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):

Roland Zell on behalf of the *Picornaviridae* Study Group

Corresponding author with e-mail address:

Roland Zell (roland.zell@med.uni-jena.de)

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:

Genus:	***Limnipivirus*** (new)
Subfamily:	-
Family:	***Picornaviridae***
Order:	***Picornavirales***

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.

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:
JX132222_BGPV-1_isolate_04-032               100.00   49.88   48.97   48.97   48.97   49.20
KF306267_CPV-1_isolate_F37/06                 49.88  100.00   58.71   58.88   58.77   59.00
KF874490_FHMPV-1_isolate_fhm/20/IL/USA/2010   48.97   58.71  100.00   99.72   98.82   98.26
KC465953_FHMPV-1_isolate_fhm/1/MN/USA/2010    48.97   58.77   98.82   98.88  100.00   99.27
```

KF183916_FHMPV-1_isolate_fhm/2/MN/USA/201	49.20	59.00	98.26	98.32	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:

Subfamily:	-
Family:	***Picornaviridae***
Order:	***Picornavirales***

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

naming a new genus

Code		(assigned by ICTV officers)

To name the new genus: *Limnipivirus*

Assigning the type species and other species to a new genus

Code		(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.

MODULE 10: **APPENDIX**: supporting material

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:

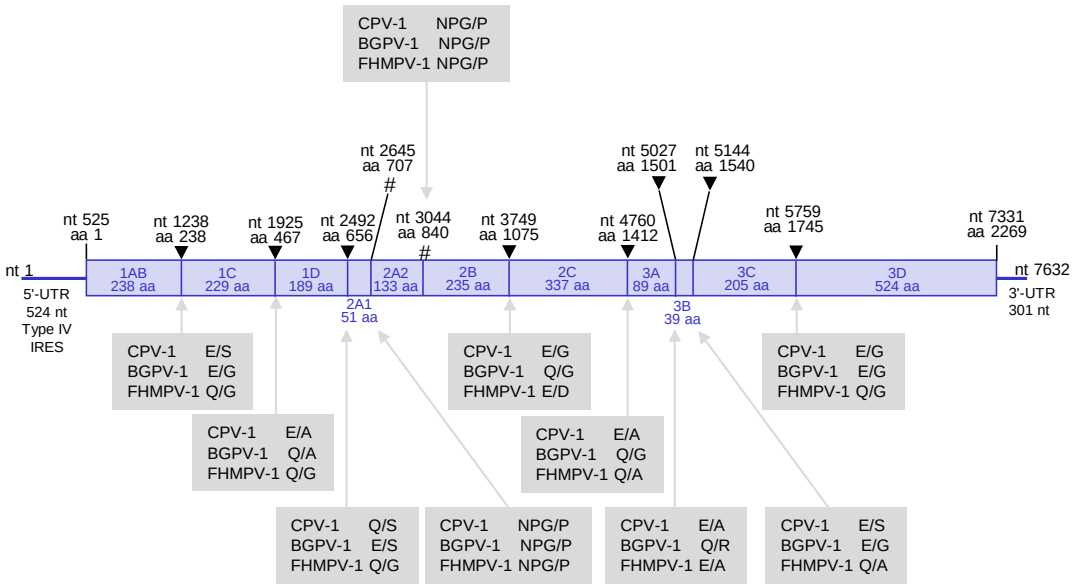

Figure 1: Schematic depiction of the *Limnipivirus* genome (example CPV-1). The open reading frame is indicated by a box. Positions of putative nt and aa cleavage sites of CPV-1 and the lengths of the deduced proteins are shown. Grey boxes show a comparison of the cleavage sites. Triangles (▼) indicate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

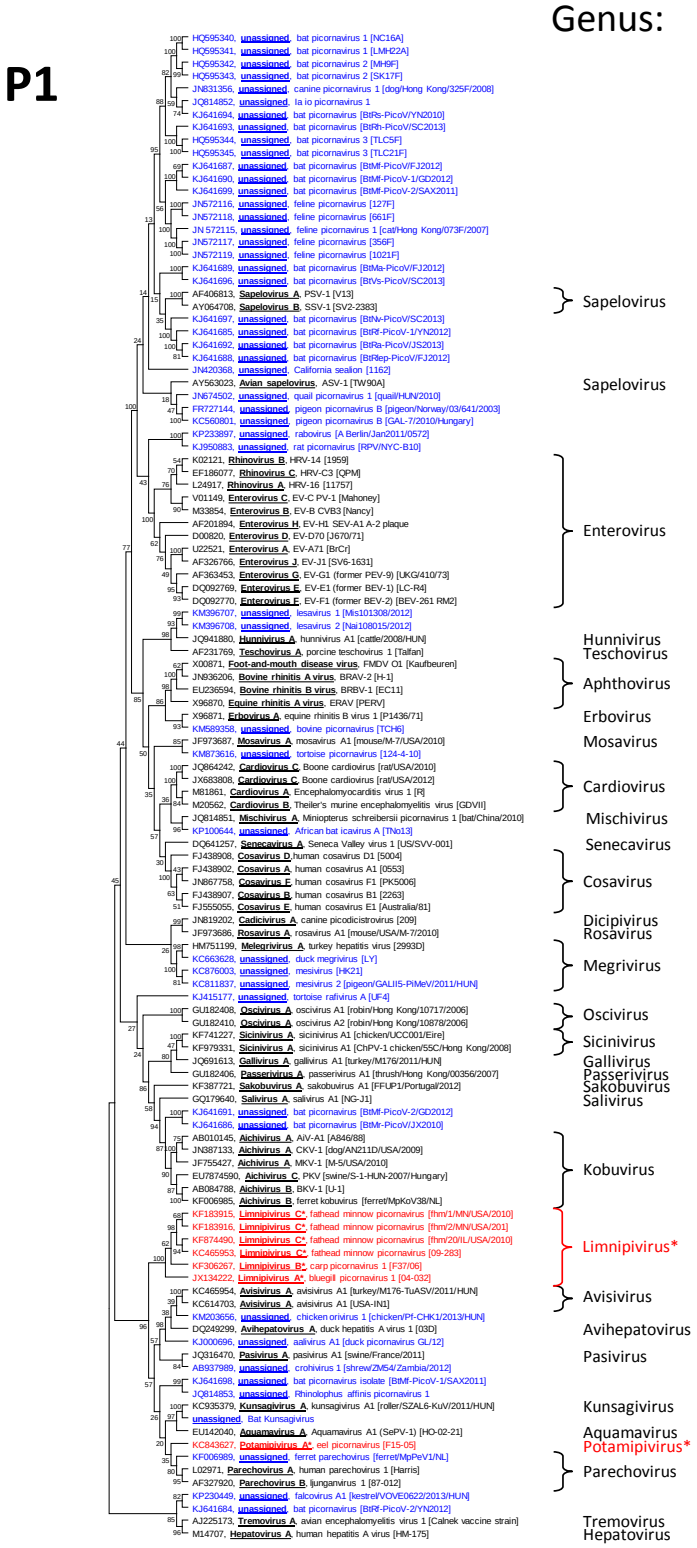

Figure 2: Maximum likelihood tree of picornavirus P1 gene region. 118 picornavirus sequences retrieved from GenBank were included. Presented are GenBank accession numbers, species names (in bold print and underlined) and type designations. If available, designations of isolates and sequenced specimens, 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.

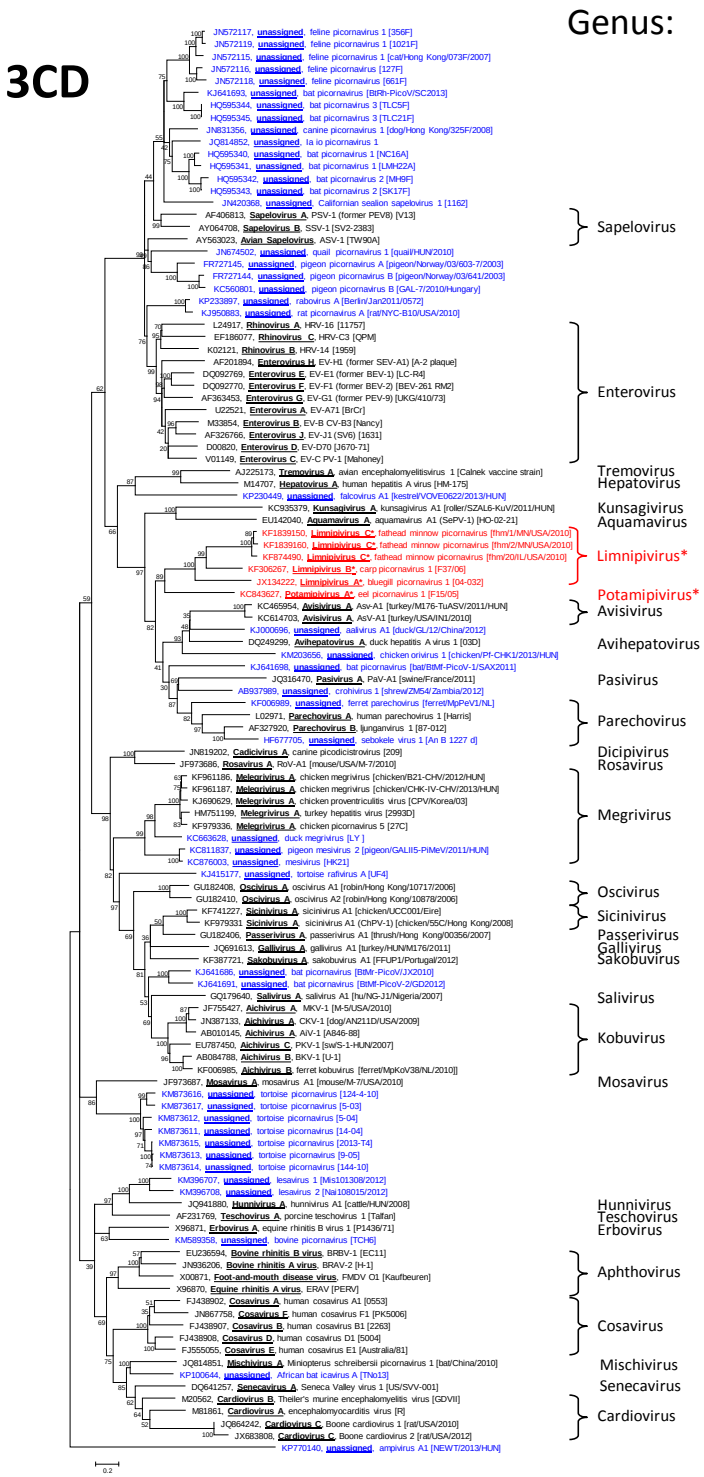

Figure 3: Maximum likelihood tree of picornavirus 3CD gene region. 117 picornavirus sequences retrieved from GenBank were included. Presented are GenBank accession numbers, species names (in bold print and underlined) and type designations. If available, designations of isolates and sequenced specimens, 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.