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:	*2015.007a-dS*	(to be completed by ICTV officers)

Short title: Creation of three new species (*Limnipivirus A, Limnipivirus B, Limnipivirus C*) in a new genus (*Limnipivirus*).
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	1 ☒	2 ☒	3 ☒	4 ☐	5 ☐
	6 ☐	7 ☐	8 ☐	9 ☐	10 ☒

Author(s):

R. Zell, E. Delwart, A.E. Gorbalenya, T. Hovi, A.M.Q. King, N.J. Knowles, A.M. Lindberg, M.A. Pallansch, A.C. Palmenberg, G. Reuter, P. Simmonds, T. Skern, G. Stanway, T. 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:	29/06/2015
Date of this revision (if different to above):	06/07/2015

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	*2015.007aS*		(assigned by ICTV officers)

To create 3 new species within:

		Fill in all that apply.
Genus:	*Limnipivirus* (new)	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:	*-*	
Family:	*Picornaviridae*	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Picornavirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Limnipivirus A	BGPV-1 bluegill/USA/04-032/2003 (bluegill picornavirus 1)	JX134222
Limnipivirus B	CPV-1 F37/06 (carp picornavirus 1)	KF306267
Limnipivirus C	FHMPV-1 fhm/1/MN/USA/2010 (fathead minnow picornavirus 1)	KF183915

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 three *Limnipivirus* species are new picornaviruses isolated from teleost fish of the Cyprinidae and Centrarchidae families from freshwater lakes and ponds in the USA and Germany. These viruses are most closely related to eel picornavirus 1, *Avihepatovirus*, *Parechovirus* and *Pasivirus* but show low amino acid identity with the orthologous proteins of these and other picornaviruses (capsid proteins 1AB, 1C, 1D: <25%, $2C^{Hel}$: <26%, $3C^{pro}$: <20%, $3D^{pol}$: <41%).

The three *Limnipivirus* species have in common and unique genome organization: VPg+5'UTR^{typeIV}[1AB-1C-1D-2A1^{NPGP}/2A2^{NPGP}/2B-2C^{Hel}/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3'UTR-poly(A)

All limnipiviruses share a characteristic, truncated type IV IRES relative to hepatitis C virus (Asnani et al., Virology 478:61-74, 2015) and two aphthovirus-like 2A proteins with NPG↓P motif. Within the genus, 2B, 3A and 3B exhibit no similarity; amino acid identities of the concatenated sequences of the orthologous proteins is greater 48%:

```
Percent Identity  Matrix – 1AB-1C-1D-2C-3C-3D – created by Clustal2.1:
JX134222_Bluegill_picornavirus_04-032          100.00   50.23   49.74   49.74   49.74   49.97
KF306267_Carp_picornavirus_1_F37/06             50.23  100.00   59.70   59.53   59.64   59.64
KC465953_Fathead_minnow_09-283                  49.74   59.70  100.00   99.72   98.88   98.32
KF874490_Fathead_minnow_fhm/20/IL/USA/2010      49.74   59.53   99.72  100.00   98.82   98.26
KF183915_Fathead_minnow_fhm/1/MN/USA/2010       49.74   59.64   98.88   98.82  100.00   99.27
KF183916_Fathead_minnow_fhm/2/MN/USA/201        49.97   59.64   98.32   98.26   99.27  100.00
```

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.007bS***	(assigned by ICTV officers)

To create a new genus within:

		Fill in all that apply.
Subfamily:	**-**	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Family:	***Picornaviridae***	
Order:	***Picornavirales***	• If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.007cS***	(assigned by ICTV officers)

To name the new genus: *Limnipivirus*

Assigning the type species and other species to a new genus

Code	***2015.007dS***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Limnipivirus A	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:**

3

Reasons to justify the creation of a new genus:
Additional material in support of this proposal may be presented in the Appendix, Module 9

Limnipivirus has a unique picornavirus genome layout (3-4-4 type) and low amino acid identity to the conserved proteins of other picornaviruses. The capsid polypeptide VP0 is predicted to be uncleaved. There are two aphthovirus-like 2A proteins with a NPG↓P sequence motif separated by a stretch of more than 120 amino acids in all three species.

