



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:	2016.018a-dS	(to be completed by ICTV officers)
Short title: Create 1 new species (<i>Torchivirus A</i>) in a new genus (<i>Torchivirus</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):

Roland Zell, Eric Delwart, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, Mark A. Pallansch, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Glyn Stanway and Teruo Yamashita

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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:

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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	2016.018aS	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Torchivirus</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>Torchivirus A</i>	tortoise picornavirus [14/04]	KM873611

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

Novel picornaviruses were isolated from various tortoise species (*Testudo graeca*, *Testudo hermanni*, *Geochelone sulcata*, *Pyxis arachnoides*) in Hungary and Germany Heuser et al., 2014; Farkas et al., 2015. Viruses were propagated in Terrapene heart permanent cell line (ATCC CCL-50) (Heuser et al., 2014; Farkas et al., 2015). The virus, referred to in the literature as “virus X”, has been associated with disease (soft plastron, soft carapace with skeletal abnormality) and death in young tortoises (Heuser et al., 2014).

Sequences of seven torchiviruses are known (KM873611-KM873617; Farkas et al., 2015); the amino acid identity of the P1 genome region is greater 92% suggesting that they belong to a single type (compare Appendix Table 1).

Typical L-4-3-4 picornavirus genome layout (compare Appendix Figure 1):

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

Torchiviruses are most closely related to *Mosavirus* (amino acid identity: P1 ~39%, 3CD ~40%; compare Appendix Tables 1 and 2), but P1 and 3CD show lower amino acid identities with the orthologous proteins of other picornaviruses.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	2016.018bS	(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:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	

naming a new genus

Code	2016.018cS	(assigned by ICTV officers)
To name the new genus: <i>Torchivirus</i>		

Assigning the type species and other species to a new genus

Code	2016.018dS	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Torchivirus 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

Torchiviruses are most closely related to *Mosavirus* (P1 and 3CD phylogenetic trees) but exhibit significant distinctive features (compare Appendix Figure 1):

Feature	Torchivirus A1 (KM873611)	Mosavirus A2 (KF958461)
Host	various tortoise species	mouse, European roller (probably dietary)
L protein	52 aa,	452 aa
2A protein	145 aa	39 aa
VPg	1 (19 aa)	2 (20 aa, 43 aa)
3' UTR	231 nt	86 nt

2B and 3A proteins show very little or no significant homology.

The 5' UTR of *Torchivirus A1* is incomplete; thus, the IRES type is presently unknown.

Origin of the new genus name:

Torchivirus: from **tort**oise virus X (Greek **chi**)

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:

Torchivirus:

Farkas SL, Ihasz K, Feher E, Bartha D, Jakab F, Gal, J, Banyai K, Marschang RE. 2015. Sequencing and phylogenetic analysis identifies candidate members of a new picornavirus genus in terrestrial tortoise species. Arch. Virol. 160:811-816.

Heuser W, Pendl H, Knowles NJ, Keil G, Herbst W, Lierz M, Kaleta EF. 2014. Soft plastron, soft carapace with skeletal abnormality in juvenile tortoises. Histopathology and isolation of a novel picornavirus from *Testudo graeca* and *Geochelone elegans*. Tierarztl Prax Ausg K Kleintiere Heimtiere. 42: 310-320.

Mosavirus A2:

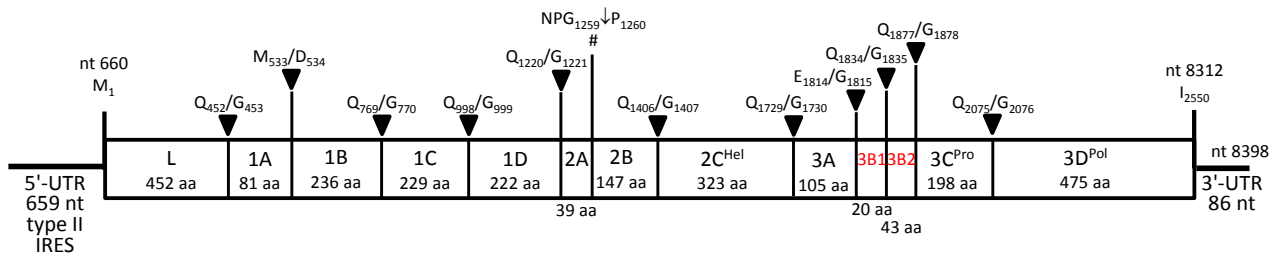
Reuter G, Boros A, Kiss T, Delwart E, Pankovics P. 2014. Complete genome characterization of mosavirus (family *Picornaviridae*) identified in droppings of a European roller (*Coriacias garrulus*) in Hungary. Arch Virol 159:2723-2729.

