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.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.004S*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **1 new picornavirus genus (*Livupivirus*) with 1 species (*Livupivirus A*)** | | | |
|  | | | |
| **Author(s):** | | | |
| Roland Zell, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, M. Steven Oberste, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Caroline Tapparel, Katja C. Wolthers, Patrick C.Y. Woo | | | |
| **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 (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: | | | 15/06/2018 |
| Date of this revision (if different to above): | | |  |

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| **ICTV-EC comments and response of the proposer:** |
|  |

**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: 2018.004S.N.v1.Livupivirus** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_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, try to provide a tree where branch length is related to genetic distance. |

**Create 1 new species (*Livupivirus A*) in a new genus (*Livupivirus*)**

A novel picornavirus—named livupivirus—has been detected in faecal specimens of smooth newts (*Lissotriton vulgaris*). No virus was isolated yet. Livupiviruses differ significantly from ampivirus, another amphibian picornavirus.

**Relation to other picornaviruses:**

- Livupiviruses have a typical picornavirus genome layout:

5'-UTRIRES-IV[L-1AB-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

(compare Fig. 1 of supporting material)

- Livupiviruses possess typical hallmarks of picornaviruses:

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

2A: **H-box/NC** sequence motif,

2Chel: **G**xx**G**x**GKS** motif of helicases,

3BVPg: **Y-3** residue,

3Cpro: **C**x**CG**x14**G**x**H** motif,

3Dpol: **KDE**, **PSG**, **YGDD**, **FLKR** motifs

- Phylogenetic analyses indicate a distinct branch that clusters with picornaviruses of supergroup 2 (*Aichivirus, Dicipivirus, Gallivirus, Megrivirus, Oscivirus, Passerivirus, Rosavirus, Sakobuvirus, Salivirus, Sicinivirus*) in the P1, 2C, 3C, and 3D trees (compare Figs. 2-5 of supporting material).

- The P1 region, 2B-2Chel and 3BVPg-3Cpro-3Dpol proteins shares closest sequence similarity to the osciviruses and the unassigned rafiviruses, but IRES, L protein, 2A and the 3'-UTR differ significantly.

**Distinguishing features of livupiviruses compared to osciviruses:**

1. Livupiviruses have a type IV IRES (vs. type V IRES of osciviruses);

2. Livupiviruses have distinct **L** and **2A proteins**;

3. Livupiviruses have a distinct 3'-UTR;

4. **Sequence divergence** (uncorrected p-distances) of all relevant genome regions is high in pairwise comparisons (Table 1):

**Table 1: Nucleotide and amino acid divergence\***

**P1 2Chel 3Cpro 3Dpol**

**Livupivirus vs. nt aa nt aa nt aa nt aa**

Cadicivirus A 62.9% 78.6% 57.3% 69.2% 60.4% 76.9% 51.1% 65.3%

Cadicivirus B\*\* 62.9% 76.3% 56.9% 69.3% 61.7% 76.4% 51.4% 62.4%

Gallivirus A 66.4% 81.3% 51.4% 66.2% 60.4% 79.5% 46.9% 53.2%

Kobuvirus A 55.7% 66.8% 54.4% 63.7% 59.5% 73.5% 46.1% 50.2%

Megrivirus A 64.3% 82.7% 55.3% 68.1% 61.1% 73.9% 48.9% 56.7%

Oscivirus A1 56.8% 71.9% 53.3% 59.6% 54.4% 68.9% 41.9% 40.2%

Passerivirus A 60.9% 75.2% 54.1% 67.3% 66.1% 78.7% 47.2% 48.5%

Passerivirus B\*\* 61.5% 75.8% 54.2% 68.7% 65.4% 76.4% 45.6% 49.5%

Poecivirus A\*\* 66.7% 81.7% 56.4% 68.2% 59.9% 80.2% 51.2% 59.3%

Rafivirus A\*\* 55.4% 66.8% 54.7% 62.5% 62.6% 78.7% 47.8% 50.1%

Rafivirus B\*\* 55.3% 64.7% 55.2% 64.1% 63.1% 80.7% 47.9% 52.3%

Rosavirus A 63.9% 80.2% 54.6% 64.3% 62.7% 78.7% 51.4% 57.0%

Rosavirus B\*\* 63.8% 80.4% 53.1% 66.9% 61.4% 73.8% 51.1% 57.6%

Rosavirus C\*\* 64.1% 80.0% 52.3% 62.7% 64.7% 76.5% 50.8% 57.5%

Sakobuvirus A 55.9% 67.5% 55.0% 63.1% 63.3% 78.8% 45.8% 50.0%

Salivirus A 56.7% 65.9% 53.1% 61.6% 61.4% 75.5% 51.3% 60.0%

Sicinivirus A 62.3% 77.1% 56.5% 64.5% 62.6% 78.2% 46.0% 49.7%

\* number of base and amino acid differences per site

\*\* to be proposed

**Type species of genus:**

**Livupivirus A**, livupivirus A1 [newt/II-5-Pilis/2014/HUN], GenBank acc. no. KX463670

**Species demarcation criteria:**

not applicable

**Origin of name:**

**livupivirus**: ***Li****ssotriton* ***vu****lgaris* (host) **pi**corna**virus**,

| **References:** |
| --- |
| Pankovics P, Boros A, Toth Z, Phan TG, Delwart E, Reuter G. 2017. Genetic characterization of a second novel picornavirus from an amphibian host, smooth newt (*Lissotriton vulgaris*). Arch Virol 162:1043-1050  . |



**Figure 1:** Comparison of the genome organisation of livupiviruses (proposed genus: Livupivirus) and *Oscivirus A* (schematic depiction). The open reading frames are indicated by boxes. Positions of putative 3Cpro cleavage sites are indicated by ▼. The names and lengths of the deduced proteins are presented.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Seventy-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/ Sakobuvirus/Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus 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. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 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 **2Chel** using Bayesian tree inference (MrBayes 3.2). Seventy-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/ Salivirus/Sakobuvirus/Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus 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. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 4:**  Phylogenetic analysis of picornavirus **3Cpro** using Bayesian tree inference (MrBayes 3.2). Seventy-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/ Salivirus/Sakobuvirus/Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus 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. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 5:**  Phylogenetic analysis of picornavirus **3Dpol** using Bayesian tree inference (MrBayes 3.2). Seventy-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/ Salivirus/Sakobuvirus/Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus 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. 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.