The phylogenetic relationship of the capsid-encoding P1 region and the 3CD region with other picornaviruses is shown in Appendix Figures 2 and 3.

Origin of the new genus name:

Limnipi: from Greek *limne* (λιμνη), "lake", and *pi* from *pi*cornavirus.

Reasons to justify the choice of type species:

Limnipvirus A is easily isolated and frequently detected in bluegills; it was also detected in other fish of the Centrarchidae family and from common carp and channel catfish.

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.

According to current knowledge, members of the proposed *Limnipivirus* genus share less than 60% amino acid identity for the concatenated orthologous proteins 1AB-1C-1D-2C-3C-3D.

additional material in support of this proposal

References:

Barbknecht M, Sepsenwol S, Leis E, Tuttle-Lau M, Gaikowski M, Knowles NJ, Lasee B, Hoffman MA. 2014. Characterization of a new picornavirus isolated from the freshwater fish *Lepomis macrochirus*. J. Gen. Virol. 95:601-613.

Lange J, Groth M, Fichtner D, Granzow H, Keller B, Walther M, Platzer M, Sauerbrei A, Zell R. 2014. Virus isolate from carp: genetic characterization reveals a novel picornavirus with two apthovirus 2A-like sequences. J. Gen. Virol. 95:80-90.

Phelps NBD, Mor SK, Armien AG, Batts W, Goodwin AE, Hopper L, McCann R, Ng TFF, Puzach C, Waltzek TB, Delwart E, Winton J, Goyal SM. 2014. Isolation and molecular characterization of a novel picornavirus from baitfish in the USA. PLoS One 9(2):e87593.

Asnani M, Kumar P, Hellen CUT. 2015. Widespread distribution and structural diversity of type IV IRESs in members of *Picornaviridae*. Virology 478:61-74.

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 Organisation:

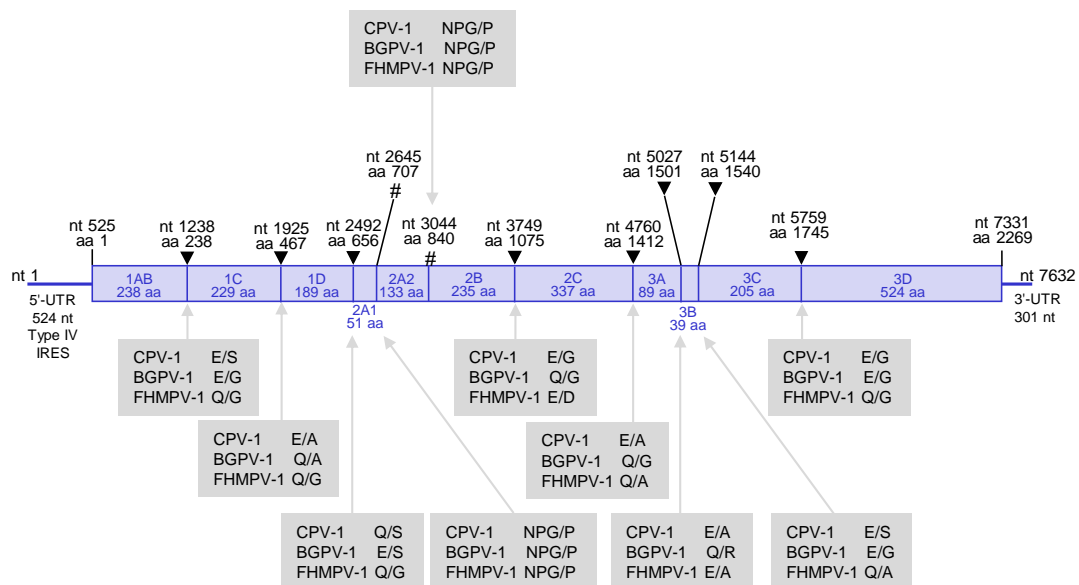**Figure 1:** Schematic depiction of the *Limnipivirus* genome (example CPV-1). The open reading frame is indicated by a box. Positions of putative nt and aa cleavage sites of CPV-1 and the lengths of the deduced proteins are shown. Grey boxes show a comparison of the cleavage sites. Triangles (▼) indicate the 3C^{pro} cleavage sites; the hash (#) indicates both ribosomal skipping sites at the NPG↓P motif.