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:

Mosavirus A2, European roller mosavirus [SZAL6-MoV/2011/HUN], GenBank acc. no. KF958461



Proposed: *Torchivirus* A, tortoise picornavirus [14-04], GenBank acc. no. KM873611

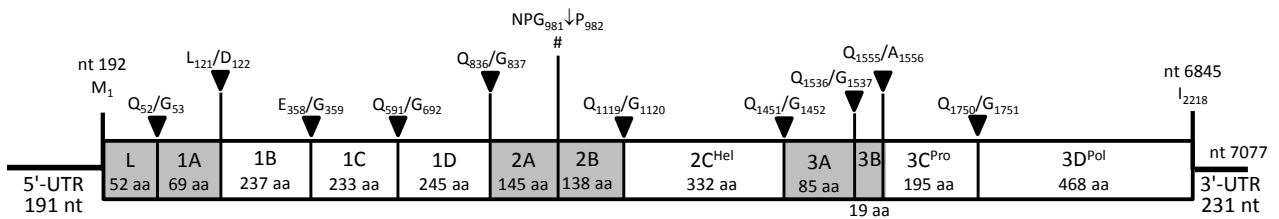


Figure 1: Comparison of *Mosavirus* (top) and *Torchivirus* (below) genome organisation (schematic depiction). The open reading frames are indicated by boxes. Positions of putative aa cleavage sites and the lengths of the deduced proteins are shown as proposed by Reuter et al. (2014) and Farkas et al (2015). Triangles (▼) indicate the putative 3C^{Pro} cleavage sites. Genome regions lacking significant sequence homology are shaded. The 5' UTR of *Torchivirus* is incomplete.

