



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**

<b>Code assigned:</b>	<b>2015.008a-dS</b>	(to be completed by ICTV officers)			
<b>Short title:</b> Creation of a new species ( <i>Potamipivirus A</i> ) in a new genus ( <i>Potamipivirus</i> ). (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	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 checked="" type="checkbox"/>

**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

**Corresponding author with e-mail address:**

Roland Zell ([roland.zell@med.uni-jena.de](mailto: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): 02/09/2015

**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	<b>2015.008aS</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<b><i>Potamipivirus</i></b> (new)	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:	-	
Family:	<b><i>Picornaviridae</i></b>	
Order:	<b><i>Picornavirales</i></b>	
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Potamipivirus A</i>	F15/05 (eel picornavirus 1)	KC843627

**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

Eel picornavirus 1 (EPV-1) is a new picornavirus detected in eels in Germany. EPV-1 is most closely related to *Avihepatovirus*, *Parechovirus* and *Pasivirus* but shows low amino acid identity with proteins of these picornaviruses:

**Table:** Percent amino acid identity with protein from:

	<i>Parechovirus</i>	<i>Parechovirus</i>	<i>Avihepatovirus</i>	<i>Aquamavirus</i>	<i>Pasivirus</i>
EPV-1 protein	HPeV-1 (L02971)	LV-1 (AF327920)	DHAV-1 (DQ249299)	SePV-1 (EU142040)	SPaV-1 (JQ316470)
1AB	30.1	33.6	25.3	27.7	24.5
1C	26.6	31.2	22.7	31.1	30.8
1D	22.8	22.7	18.7	15.9	21.5
2A1	24.0	52.2	20.7	36.4	40.0
2A2	27.9	33.8	30.0	-	-
2B	28.6	25.8	21.3	13.3	19.7
2C	27.6	27.3	29.9	26.5	27.3
3A	8.8	20.3	12.9	11.0	12.2
3C	18.3	19.1	21.0	26.1	19.1
3D	34.6	41.6	38.6	29.0	31.3

**Genome organisation:**

VPg+5'UTR[1AB-1C-1D-2A1<sup>NPGP</sup>/2A2<sup>H-Box/NC</sup>-2B-2C<sup>Hel</sup>/3A-3B<sup>VPg</sup>-3C<sup>pro</sup>-3D<sup>pol</sup>]3'UTR-poly(A)

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	<b>2015.008bS</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
Subfamily:	-	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no family is specified, enter “ <b>unassigned</b> ” in the family box
Family:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	

naming a new genus

Code	<b>2015.008cS</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Potamipivirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2015.008dS</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<i>Potamipivirus 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). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
<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

Although Potamipivirus has a typical picornavirus genome layout (3-4-4 type) that is comparable to the Parechovirus genome, it has low amino acid identity to the orthologous proteins of other picornaviruses. The capsid polypeptide VP0 is predicted to be uncleaved. There are two 2A proteins: 2A1 has a NPG↓P sequence motif, 2A2 contains the H-Box/NC motifs.

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:**

*Potamipi*: from Greek potami (ποταμι), "river", and *pi* from picornavirus.

**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 10: **APPENDIX**: supporting material

additional material in support of this proposal

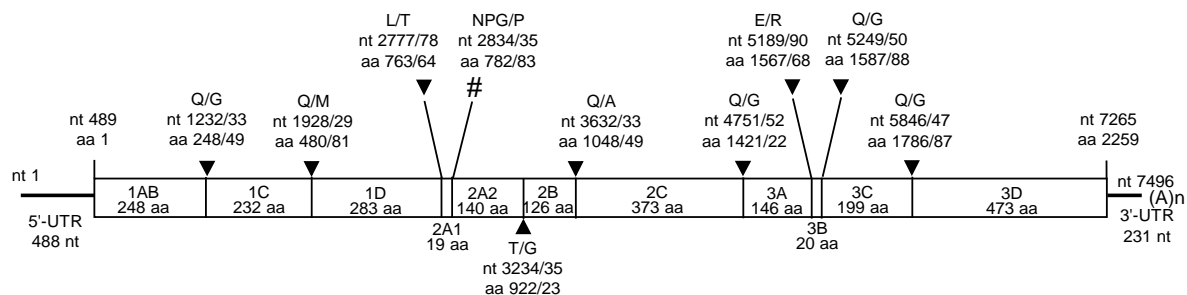
### References:

Fichtner D, Philipps A, Groth M, Schmidt-Posthaus H, Granzow H, Dauber M, Platzer M, Bergmann SM, Schrudde D, Sauerbrei A, Zell R. (2013). Characterization of a novel picornavirus isolate from a diseased European eel (*Anguilla anguilla*). *J. Virol.* 87: 10895-10899.