P1

Genus:

100 HQ595340, **unassigned**, bat picornavirus 1 [NC16A]
100 HQ595341, **unassigned**, bat picornavirus 1 [LMH22A]
99 HQ595342, **unassigned**, bat picornavirus 2 [MH9F]
82 HQ595343, **unassigned**, bat picornavirus 2 [SK17F]
JN831356, **unassigned**, canine picornavirus 1 [dog/Hong Kong/325F/2008]
88 59 JQ814852, **unassigned**, Ia io picornavirus 1
74 KJ641694, **unassigned**, bat picornavirus [BtRs-PicoV/YN2010]
KJ641693, **unassigned**, bat picornavirus [BtRh-PicoV/SC2013]
95 HQ595344, **unassigned**, bat picornavirus 3 [TLC5F]
100 HQ595345, **unassigned**, bat picornavirus 3 [TLC21F]
69 KJ641687, **unassigned**, bat picornavirus [BtMf-PicoV/FJ2012]
100 KJ641690, **unassigned**, bat picornavirus [BtMf-PicoV-1/GD2012]
KJ641699, **unassigned**, bat picornavirus [BtMf-PicoV-2/SAX2011]
58 100 JN572116, **unassigned**, feline picornavirus [127F]
JN572118, **unassigned**, feline picornavirus [661F]
13 100 JN 572115, **unassigned**, feline picornavirus 1 [cat/Hong Kong/073F/2007]
100 JN572117, **unassigned**, feline picornavirus [356F]
100 JN572119, **unassigned**, feline picornavirus [1021F]
100 KJ641689, **unassigned**, bat picornavirus [BtMa-PicoV/FJ2012]
KJ641696, **unassigned**, bat picornavirus [BtVs-PicoV/SC2013]
14 100 AF406813, **Sapelovirus A**, PSV-1 [V13] ⎫ Sapelovirus
15 AY064708, **Sapelovirus B**, SSV-1 [SV2-2383] ⎬
24 35 KJ641697, **unassigned**, bat picornavirus [BtNv-PicoV/SC2013]
91 KJ641685, **unassigned**, bat picornavirus [BtRf-PicoV-1/YN2012]
100 KJ641692, **unassigned**, bat picornavirus [BtRa-PicoV/JS2013]
81 KJ641688, **unassigned**, bat picornavirus [BtRlep-PicoV/FJ2012]
JN420368, **unassigned**, California sealion [1162]
100 AY563023, **Avian sapelovirus**, ASV-1 [TW90A]   Sapelovirus
18 JN674502, **unassigned**, quail picornavirus 1 [quail/HUN/2010]
47 FR727144, **unassigned**, pigeon picornavirus B [pigeon/Norway/03/641/2003]
100 KC560801, **unassigned**, pigeon picornavirus B [GAL-7/2010/Hungary]