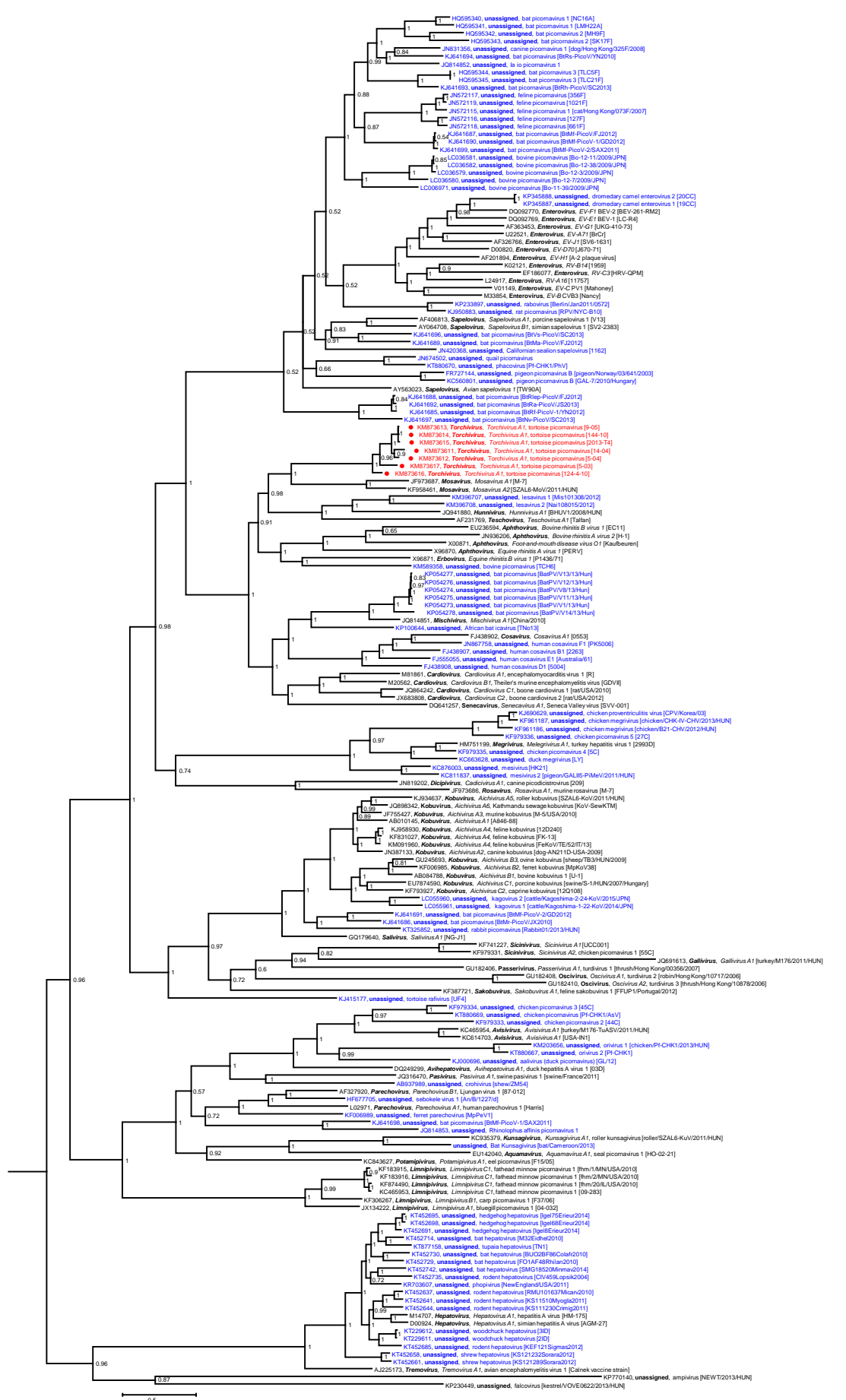


Figure 2 (previous page): Phylogenetic analyses of picornavirus P1 using Bayesian tree inference (MrBayes 3.2). 178 picornavirus sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square brackets] are given. Yet unassigned viruses are printed in blue. Proposed names are 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.