### 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.

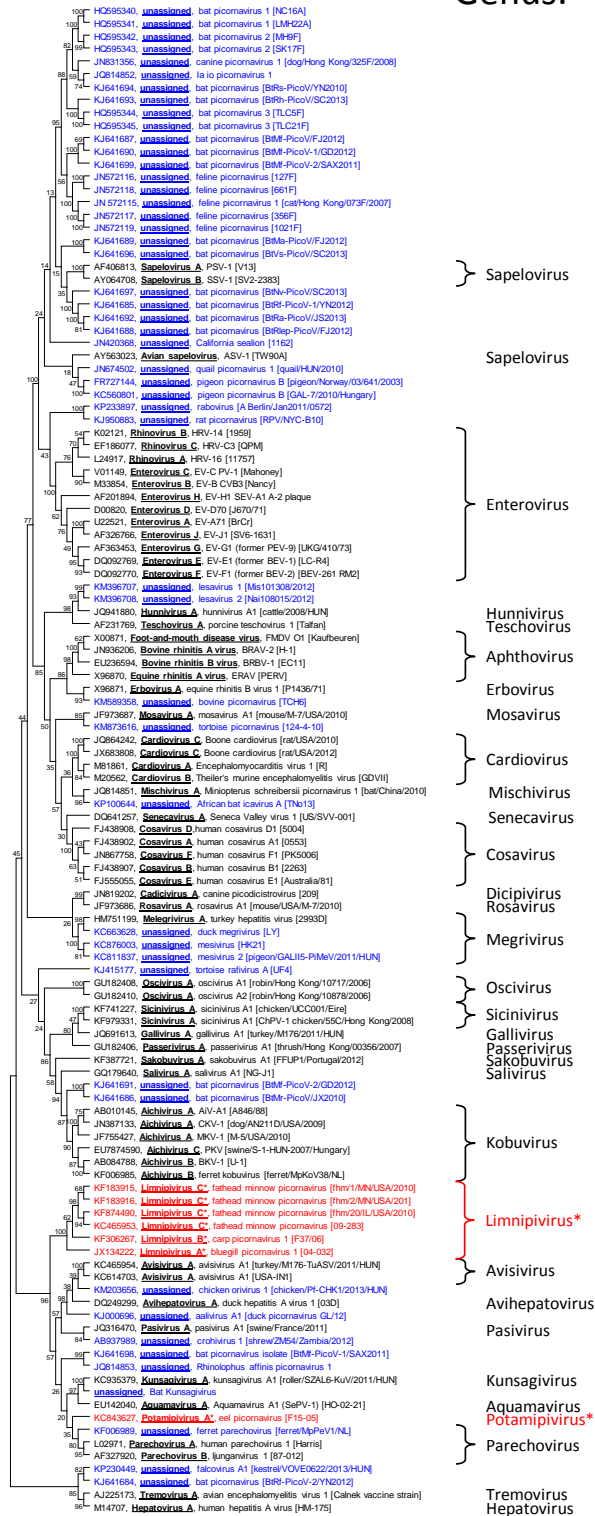
Genome organisation:



**Figure 1:** Schematic depiction of the Potamipivirus genome. The open reading frame is indicated by a box. Positions of putative nt and aa cleavage sites of EPV-1 and the lengths of the deduced proteins are shown. Triangles (▼) indicate the 3C<sup>pro</sup> cleavage sites; the hash (#) indicates the ribosomal skipping site at the NPG↓P motif.

P1

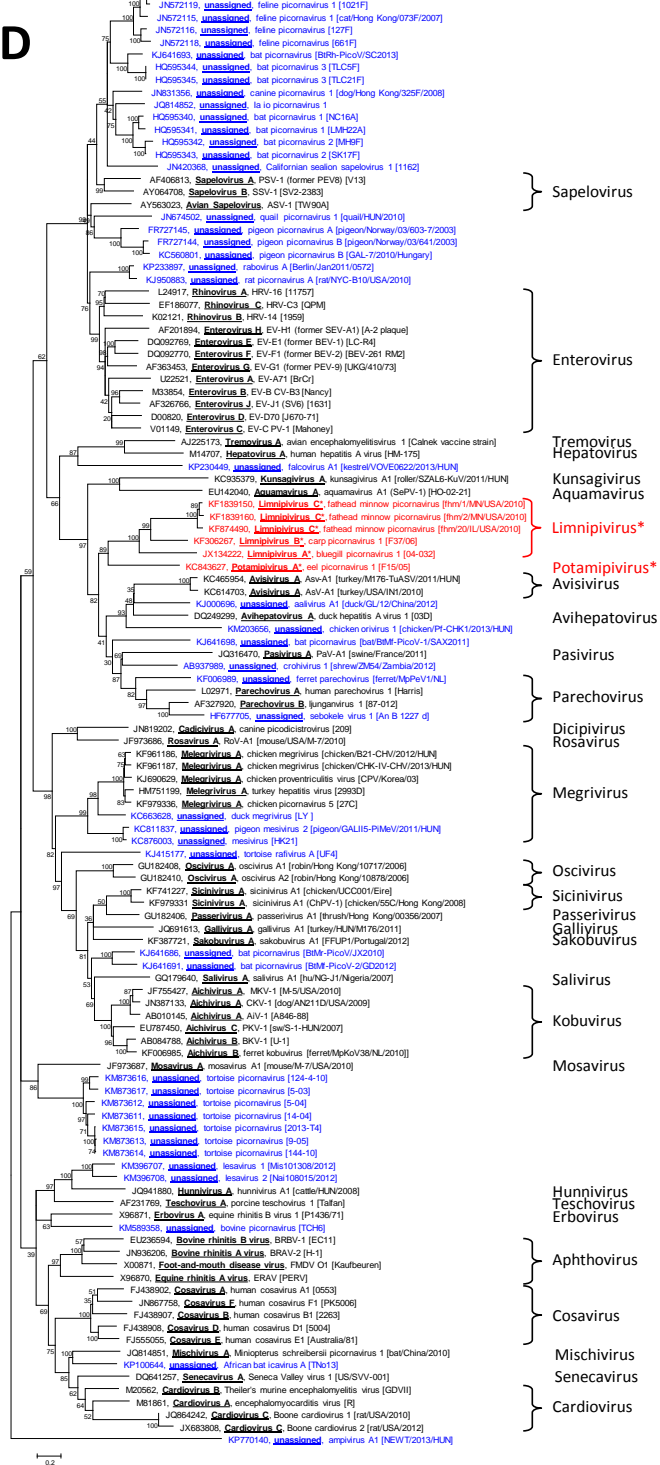
Genus:



**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 nucleotide substitutions/site.

3CD

Genus:



**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 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.