100 KP233897, **unassigned**, rabovirus [A Berlin/Jan2011/0572]
KJ950883, **unassigned**, rat picornavirus [RPV/NYC-B10]
54 K02121, **Rhinovirus B**, HRV-14 [1959]
70 EF186077, **Rhinovirus C**, HRV-C3 [QPM]
43 76 L24917, **Rhinovirus A**, HRV-16 [11757]
V01149, **Enterovirus C**, EV-C PV-1 [Mahoney]
90 M33854, **Enterovirus B**, EV-B CVB3 [Nancy]
100 AF201894, **Enterovirus H**, EV-H1 SEV-A1 A-2 plaque
62 D00820, **Enterovirus D**, EV-D70 [J670/71]
77 100 U22521, **Enterovirus A**, EV-A71 [BrCr]   Enterovirus
76 AF326766, **Enterovirus J**, EV-J1 [SV6-1631]
49 AF363453, **Enterovirus G**, EV-G1 (former PEV-9) [UKG/410/73]
94 DQ092769, **Enterovirus E**, EV-E1 (former BEV-1) [LC-R4]
93 DQ092770, **Enterovirus F**, EV-F1 (former BEV-2) [BEV-261 RM2]
99 KM396707, **unassigned**, lesavirus 1 [Mis101308/2012]
93 KM396708, **unassigned**, lesavirus 2 [Nai108015/2012]
98 JQ941880, **Hunnivirus A**, hunnivirus A1 [cattle/2008/HUN]   Hunnivirus
AF231769, **Teschovirus A**, porcine teschovirus 1 [Talfan]   Teschovirus
62 X00871, **Foot-and-mouth disease virus**, FMDV O1 [Kaufbeuren]
100 JN836206, **Bovine rhinitis A virus**, BRAV-2 [H-1] ⎫ Aphthovirus
98 EU236594, **Bovine rhinitis B virus**, BRBV-1 [EC11] ⎬
85 86 X96870, **Equine rhinitis A virus**, ERAV [PERV]
X96871, **Erbovirus A**, equine rhinitis B virus 1 [P1436/71]   Erbovirus
44 93 KM398358, **unassigned**, bovine picornavirus [TCH6]
85 JF973687, **Mosavirus A**, mosavirus A1 [mouse/M-7/USA/2010]   Mosavirus
50 KM873616, **unassigned**, tortoise picornavirus [124-4-10]
100 JQ864242, **Cardiovirus C**, Boone cardiovirus [rat/USA/2010]
100 JX683808, **Cardiovirus C**, Boone cardiovirus [rat/USA/2012]   Cardiovirus
35 M81861, **Cardiovirus A**, Encephalomyocarditis virus 1 [R]
84 M20562, **Cardiovirus B**, Theiler's murine encephalomyelitis virus [GDVII]
JQ814851, **Mischivirus A**, Miniopterus schreibersii picornavirus 1 [bat/China/2010]   Mischivirus
96 KP100644, **unassigned**, African bat icavirus A [TNo13]
