



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:	2016.009aS	(to be completed by ICTV officers)
Short title: Create 8 new species (<i>Hepatovirus B-I</i>) in the genus <i>Hepatovirus</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 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	2016.009aS	(assigned by ICTV officers)
To create 8 new species within:		
Genus:	<i>Hepatitis</i>	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>Hepatitis B</i>	Phopivirus [New England/USA/2011]	KR703607
<i>Hepatitis C</i>	Bat hepatitis [SMG18520Minmav2014]	KT452742
<i>Hepatitis D</i>	Rodent hepatitis [RMU101637Micarv2010]	KT452637
<i>Hepatitis E</i>	Rodent hepatitis [CIV459Lopsik2004]	KT452735
<i>Hepatitis F</i>	Rodent hepatitis [KEF121Sigmas2012]	KT452685
<i>Hepatitis G</i>	Bat hepatitis [BUO2BF86Colafr2010]	KT452730
<i>Hepatitis H</i>	Hedgehog hepatitis [Igel8Erieur2014]	KT452691
<i>Hepatitis I</i>	Shrew hepatitis [KS121232Sorara2012]	KT452658

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 detected in seals (*Phoca vitulina vitulina*), woodchucks (*Marmota himalayana*), bats (*Miniopterus cf. manavi*, *Coleura afra*, *Eidolon helvum*, *Rhinolophus landeri*), hedgehogs (*Erinaceus europaeus*), rodents (*Microtus arvalis*, *Myodes glareolus*, *Cricetulus migratorius*, *Sigmodon mascotensis*, *Lophuromys sikapusi*), shrews (*Sorex araneus*) and tupajas (*Tupaia belangeri chinensis*). These viruses show a global distribution.

The proposed hepatitisviruses share significant similarities to *Hepatitis A1*, i.e.

- similar genome layout:
 VPg+5'UTR^{IRES-III}[1A-1B-1C-1D/2A-2B-2C^{Hel}/3A-3B^{VPg}-3C^{Pro}-3D^{Pol}]3'UTR-poly(A);
- significant amino acid identities of capsid proteins (>60%) and 3CD (>50%) protein (compare Appendix Tables 1 and 2);
- clustering with *Hepatitis A* in phylogenetic trees (compare Appendix Figures 1-4).

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Anthony SJ, St. Leger JA, Liang E, Hicks AL, Sanchez-Leon MD, Jain K, Lefkowitz JH, Navarete-Macias I, Knowles N, Goldstein T, Puglianes K, Ip HS, Rowles T, Lipkin WI. 2015. Discovery of a novel hepatovirus (phopivirus of seals) related to human hepatitis A virus. *mBio* 6(4):e01180-15.
- Drexler JF, Corman VM, Lukashev AN, van den Brand JMA, Gmyl AP, Brünink S, Rasche A, Seggewiß N, Feng H, Leijten LM, Vallo P, Kuiken T, Dotzauer A, Ulrich RG, Lemon SM, Drosten C, and the Hepatovirus Ecology Consortium. 2015. Evolutionary origins of hepatitis A virus in small mammals. *Proc. Natl. Acad. Sci. USA* 112(49):15190-15195.
- Yu JM, Li LL, Zhang CY, Lu S, Ao YY, Gao HC, Xie ZP, Xie GC, Sun XM, Pang LL, Xu JG, Lipkin WI, Duan ZJ. 2016. A novel hepatovirus identified in wild woodchuck *Marmota himalayana*. *Sci. Rep.* 6:22361.