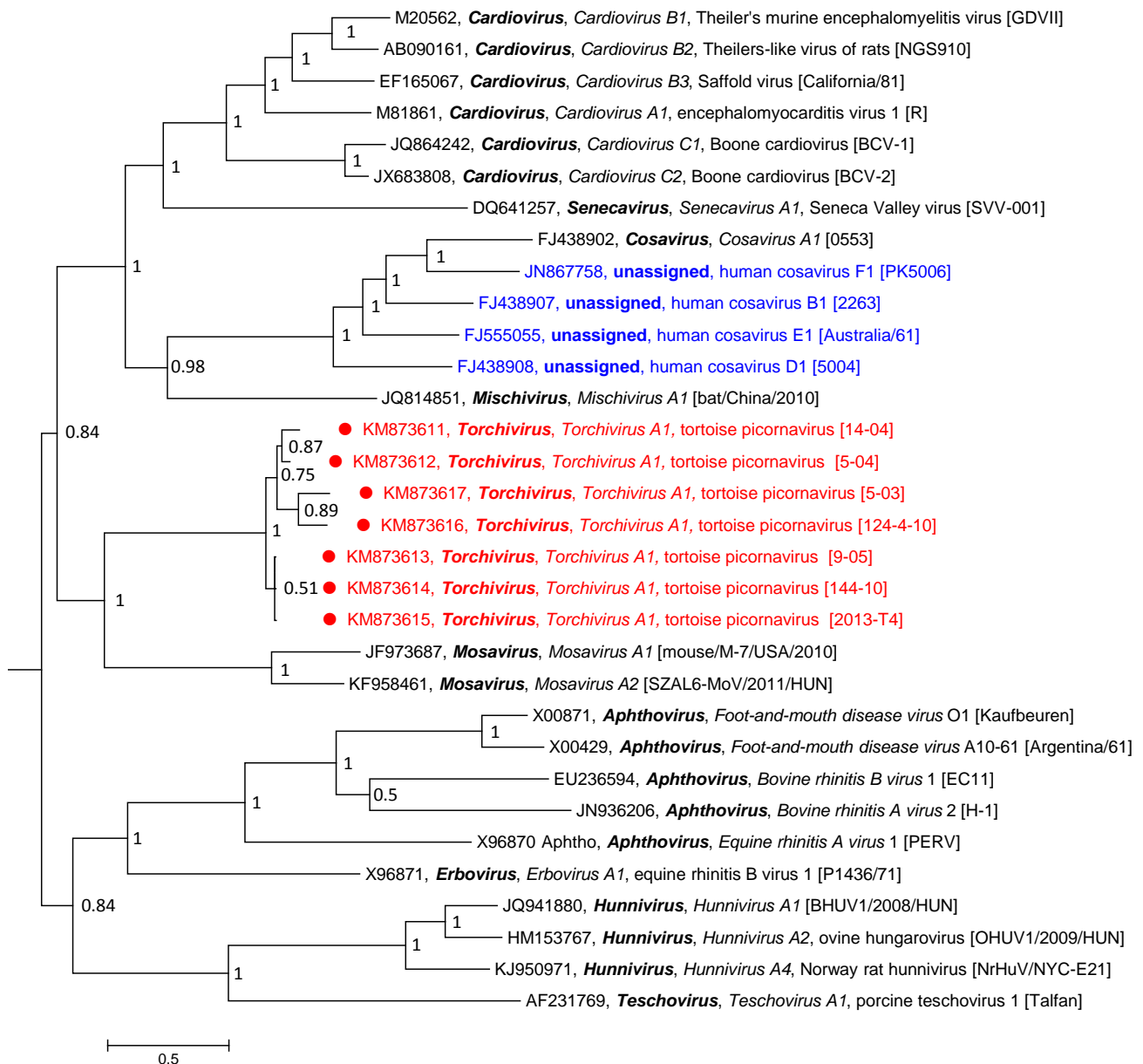


Figure 3: Phylogenetic analyses of picornavirus P1 using Bayesian tree inference (MrBayes 3.2). 32 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square brackets] are 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 1,000,000 generations. The optimal substitution model (GTR+G) was determined with MEGA 5. The scale indicates substitutions/site.

