This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.015S*** |  |
| **Short title:**Create 1 new species (*Potamipivirus B*) in the genus *Potamipivirus* |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Zell R, Gorbalenya AE, Hovi T, Knowles NJ, Lindberg M, Oberste S, Palmenberg AC, Reuter G, Simmonds P, Skern T, Tapparel C, Wolthers K, Woo P | roland.zell@med.uni-jena.de; a.e.gorbalenya@lumc.nl; tapani.hovi@thl.fi; nick.knowles@pirbright.ac.uk; michael.lindberg@lnu.se; soberste@cdc.gov; acpalmen@wisc.edu; reuter.gabor@gmail.com; peter.simmonds@ndm.ox.ac.uk; timothy.skern@meduniwien.ac.at; caroline.tapparel@unige.ch; k.c.wolthers@amc.uva.nl; pcywoo@hkucc.hku.hk |
| **Author(s) institutional address(es) (optional):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| Jena University Hospital [RZ]Leiden University Medical Center [AEG]National Institute for Health and Welfare [TH]The Pirbright Institute [NJK]Linnaeus University Kalmar [ML]Centers for Disease Control and Prevention [SO]University of Wisconsin [ACP]University of Pécs [GR]University of Oxford [PS]Medical University of Vienna [TS]University of Geneve [CT]Universiteit van Amsterdam [KW]University of Hong Kong [PW] |

 |
| **Corresponding author** |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ***Picornaviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 21/05/2019 |
| Date of this revision (if different to above): | 20/08/2019 |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
| None.New version since reference was corrected. |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.015S.A.v1.1newsp\_Potamipivirus\_B.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

**Create one new species (*Potamipivirus B*) in the genus *Potamipivirus***

The genus *Potamipivirus* presently consists of 1 species, *Potamipivirus A*.

Three novel, potamipi-like picornaviruses were detected in ...

(i) samples of threespine sticklebacks (*Gasterosteus aculeatus*) in Alaska, USA (Hahn and Dheilly, 2019)

(ii) organ pools (gut, liver, gill) of threadfin breams (*Pentapodus spec.*) captured in Beihai, Guangxi province of China (Shi et al., 2018)

(iii) unspecified flatfish (order *Pleuronectiformes*) captured in Wenling, Zhejiang province of China (Shi et al., 2018).

No virus was isolated yet. Only the genome of the **threespine stickleback picornavirus (TSPV)** was completely sequenced and is considered here. High genetic diversity (54.8% of polyprotein) indicates that TSPV belongs to a novel potamipivirus species.

**Relation of TSPV to *Potamipivirus A* and other picornaviruses:**

- Genome layout of threespine stickleback picornavirus:

 5'-UTR[1AB-1C-1D-2A1npgp/2A2npgp/2A3H-box/NC-2B-2Chel/3A1-3A2-3BVPg-3Cpro-3Dpol]3'-UTR

 (compare Fig. 1 of supporting material)

- The novel potamipivirus has typical hallmarks of picornaviruses:

 - capsid proteins 1AB, 1C, 1D have **rhv** domains with drug-binding site,

 - 2A1 and 2A2 have a **NPGP**-motif, 2A3 has a **H-box/NC** motiv,

 - 2Chel with **GxxGxGKS** motif of helicases,

 - 3BVPg peptide with **Y-3** residue,

 - 3Cpro with **GxCGx14GxH** motif,

 - 3Dpol with **KDE**, **PSG**, **YGDD** and **FLKR** motifs,

- P1 and 3CD sequences of TSPV cluster with the potamipivirus A1 (eel picornavirus) sequence in phylogenetic analyses (compare Figs. 2 & 3 of supporting material).

**Distinguishing features of TSPV compared to potamipivirus A1:**

- TSPV has **two 2A** proteins with **NPGP**-motif (potamipivirus A1 has only one 2Anpgp protein),

- TSPV has **two 3A** proteins, the latter of which has similarity to 3A of potamipivirus A1,

- **Sequence divergence** (uncorrected p-distance) of complete genomes suggests a novel potamipivirus species, ***Potamipivirus B***: genetic distance of *between-species* comparison equals 54.8% (compare Table 1):

- **Sequence divergences** (uncorrected p-distances) of orthologous proteins in pairwise comparisons of TSPV with representative picornavirus supergroup 4 viruses (*Aalivirus/ Aquamavirus/Avihepatovirus/Avisivirus/Crohivirus/Kunsagivirus/Limnipivirus/Orivirus/ Parechovirus/Pasivirus/Potamipivirus/Shanbavirus*) justify creation of a new species (compare Table 1).