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
P1

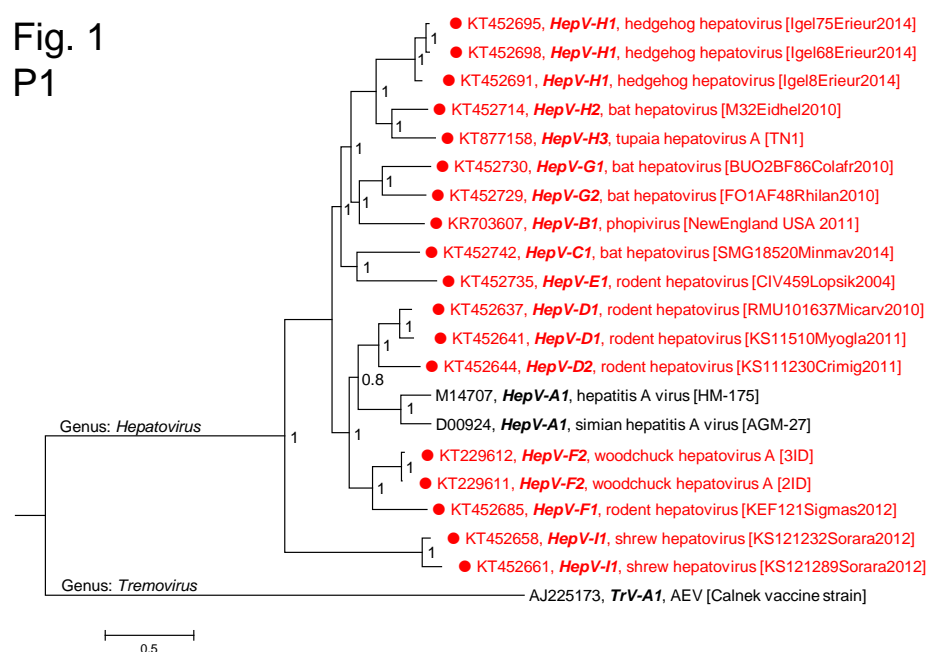


Figure 1: Phylogenetic analyses of *Hepatovirus* P1 gene regions using Bayesian tree inference (MrBayes 3.2). 20 hepatovirus (HepV) sequences and 1 *Tremovirus* (TrV) sequence (outgroup) were retrieved from GenBank. Proposed names are printed in red and indicated by a dot (●). Presented are GenBank accession numbers, *species names* and type designations. If available, designations of isolates are given in square brackets. 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. Abbreviations: HepV, *Hepatovirus*; TrV, *Tremovirus*.