57 DQ641257, **Senecavirus A**, Seneca Valley virus 1 [US/SVV-001]   Senecavirus
30 FJ438908, **Cosavirus D**, human cosavirus D1 [5004]
43 100 FJ438902, **Cosavirus A**, human cosavirus A1 [0553]
JN867758, **Cosavirus F**, human cosavirus F1 [PK5006]   Cosavirus
83 FJ438907, **Cosavirus B**, human cosavirus B1 [2263]
51 FJ555055, **Cosavirus E**, human cosavirus E1 [Australia/81]
98 JN819202, **Cadicivirus A**, canine picodicistrovirus [209]   Dicipivirus
98 JF973686, **Rosavirus A**, rosavirus A1 [mouse/USA/M-7/2010]   Rosavirus
26 HM751199, **Melegrivirus A**, turkey hepatitis virus [2993D]
KC663628, **unassigned**, duck megrivirus [LY]   Megrivirus
100 KC876003, **unassigned**, mesivirus [HK21]
81 KC811837, **unassigned**, mesivirus 2 [pigeon/GALI5-PiMeV/2011/HUN]
KJ415177, **unassigned**, tortoise rafivirus A [UF4]   Oscivirus
100 GU182408, **Oscivirus A**, oscivirus A1 [robin/Hong Kong/10717/2006]
27 GU182410, **Oscivirus A**, oscivirus A2 [robin/Hong Kong/10878/2006]
24 100 KF741227, **Sicinivirus A**, sicinivirus A1 [chicken/UCC001/Eire]   Sicinivirus
47 KF979331, **Sicinivirus A**, sicinivirus A1 [ChPV-1 chicken/55C/Hong Kong/2008]
80 JQ691613, **Gallivirus A**, gallivirus A1 [turkey/M176/2011/HUN]   Gallivirus
GU182406, **Passerivirus A**, passerivirus A1 [thrush/Hong Kong/00356/2007]   Passerivirus
88 KF387721, **Sakobuvirus A**, sakobuvirus A1 [FFUP1/Portugal/2012]   Sakobuvirus
GQ179640, **Salivirus A**, salivirus A1 [NG-J1]   Salivirus
58 100 KJ641691, **unassigned**, bat picornavirus [BtMf-PicoV-2/GD2012]
94 KJ641686, **unassigned**, bat picornavirus [BtMr-PicoV/JX2010]
75 AB010145, **Aichivirus A**, AiV-A1 [A846/88]
87 100 JN387133, **Aichivirus A**, CKV-1 [dog/AN211D/USA/2009]
JF755427, **Aichivirus A**, MKV-1 [M-5/USA/2010]   Kobuvirus
90 EU787590, **Aichivirus C**, PKV [swine/S-1-HUN-2007/Hungary]
87 AB084788, **Aichivirus B**, BKV-1 [U-1]
100 KF006985, **Aichivirus B**, ferret kobuvirus [ferret/MpKoV38/NL]