**Table 1: Amino acid divergence\***

 P1 2Chel 3Cpro 3Dpol

**threespine stickleback potamipivirus vs. member of ...**

*within-genus* comparisons:

*Potamipivirus Potamipivirus A* 48.8% 53.7% 46.6% 40.8%

*between-genus* comparisons:

*Aalivirus Aalivirus* A 60.2% 53.9% 64.4% 53.6%

*Aquamavirus Aquamavirus A* 58.4% 57.5% 66.1% 60.2%

*Avihepatovirus Avihepatovirus A*  59.9% 55.7% 63.8% 53.8%

*Avisivirus Avisivirus A*  62.7% 56.3% 64.5% 55.5%

*Crohivirus Crohivirus A*  57.4% 52.8% 65.8% 51.5%

 *Crohivirus B*  57.0% 56.0% 64.6% 51.2%

*Grusopivirus*† *Grusopivirus A*† 61.1% 53.5% 66.5% 54.7%

 *Grusopivirus B*† 62.8% 54.5% 62.0% 55.8%

unassigned crane picornavirus 4 62.0% 54.1% 64.9% 53.2%

*Kunsagivirus Kunsagivirus A*  63.3% 57.0% 64.8% 60.4%

 *Kunsagivirus B*  62.5% 58.4% 66.9% 57.3%

 *Kunsagivirus C*  61.9% 58.5% 66.7% 58.5%

*Limnipivirus Limnipivirus A*  63.0% 60.6% 60.0% 53.2%

 *Limnipivirus B*  61.1% 58.9% 59.2% 53.5%

 *Limnipivirus C*  62.5% 60.0% 58.5% 53.8%

*Orivirus Orivirus A*  62.6% 58.0% 68.4% 55.6%

*Parechovirus Parechovirus A*  57.2% 53.7% 66.8% 52.9%

 *Parechovirus B*  55.4% 53.7% 66.8% 52.5%

 *Parechovirus C*  57.3% 55.3% 68.7% 53.4%

 *Parechovirus D*  58.4% 54.2% 67.4% 50.1%

 *Parechovirus E*† 57.8% 51.5% 67.4% 54.2%

 *Parechovirus F*† 57.2% 55.8% 63.9% 52.7%

*Pasivirus Pasivirus A*  57.5% 58.0% 65.5% 56.3%

 *Shanbavirus Shanbavirus A*  61.4% 57.6% 61.7% 53.0%

\* number of amino acid differences per site

† proposed taxa

**Exemplar:**

*Potamipivirus B*, potamipivirus B1 (threespine stickleback picornavirus) strain TSPV, GenBank acc. no. MK189163

**Species demarcation criteria:**

Members of a species of the genus *Potamipivirus*:

- are less than 30% divergent in polyprotein aa sequence,

-are less than 30% divergent in P1 aa sequence,

-are less than 30% divergent in 2C+3CD aa sequence,

- share a common genome organization,

| **References:** |
| --- |
| 1. Hahn MA, Dheilly NM. 2019. Genome characterization, prevalence and transmission mode of a novel picornavirus associated with the threespine stickleback fish (*Gasterosteus aculeatus*). J Virol 93:e02277-18. doi: 10.1128/JVI.02277-18. [Epub ahead of print] PubMed PMID: 30760574.2. Shi et al. 2018. The evolutionary history of vertebrate RNA viruses. Nature 556:197-202. |

**Supporting Material**



**Figure 1:** Genome organization of potamipivirus A1 (eel picornavirus) and B1 (threespine stickleback picornavirus), schematic depiction. The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by a ▼ and the site of termination/reinitiation of RNA translation at the NPGP sequence motif is indicated by a hash (#). The names and lengths of the deduced proteins are presented. The 5'-UTRs may be incomplete. The significance of the 3A1/3A2 cleavage is unclear.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Forty-five picornavirus sequences of the *Aalivirus/Aquamavirus/Avihepatovirus/Avisivirus/Crohivirus/ Kunsagivirus/Limnipivirus/Orivirus/Parechovirus/Pasivirus/Potamipivirus/Shanbavirus* supergroup were retrieved from GenBank; the cardiovirus sequence served as outgroup. [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC).] Presented are GenBank accession numbers, ***genus*** ***names***, *species names*, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 3:**  Phylogenetic analysis of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Forty-six picornavirus sequences of the *Aalivirus/Aquamavirus/Avihepatovirus/Avisivirus/ Crohivirus/Kunsagivirus/Limnipivirus/Orivirus/Parechovirus/Pasivirus/Potamipivirus/Shanbavirus* supergroup were retrieved from GenBank; the cardiovirus sequence served as outgroup. [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC).] Presented are GenBank accession numbers, ***genus*** ***names***, *species names*, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.