Fig. 2
3CD

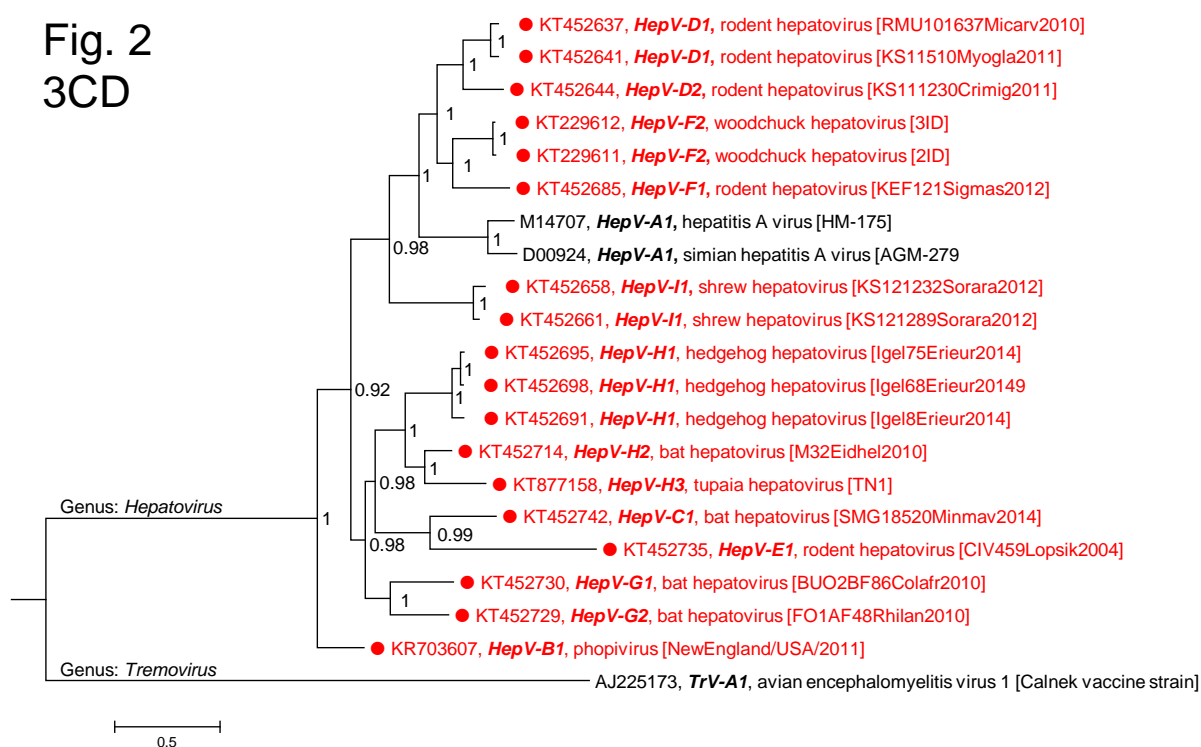


Figure 2: Phylogenetic analyses of *Hepatovirus* 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 20 hepatovirus (HepV) sequences and 1 *Tremovirus* (TrV) sequence (outgroup) were retrieved from GenBank. Proposed names are printed in red and indicated by a dot (●). Presented are GenBank accession numbers, *species names* and *types*. If available, designations of isolates are given in square brackets. 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. Abbreviations: HepV, *Hepatovirus*; TrV, *Tremovirus*.