68 KF183915, **Limnipivirus C***, fathead minnow picornavirus [fhm/1/MN/USA/2010]
98 KF183916, **Limnipivirus C***, fathead minnow picornavirus [fhm/2/MN/USA/201]
62 KF874490, **Limnipivirus C***, fathead minnow picornavirus [fhm/20/IL/USA/2010] ⎫ Limnipivirus*
94 KC465953, **Limnipivirus C***, fathead minnow picornavirus [09-283] ⎬
100 KF306267, **Limnipivirus B***, carp picornavirus 1 [F37/06]
JX134222, **Limnipivirus A***, bluegill picornavirus 1 [04-032]
100 KC465954, **Avisivirus A**, avisivirus A1 [turkey/M176-TuASV/2011/HUN] ⎫ Avisivirus
39 KC614703, **Avisivirus A**, avisivirus A1 [USA-IN1] ⎬
98 KM203656, **unassigned**, chicken orivirus 1 [chicken/Pf-CHK1/2013/HUN]
96 57 DQ249299, **Avihepatovirus A**, duck hepatitis A virus 1 [03D]   Avihepatovirus
KJ000696, **unassigned**, aalivirus A1 [duck picornavirus GL/12]
JQ316470, **Pasivirus A**, pasivirus A1 [swine/France/2011]   Pasivirus
84 AB937989, **unassigned**, crohivirus 1 [shrew/ZM54/Zambia/2012]
57 99 KJ641698, **unassigned**, bat picornavirus isolate [BtMf-PicoV-1/SAX2011]
JQ814853, **unassigned**, Rhinolophus affinis picornavirus 1
100 KC935379, **Kunsagivirus A**, kunsagivirus A1 [roller/SZAL6-KuV/2011/HUN]   Kunsagivirus
26 97 **unassigned**, Bat Kunsagivirus
EU142040, **Aquamavirus A**, Aquamavirus A1 (SePV-1) [HO-02-21]   Aquamavirus
20 KC843627, **Potamipivirus A***, eel picornavirus [F15-05]   Potamipivirus*
35 KF006989, **unassigned**, ferret parechovirus [ferret/MpPeV1/NL] ⎫
80 L02971, **Parechovirus A**, human parechovirus 1 [Harris] ⎬ Parechovirus
95 AF327920, **Parechovirus B**, ljunganvirus 1 [87-012]
92 KP230449, **unassigned**, falcovirus A1 [kestrel/VOVE0622/2013/HUN]
KJ641684, **unassigned**, bat picornavirus [BtRf-PicoV-2/YN2012]
85 AJ225173, **Tremovirus A**, avian encephalomyelitis virus 1 [Calnek vaccine strain]   Tremovirus
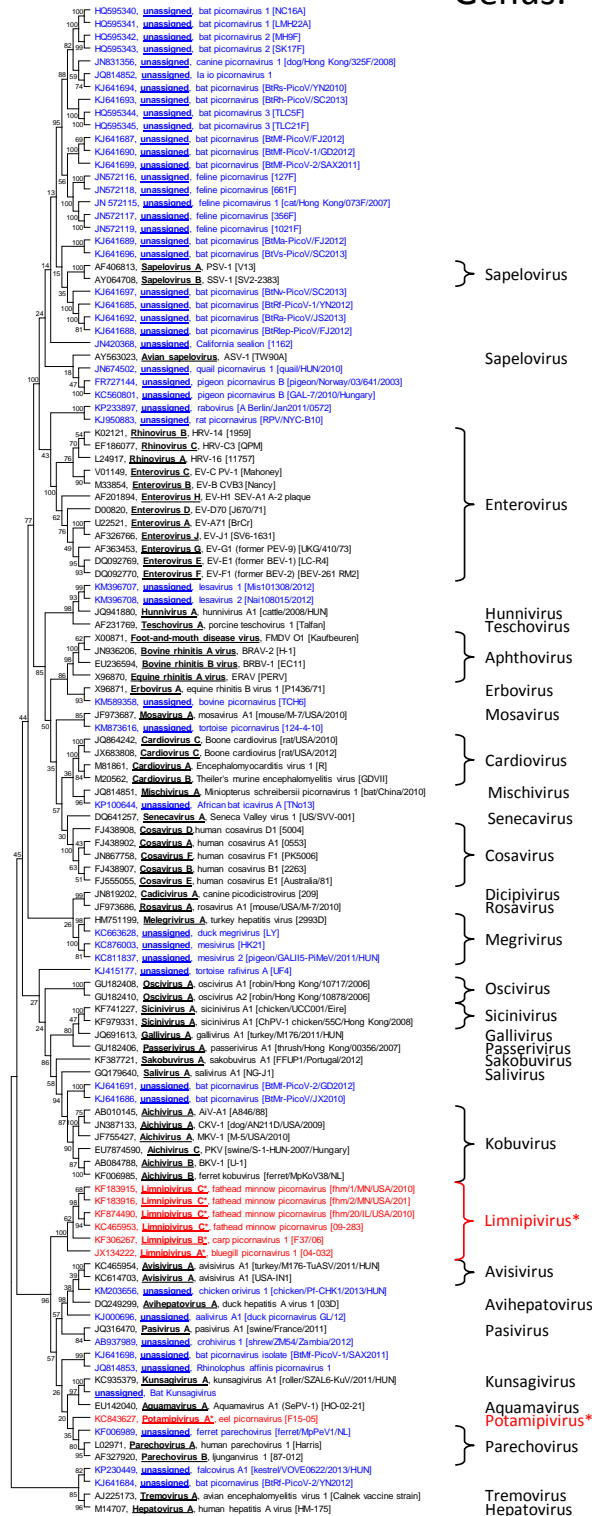96 M14707, **Hepatovirus A**, human hepatitis A virus [HM-175]   Hepatovirus

