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:** | ***2019.012S*** | |  |
| **Short title:** Create one new genus (*Mupivirus*) with one species (*Mupivirus A*) | | | |
|  | | | |
| **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): | | |  |

|  |
| --- |
| **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:** **2019.012S.N.v1.1newgen\_Mupivirus\_A.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 genus (*Mupivirus*) with one species (*Mupivirus A*)**

Novel rodent picornaviruses have been described by Wu et al. (2018). The viruses were detected in pharyngeal and anal swabs of Ryukyu mice (*Mus caroli*) and Chinese white-bellied rats (*Niviventer confucianus*) captured in the Yunnan and Hubei provinces of China, respectively. These picornaviruses differ significantly from the known rodent picornaviruses. No virus was isolated yet.

**Relation to other picornaviruses:**

- Mupiviruses have a typical picornavirus genome layout:

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

(compare Fig. 1 of supporting material)

- Mupiviruses possess typical hallmarks of picornaviruses:

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

**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 sequences of picornavirus supergroup 1 (*Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/ Malagasivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus/Tottorivirus*) in the P1 and 3CD trees (compare Figs. 2 & 3 of supporting material).

- The polyproteins of both mupiviruses show 23.2% diversity suggesting one species, *Mupivirus A*, with 2 types, mupivirus A1 and A2 (GenBank acc. nos. KY432924, KY432934).

**Distinguishing features of mupiviruses compared to other viruses of picornavirus supergroup 1:**

1. Mupiviruses have unique **L** and **2B proteins** with unknown function; the **2B protein** is highly divergent.

2. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 34 acknowledged and proposed species of picornavirus supergroup 1. The amino acid divergences range from 57.1 to 73.6% for P1, 53.2-68.9% for 2Chel, 62.6-83.7% for 3Cpro and 44.1-62.1% for 3Dpol (compare Table 1). Divergence to sequences of other picornavirus supergroups is even greater.

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

**mupivirus A1 vs. member of P1 2Chel 3Cpro 3Dpol**

*Ailurivirus* *Ailurivirus A* 64.9% 60.8% 71.0% 48.9%

*Aphthovirus* *Bovine rhinitis A virus* 73.2% 63.4% 73.4% 56.4%

*Bovine rhinitis B virus* 73.6% 65.6% 76.2% 53.8%

*Equine rhinitis A virus* 68.9% 63.7% 74.1% 54.2%

*Foot-and-mouth disease virus* 71.2% 65.2% 76.1% 55.3%

*Bopivirus* *Bopivirus A* 64.1% 61.8% 76.1% 60.7%

*Cardiovirus* *Cardiovirus A* 57.8% 55.2% 64.1% 50.0%

*Cardiovirus B* 57.5% 57.7% 62.6% 47.8%

*Cardiovirus C* 58.0% 57.7% 65.4% 49.1%

*Cardiovirus D*† 57.1% 56.0% 64.5% 48.0%

*Cardiovirus E*† 57.5% 53.9% 67.8% 49.4%

*Cardiovirus F*† 60.4% 53.2% 63.7% 44.1%

*Cardiovirus G*† 58.1% 57.4% 65.8% 47.4%

*Cardiovirus H*† 56.8% 53.8% 68.6% 45.9%

*Cosavirus* *Cosavirus A* 64.0% 59.4% 77.0% 53.7%

*Cosavirus B* 61.7% 58.4% 77.4% 52.3%

*Cosavirus D* 63.7% 58.7% 76.0% 53.6%

*Cosavirus E* 63.7% 57.8% 76.0% 53.8%

*Cosavirus F* 61.3% 58.4% 78.6% 53.9%

*Erbovirus* *Erbovirus A* 66.8% 64.1% 83.7% 58.7%

*Hunnivirus* *Hunnivirus A* 71.0% 64.0% 77.7% 59.2%

*Malagasivirus* *Malagasivirus A* 69.4% 68.1% 82.7% 57.3%

*Malagasivirus B* 69.0% 68.5% 82.6% 58.4%

*Mischivirus* *Mischivirus A* 58.4% 56.4% 71.6% 47.5%

*Mischivirus B* 57.8% 57.3% 73.1% 49.5%

*Mischivirus C* 62.4% 55.1% 76.1% 49.9%

*Mischivirus D* 62.5% 56.5% 70.0% 51.6%

*Mosavirus* *Mosavirus A* 60.7% 60.7% 78.5% 60.5%

*Mosavirus B*† 61.5% 61.4% 81.1% 62.1%

*Senecavirus* *Senecavirus A* 63.4% 60.8% 72.8% 46.2%

*Teschovirus* *Teschovirus A* 72.0% 68.2% 79.3% 59.1%

*Teschovirus B*† 71.1% 68.9% 80.3% 59.6%

*Torchivirus* *Torchivirus A* 63.6% 60.1% 78.4% 59.8%

*Tottorivirus* *Tottorivirus A* 70.6% 66.8% 76.6% 59.7%

\* number of amino acid differences per site

† proposed species

**Type species of genus:**

**Mupivirus A**, mupivirus A1 strain RtRn-PicoV/YN2014, GenBank acc. no. KY432924

**Species demarcation criteria:**

not applicable

**Origin of name:**

**mupivirus**: derived from ***Mu****ridae* (the two hosts are of the family *Muridae*) and **pi**corna**virus**

| **References:** |
| --- |
| Wu Z, Lu L, Du J, Yang L, Ren X, Liu B, Jiang J, Yang J, Dong J, Sun L, Zhu Y, Li Y, Zheng D, Zhang C, Su H, Zheng Y, Zhou H, Zhu G, Li H, Chmura A, Yang F, Daszak P, Wang J, Liu Q, Jin Q. 2018. Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome 6:178. |

**Supplementary material**



**Figure 1:** Genome of mupivirus A1 (schematic depiction). The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by a ▼ and the VP0 processing site by a ¶. The names and lengths of the deduced proteins are presented. The 5'-UTR may be incomplete.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Seventy-six picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/Erbovirus/ Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus/Tottorivirus* supergroup were retrieved from GenBank; the enterovirus 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 1,000,000 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). Seventy-two picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/Erbovirus/ Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus/Tottorivirus* supergroup were retrieved from GenBank; the enterovirus 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 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.