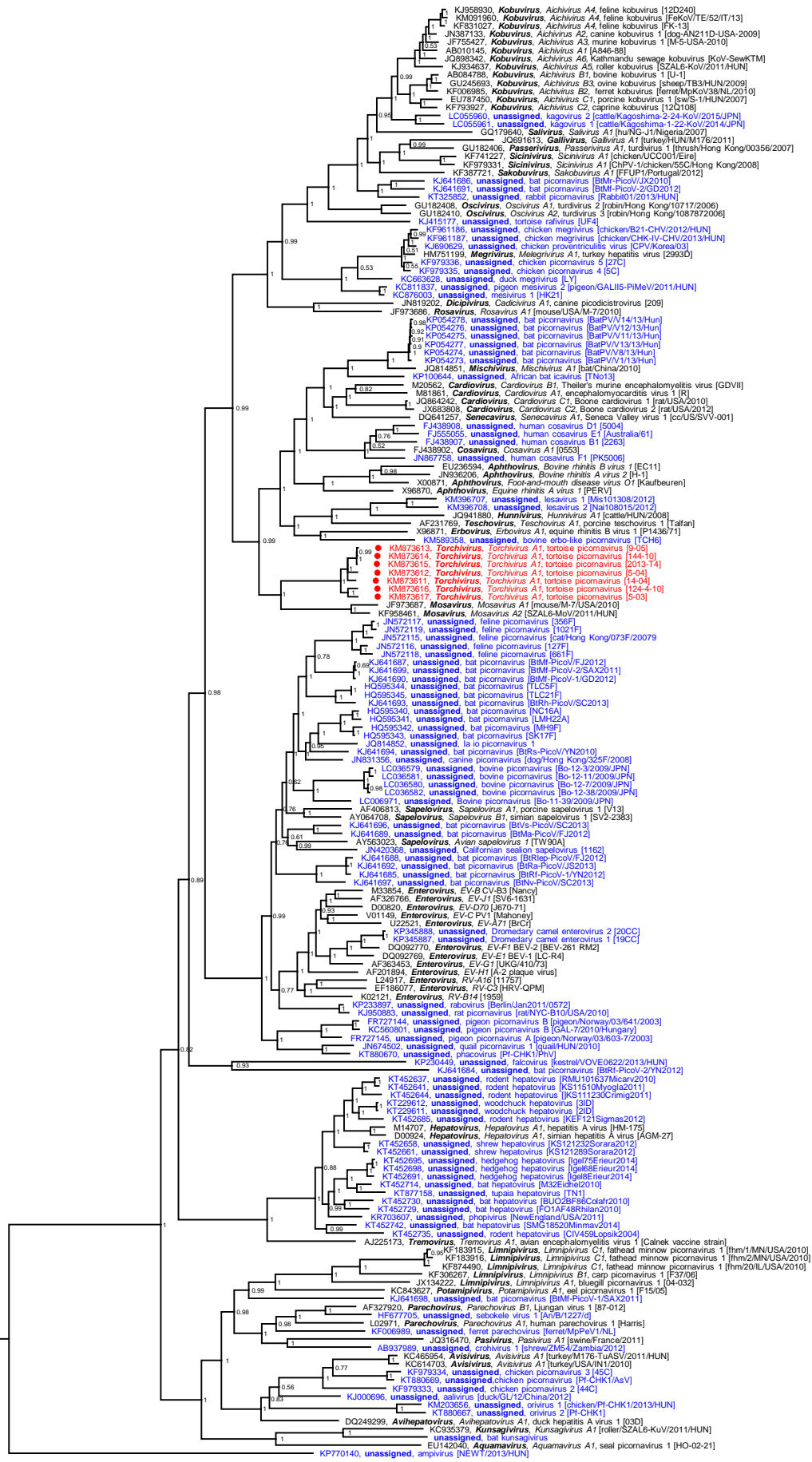


Figure 4 (previous page): Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of 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.