Figure 2: Maximum likelihood tree of picornavirus P1 gene region. 118 picornavirus sequences retrieved from GenBank were included. Presented are GenBank accession numbers, species names (in bold print and underlined) and type designations. If available, designations of isolates and sequenced specimens, respectively, are given in square brackets. Unassigned viruses are printed in blue. Proposed names are printed in red and indicated by an asterisk (*). Braces indicate acknowledged and proposed (*) genera. Numbers at nodes indicate bootstrap support obtained after 1000 replicates. The scale indicates substitutions/site.
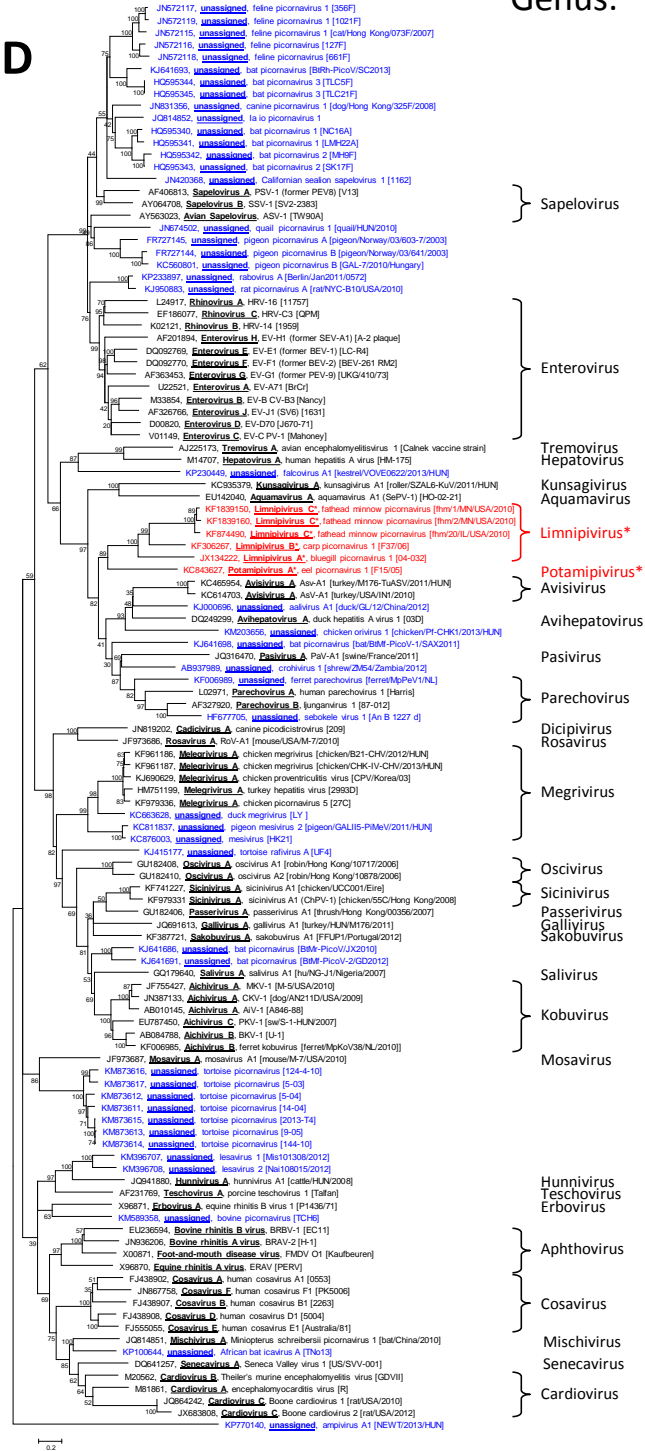
Figure 3: Maximum likelihood tree of picornavirus 3CD gene region. 117 picornavirus sequences retrieved from GenBank were included. Presented are GenBank accession numbers, species names (in bold print and underlined) and type designations. If available, designations of isolates and sequenced specimens, respectively, are given in square brackets. Unassigned viruses are printed in blue. Proposed names are indicated by an asterisk (*). Braces indicate acknowledged and proposed (*) genera. Numbers at nodes indicate bootstrap support obtained after 1000 replicates. The scale indicates substitutions/site.