Fig. 3
P1

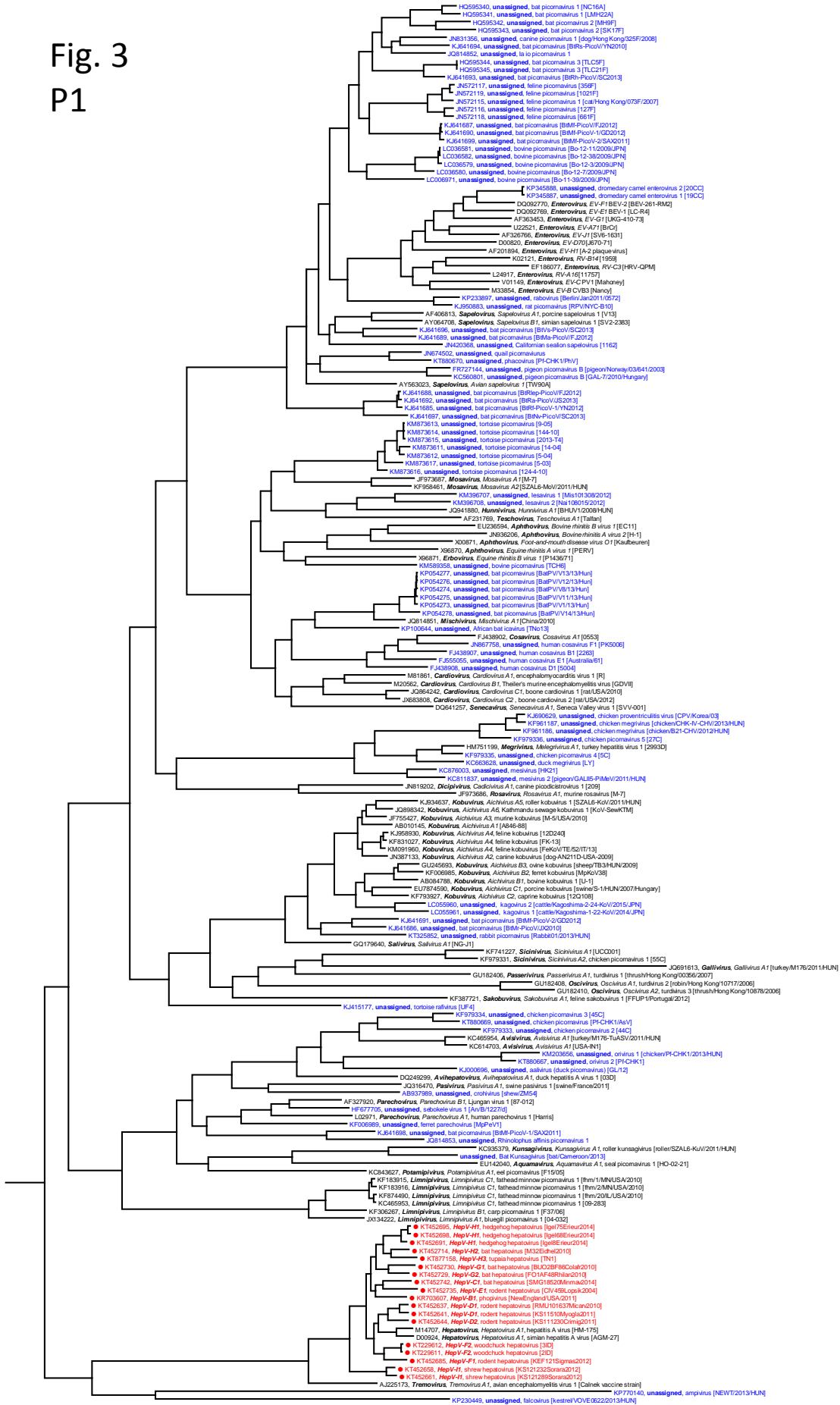


Figure 3: Phylogenetic analyses of picornavirus P1 gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square 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 6,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

Fig. 4
3CD

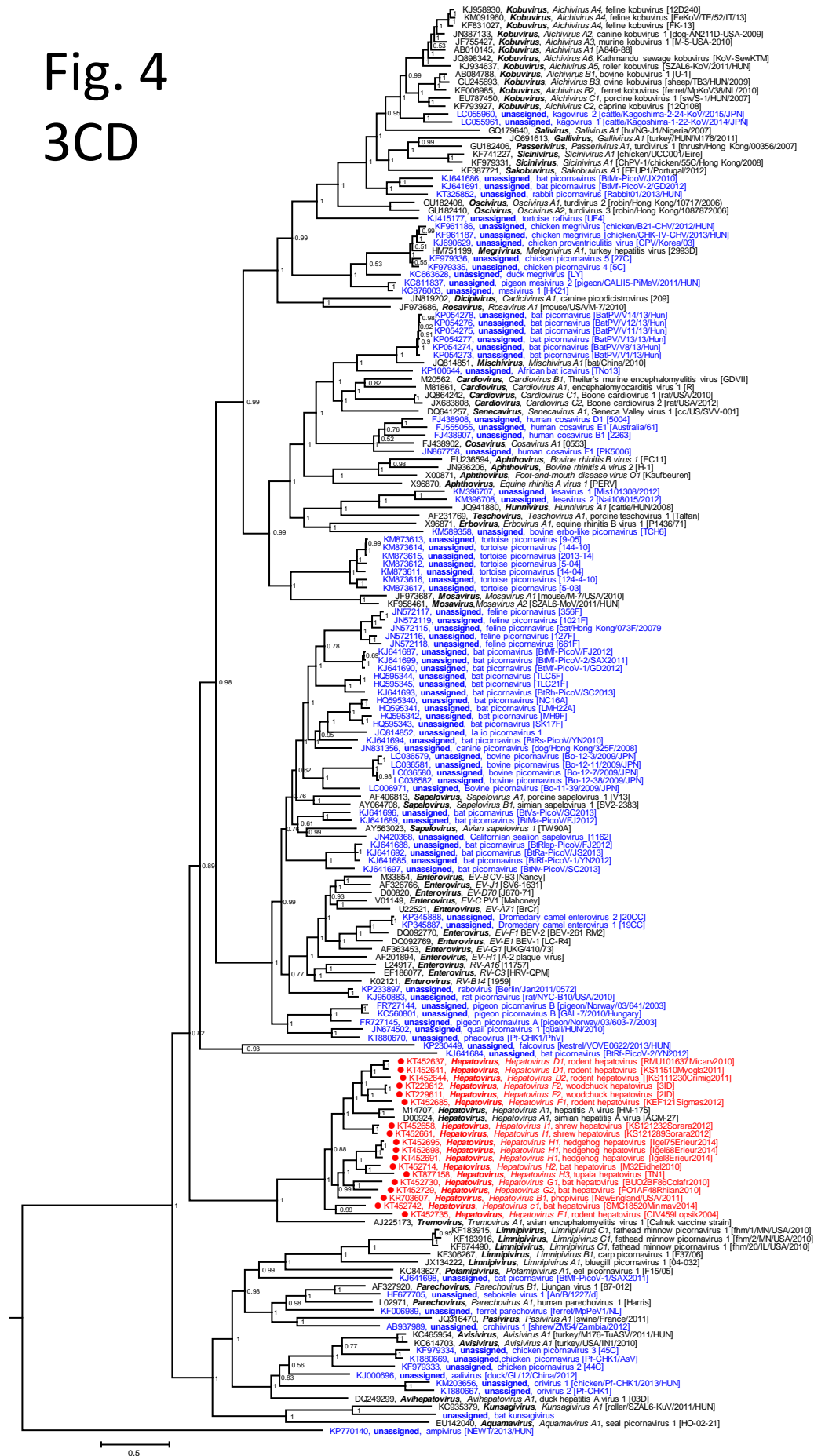


Figure 4: Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of isolates [in square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