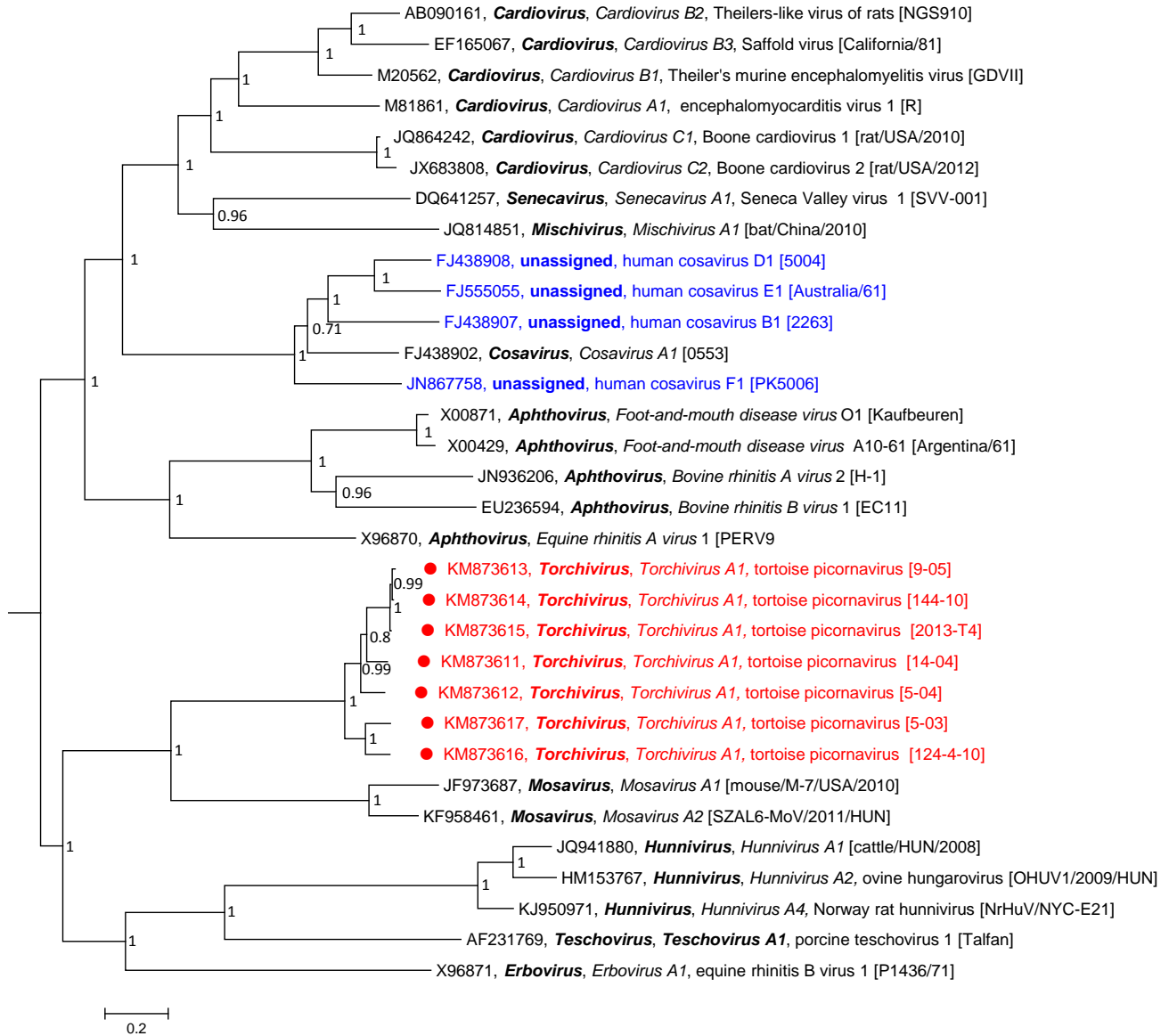


Figure 5: Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 32 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square 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 1,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

The number of amino acid differences per site from between sequences are shown. The analysis involved 32 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 1043 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

1. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution* 28: 2731-2739.

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Table 2: Estimates of Evolutionary Divergence between 3CD Sequences

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[ 1] #JF973687_Mosavirus_A1_mouse/M-7/USA/2010
[ 2] #KF958461_Mosavirus_A2_strain_SZAL6-Mov/2011/HUN
[ 3] #KM873613_Tortoise_picornavirus_strain_9-05
[ 4] #KM873614_Tortoise_picornavirus_strain_144-10
[ 5] #KM873615_Tortoise_picornavirus_strain_2013-T4
[ 6] #KM873611_Tortoise_picornavirus_strain_14-04
[ 7] #KM873612_Tortoise_picornavirus_strain_5-04
[ 8] #KM873617_Tortoise_picornavirus_strain_5-03
[ 9] #KM873616_Tortoise_picornavirus_strain_124-4-10
[10] #M81861_Cardiovirus_EMCV-R
[11] #M20562_Cardiovirus_TMEV_GDVII
[12] #gi|28804493|dbj|AB090161.1_Theilers-like_virus_of_rats_NGS910_genomic_RNA_complete_genome
[13] #gi|172050184|gb|EF165067.2|_Saffold_virus_complete_genome
[14] #JQ864242_Boone_cardiovirus_1_isolate_rat/USA/2010
[15] #JX683808_Boone_cardiovirus_2_isolate_rat/USA/2012
[16] #DQ641257_Senecavirus_A_SVV-1_cc/US/SVV-001
[17] #JQ814851_Mischivirus_A1_M_schreibersii_picornavirus_1_bat/China/2010
[18] #FJ438902_Cosavirus_HCoSV-A1
[19] #FJ438907_Cosavirus_HCoSV-B1
[20] #FJ438908_Cosavirus_HCoSV-D1
[21] #FJ555055_Cosavirus_HCoSV-E1
[22] #JN867758_Cosavirus_HCoSV_F1_PK5006
[23] #X96870_Aphthovirus_ERAV_PERV_P2F3
[24] #X00871_Aphthovirus_FMDV_O1Kaufbeuren
[25] #X00429_Aphthovirus_FMDV_A10-61_(Argentina/61)
[26] #JN936206_BRAV-2_H-1
[27] #EU236594_BRBV-1_EC11
[28] #X96871_Erbovirus_EREBV-1_P1436/71
[29] #AF231769_Teschovirus_A_PTV-1_Talfan
[30] #JQ941880_Hunnivirus_A1_HuV-A1_cattle/HUN/2008
[31] #HM153767_Ovine_hungarovirus_OHUV1/2009/HUN
[32] #KJ950971_Norway_rat_hunnivirus_isolate_NrHuV/NYC-E21

