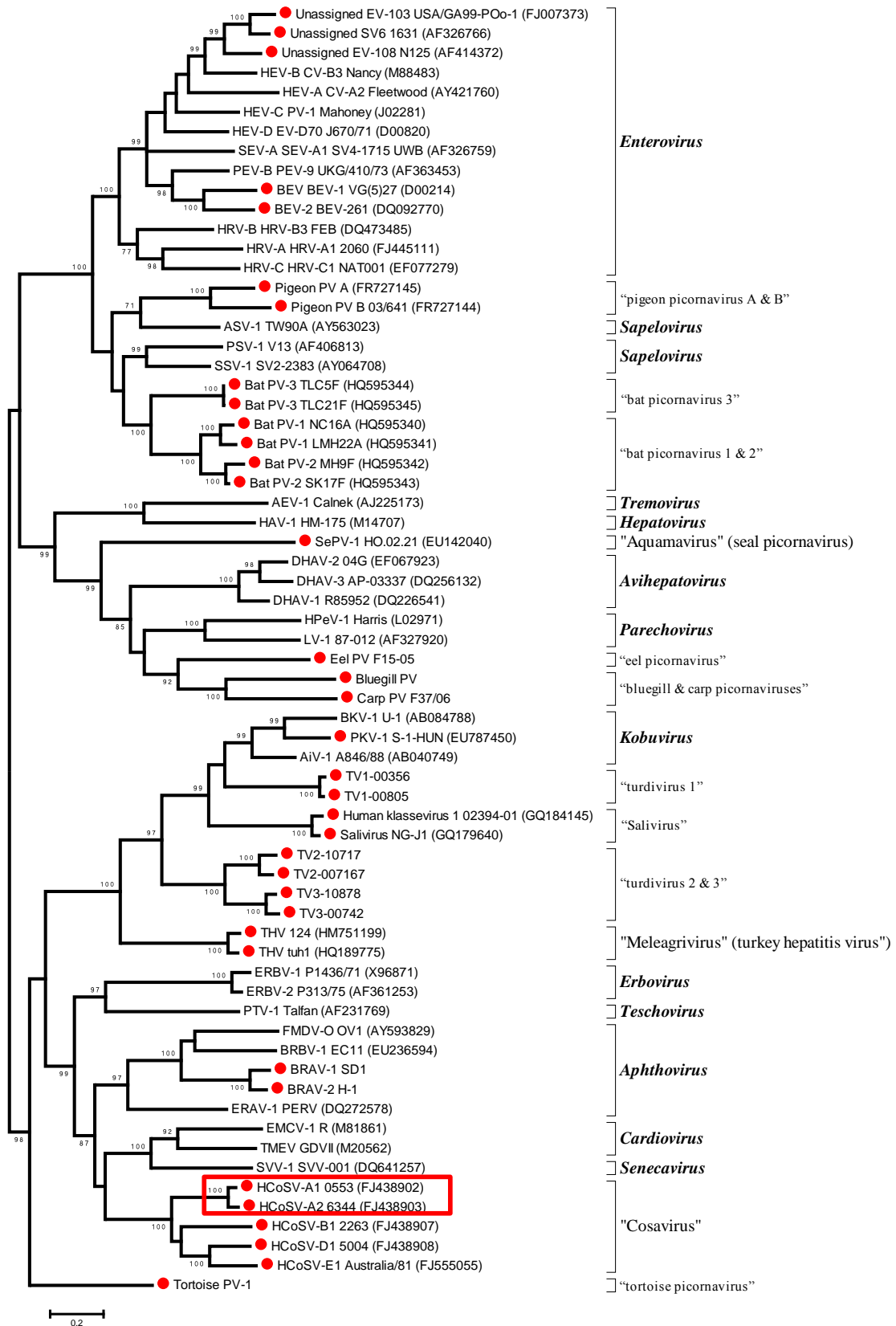


Fig. 2. Phylogenetic tree of the 3CD polypeptides of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.