Table 1. Estimates of evolutionary divergence between P1 aa sequences

```
[ 1] M14707_HepV-A1_HAV_HM-175
[ 2] D00924_HepV-A1_Simian_hepatitis_A_virus_AGM-27
[ 3] KT452637_HepV-D1_Rodent_hepatovirus_isolate_RMU101637Micarv2010
[ 4] KT452641_HepV-D1_Rodent_hepatovirus_isolate_KS11510Myogla2011
[ 5] KT452644_HepV-D2_Rodent_hepatovirus_isolate_KS111230Crimig2011
[ 6] KT452685_HepV-F1_Rodent_hepatovirus_isolate_KEF121Sigmas2012
[ 7] KT229612_HepV-F2_Woodchuck_hepatovirus_A_isolate_3ID
[ 8] KT229611_HepV-F2_Woodchuck_hepatovirus_A_isolate_2ID
[ 9] KR703607_HepV-B1_Phopivirus_strain_NewEngland_USA/2011
[10] KT452742_HepV-C1_Bat_hepatovirus_isolate_SMG18520Minnav2014
[11] KT452691_HepV-H1_Hedgehog_hepatovirus_isolate_Igel18Erieur2014
[12] KT452695_HepV-H1_Hedgehog_hepatovirus_isolate_Igel75Erieur2014
[13] KT452698_HepV-H1_Hedgehog_hepatovirus_isolate_Igel68Erieur2014
[14] KT452714_HepV-H2_Bat_hepatovirus_isolate_M32Eidhel2010
[15] KT877158_HepV-H3_Tupaia_hepatovirus_A_isolate_TN1
[16] KT452730_HepV-G1_Bat_hepatovirus_isolate_BUO2BF86Colafra2010
[17] KT452729_HepV-G2_Bat_hepatovirus_isolate_F01AF48Rhilan2010
[18] KT452735_HepV-E1_Rodent_hepatovirus_isolate_CIV459Lopsik2004
[19] KT452658_HepV-I1_Shrew_hepatovirus_isolate_KS121232Sorara2012
[20] KT452661_HepV-I1_Shrew_hepatovirus_isolate_KS121289Sorara2012
[21] AJ225173_TrV-A1_AEV_Calnek_vaccine_strain
```