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	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
[1]	0.0000																															
[2]	0.1878	0.0000																														
[3]	0.5960	0.5945	0.0000																													
[4]	0.5991	0.5976	0.0166	0.0000																												
[5]	0.5991	0.5976	0.0166	0.0060	0.0000																											
[6]	0.6006	0.5960	0.0498	0.0422	0.0422	0.0000																										
[7]	0.5915	0.5899	0.0468	0.0407	0.0407	0.0347	0.0000																									
[8]	0.5930	0.5960	0.0950	0.0905	0.0920	0.0830	0.0845	0.0000																								
[9]	0.5915	0.5930	0.1041	0.0980	0.0995	0.0935	0.0950	0.0543	0.0000																							
[10]	0.6595	0.6656	0.6316	0.6300	0.6316	0.6347	0.6316	0.6300	0.6316	0.0000																						
[11]	0.6564	0.6595	0.6373	0.6358	0.6343	0.6250	0.6281	0.6250	0.6296	0.4030	0.0000																					
[12]	0.6702	0.6733	0.6373	0.6404	0.6404	0.6327	0.6358	0.6358	0.6389	0.4090	0.1858	0.0000																				
[13]	0.6534	0.6656	0.6451	0.6466	0.6466	0.6389	0.6435	0.6358	0.6343	0.4286	0.2314	0.1711	0.0000																			
[14]	0.6733	0.6870	0.6467	0.6467	0.6482	0.6436	0.6406	0.6498	0.6467	0.4496	0.4687	0.4925	0.5015	0.0000																		
[15]	0.7591	0.7657	0.7367	0.7400	0.7400	0.7333	0.7367	0.7333	0.7300	0.5367	0.5647	0.5962	0.5931	0.0282	0.0000																	
[16]	0.6804	0.6865	0.6333	0.6348	0.6364	0.6364	0.6348	0.6410	0.6364	0.4887	0.4925	0.5060	0.5120	0.5135	0.6234	0.0000																
[17]	0.6586	0.6768	0.6462	0.6432	0.6447	0.6417	0.6401	0.6371	0.6371	0.5076	0.5397	0.5457	0.5397	0.5388	0.6519	0.5164	0.0000															
[18]	0.6866	0.6897	0.6852	0.6867	0.6867	0.6852	0.6821	0.6759	0.6790	0.5936	0.5906	0.5784	0.5951	0.5894	0.7010	0.5881	0.6067	0.0000														
[19]	0.6903	0.6995	0.6641	0.6625	0.6594	0.6548	0.6625	0.6594	0.6641	0.6037	0.6174	0.6082	0.6037	0.6191	0.7323	0.6073	0.6106	0.3042	0.0000													
[20]	0.6846	0.7031	0.6692	0.6692	0.6692	0.6662	0.6677	0.6692	0.6692	0.5997	0.6088	0.6027	0.6088	0.6076	0.6977	0.5927	0.6021	0.3368	0.3148	0.0000												
[21]	0.6877	0.6969	0.6662	0.6677	0.6677	0.6708	0.6677	0.6708	0.6739	0.6074	0.6149	0.6164	0.6195	0.6121	0.7042	0.6049	0.6188	0.3444	0.3343	0.2241	0.0000											