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
[1] HepV-A1	0.0000																				
[2] HepV-A1	0.0405	0.0000																			
[3] HepV-D1	0.1800	0.1787	0.0000																		
[4] HepV-D1	0.1787	0.1774	0.0063	0.0000																	
[5] HepV-D2	0.1904	0.1891	0.0947	0.0934	0.0000																
[6] HepV-F1	0.2229	0.2217	0.1916	0.1891	0.1774	0.0000															
[7] HepV-F2	0.1985	0.1947	0.1765	0.1765	0.1892	0.1389	0.0000														
[8] HepV-F2	0.1960	0.1922	0.1740	0.1740	0.1866	0.1364	0.0050	0.0000													
[9] HepV-B1	0.2424	0.2475	0.2376	0.2363	0.2576	0.2376	0.2273	0.2247	0.0000												
[10] HepV-C1	0.2604	0.2604	0.2469	0.2494	0.2657	0.2693	0.2447	0.2422	0.2099	0.0000											
[11] HepV-H1	0.2656	0.2745	0.2538	0.2525	0.2522	0.2392	0.2386	0.2361	0.2087	0.2582	0.0000										
[12] HepV-H1	0.2646	0.2723	0.2554	0.2541	0.2525	0.2405	0.2389	0.2364	0.2115	0.2598	0.0114	0.0000									
[13] HepV-H1	0.2638	0.2714	0.2545	0.2532	0.2529	0.2385	0.2417	0.2392	0.2103	0.2577	0.0115	0.0038	0.0000								
[14] HepV-H2	0.2519	0.2608	0.2519	0.2519	0.2516	0.2475	0.2431	0.2418	0.2015	0.2535	0.1378	0.1354	0.1338	0.0000							
[15] HepV-H3	0.2506	0.2532	0.2481	0.2468	0.2427	0.2272	0.2390	0.2365	0.1990	0.2573	0.1313	0.1315	0.1272	0.0982	0.0000						
[16] HepV-G1	0.2620	0.2749	0.2440	0.2427	0.2551	0.2535	0.2506	0.2481	0.2203	0.2645	0.2165	0.2155	0.2117	0.1980	0.2005	0.0000					
[17] HepV-G2	0.2624	0.2696	0.2408	0.2433	0.2557	0.2490	0.2449	0.2424	0.2069	0.2576	0.2180	0.2170	0.2158	0.1957	0.2033	0.1450	0.0000				
[18] HepV-E1	0.2748	0.2774	0.2605	0.2643	0.2754	0.2748	0.2522	0.2510	0.2354	0.2231	0.2668	0.2656	0.2673	0.2649	0.2636	0.2687	0.2652	0.0000			
[19] HepV-I1	0.3908	0.3921	0.3842	0.3855	0.3787	0.3980	0.3881	0.3856	0.3929	0.3802	0.3613	0.3651	0.3656	0.3723	0.3655	0.3609	0.3745	0.3520	0.0000		
[20] HepV-I1	0.3921	0.3934	0.3842	0.3855	0.3799	0.3980	0.3881	0.3856	0.3929	0.3790	0.3601	0.3639	0.3643	0.3723	0.3655	0.3609	0.3745	0.3508	0.0038	0.0000	
[21] TrV-A1	0.5067	0.5054	0.4980	0.4967	0.4953	0.4940	0.4847	0.4861	0.4926	0.5053	0.5054	0.5054	0.5047	0.4993	0.5053	0.5100	0.5107	0.4987	0.5007	0.5020	0.0000

The number of amino acid differences per site from between sequences are shown. The analysis involved 21 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 813 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

P1:	intra-typic	observed aa divergence: <5%	⇒	aa identity: >95%
	inter-typic (within species)	observed aa divergence: 6-15%	⇒	aa identity: 85-95%
	between species	observed aa divergence: 17-40%	⇒	aa identity: >60%
	between genera	observed aa divergence: >48%	⇒	aa identity: <52%

Table 2. Estimates of evolutionary divergence between 3CD aa sequences

```
[ 1] M14707_HepV-A1_HAV_HM-175
[ 2] D00924_HepV-A1_Simian_hepatitis_A_virus_AGM-27
[ 3] HepV-D1_KT452637_Rodent_hepatovirus_isolate_RMU101637Micarv2010_cg
[ 4] HepV-D1_KT452641_Rodent_hepatovirus_isolate_KS11510Myogla2011_cg
[ 5] HepV-D2_KT452644_Rodent_hepatovirus_isolate_KS111230Crimig2011_cg
[ 6] HepV-F1_KT452685_Rodent_hepatovirus_isolate_KEF121Sigmas2012_cg
[ 7] HepV-F2_KT229612_Woodchuck_hepatovirus_A_isolate_3ID
[ 8] HepV-F2_KT229611_Woodchuck_hepatovirus_A_isolate_2ID
[ 9] HepV-B1_KR703607_Phopivirus_strain_NewEngland_USA/2011
[10] HepV-C1_KT452742_Bat_hepatovirus_isolate_SMG18520Minmav2014
[11] HepV-H1_KT452691_Hedgehog_hepatovirus_isolate_Igel18Erieur2014_cg
[12] HepV-H1_KT452695_Hedgehog_hepatovirus_isolate_Igel75Erieur2014_cg
[13] HepV-H1_KT452698_Hedgehog_hepatovirus_isolate_Igel68Erieur2014_cg
[14] HepV-H2_KT452714_Bat_hepatovirus_isolate_M32Eidhel2010_cg
[15] HepV-H3_KT877158_Tupaia_hepatovirus_A_isolate_TN1
[16] HepV-G1_KT452730_Bat_hepatovirus_isolate_BUO2BF86Colafra2010_cg
[17] HepV-G2_KT452729_Bat_hepatovirus_isolate_F01AF48Rhilan2010_cg
[18] HepV-E1_KT452735_Rodent_hepatovirus_isolate_CIV459Lopsik2004_cg
[19] HepV-I1_KT452658_Shrew_hepatovirus_isolate_KS121232Sorara2012_cg
[20] HepV-I1_KT452661_Shrew_hepatovirus_isolate_KS121289Sorara2012_cg
[21] TrV-A1_AJ225173_AEV-1_Calnek_vaccine_strain
```

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
[1] HepV-A1	0.0000																				
[2] HepV-A1	0.0791	0.0000																			
[3] HepV-D1	0.3164	0.3131	0.0000																		
[4] HepV-D1	0.3164	0.3117	0.0070	0.0000																	
[5] HepV-D2	0.3263	0.3216	0.1408	0.1437	0.0000																
[6] HepV-F1	0.3644	0.3583	0.2676	0.2676	0.2789	0.0000															
[7] HepV-F2	0.3291	0.3258	0.2479	0.2507	0.2577	0.2225	0.0000														
[8] HepV-F2	0.3277	0.3244	0.2465	0.2493	0.2549	0.2225	0.0085	0.0000													
[9] HepV-B1	0.4201	0.4364	0.4006	0.4006	0.4020	0.3977	0.3738	0.3738	0.0000												
[10] HepV-C1	0.4703	0.4710	0.4619	0.4619	0.4661	0.4520	0.4280	0.4280	0.4116	0.0000											
[11] HepV-H1	0.4350	0.4415	0.4239	0.4268	0.4141	0.4268	0.4127	0.4141	0.3456	0.3912	0.0000										
[12] HepV-H1	0.4350	0.4358	0.4211	0.4239	0.4141	0.4225	0.4141	0.4155	0.3456	0.3912	0.0197	0.0000									
[13] HepV-H1	0.4350	0.4386	0.4239	0.4268	0.4169	0.4211	0.4127	0.4141	0.3470	0.3912	0.0155	0.0070	0.0000								
[14] HepV-H2	0.4054	0.4217	0.4183	0.4197	0.4169	0.4296	0.4014	0.4014	0.3470	0.3686	0.1944	0.1944	0.1915	0.0000							
[15] HepV-H3	0.4096	0.4260	0.4380	0.4366	0.4254	0.4155	0.4239	0.4254	0.3709	0.3771	0.2380	0.2408	0.2394	0.1620	0.0000						
[16] HepV-G1	0.4322	0.4358	0.4282	0.4310	0.4282	0.4268	0.4000	0.4000	0.3343	0.3785	0.3141	0.3113	0.3113	0.3014	0.3437	0.0000					
[17] HepV-G2	0.4243	0.4223	0.4217	0.4245	0.4147	0.4147	0.3921	0.3921	0.3347	0.3989	0.3159	0.3145	0.3145	0.3230	0.3456	0.2454	0.0000				
[18] HepV-E1	0.4786	0.4694	0.4744	0.4773	0.4759	0.4901	0.4673	0.4673	0.4737	0.4017	0.4545	0.4545	0.4545	0.4474	0.4673	0.4759	0.4538	0.0000			
[19] HepV-I1	0.4068	0.4076	0.3972	0.3972	0.3972	0.4042	0.3606	0.3606	0.3766	0.4364	0.3859	0.3873	0.3845	0.4000	0.4056	0.3746	0.3865	0.4901	0.0000		
[20] HepV-I1	0.4082	0.4090	0.3986	0.3986	0.3986	0.4028	0.3606	0.3606	0.3780	0.4379	0.3845	0.3859	0.3831	0.3986	0.4042	0.3761	0.3836	0.4901	0.0070	0.0000	
[21] TrV-A1	0.6121	0.6184	0.6126	0.6126	0.6155	0.6169	0.6083	0.6098	0.5991	0.5942	0.6055	0.6069	0.6055	0.5997	0.6040	0.6098	0.6078	0.6199	0.5997	0.5997	0.0000

The number of amino acid differences per site from between sequences are shown. The analysis involved 21 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 718 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

3CD:	intra-typic	observed aa divergence: <8%	⇒	aa identity: >92%
	inter-typic (within species)	observed aa divergence: 14-25%	⇒	aa identity: 75-86%
	between species	observed aa divergence: 24-50%	⇒	aa identity: >50%
	between genera	observed aa divergence: >59%	⇒	aa identity: <41%