[22]	0.6963	0.7040	0.6744	0.6728	0.6728	0.6698	0.6759	0.6698	0.6775	0.6150	0.6088	0.6073	0.6058	0.6061	0.7235	0.6064	0.6036	0.3308	0.3605	0.3614	0.3705	0.0000										
[23]	0.6467	0.6498	0.6497	0.6481	0.6466	0.6497	0.6481	0.6451	0.6420	0.6092	0.6015	0.6244	0.6153	0.5866	0.6883	0.6073	0.6277	0.6280	0.6290	0.6235	0.6159	0.6260	0.0000									
[24]	0.6692	0.6707	0.6743	0.6743	0.6728	0.6728	0.6743	0.6774	0.6758	0.6297	0.6596	0.6491	0.6551	0.6357	0.7089	0.6201	0.6617	0.6269	0.6248	0.6344	0.6375	0.6314	0.5314	0.0000								
[25]	0.6707	0.6723	0.6820	0.6789	0.6774	0.6774	0.6789	0.6820	0.6804	0.6358	0.6657	0.6536	0.6611	0.6477	0.7215	0.6276	0.6662	0.6360	0.6369	0.6390	0.6390	0.6390	0.5419	0.4433	0.0000							
[26]	0.6707	0.6692	0.6662	0.6646	0.6616	0.6585	0.6646	0.6708	0.6585	0.6434	0.6491	0.6340	0.6431	0.6447	0.7215	0.6331	0.6432	0.6420	0.6445	0.6375	0.6390	0.6526	0.5602	0.4174	0.4322	0.0000						
[27]	0.6738	0.6677	0.6590	0.6590	0.6590	0.6605	0.6621	0.6544	0.6544	0.6128	0.6415	0.6415	0.6536	0.6265	0.7134	0.6103	0.6431	0.6258	0.6282	0.6258	0.6258	0.6273	0.5452	0.3985	0.4044	0.4125	0.0000					
[28]	0.6960	0.7021	0.6733	0.6702	0.6687	0.6748	0.6779	0.6794	0.6718	0.6337	0.6528	0.6528	0.6542	0.6471	0.7333	0.6586	0.6417	0.6747	0.6848	0.6717	0.6672	0.6944	0.6425	0.6716	0.6751	0.6503	0.6637	0.0000				
[29]	0.6988	0.6972	0.6941	0.6941	0.6925	0.6957	0.6972	0.7003	0.6941	0.6573	0.6620	0.6728	0.6806	0.6903	0.7662	0.6538	0.6610	0.6817	0.6854	0.6796	0.6765	0.6791	0.6625	0.6687	0.6749	0.6995	0.6703	0.6606	0.0000			
[30]	0.6903	0.6872	0.6918	0.6903	0.6888	0.6918	0.6965	0.6857	0.6810	0.6579	0.6646	0.6615	0.6815	0.6922	0.7677	0.6692	0.6514	0.7088	0.7156	0.6991	0.6975	0.7211	0.6821	0.6789	0.6794	0.6927	0.6865	0.6657	0.5745	0.0000		
[31]	0.6903	0.6888	0.6934	0.6918	0.6903	0.6903	0.6949	0.6841	0.6810	0.6563	0.6692	0.6708	0.6862	0.6937	0.7742	0.6738	0.6621	0.7026	0.7141	0.6914	0.6929	0.7196	0.6867	0.6881	0.6916	0.7049	0.6957	0.6748	0.5895	0.1220	0.0000	
[32]	0.6909	0.6940	0.6940	0.6924	0.6909	0.6940	0.6986	0.6878	0.6862	0.6615	0.6821	0.6759	0.6883	0.6928	0.7896	0.6790	0.6626	0.7110	0.7163	0.7074	0.7028	0.7202	0.6811	0.6764	0.6845	0.6902	0.6917	0.6677	0.5747	0.1631	0.1722	0.0000

The number of amino acid differences per site from between sequences are shown. The analysis involved 32 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 724 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].