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:** | ***2019.011S*** |  |
| **Short title:** Create one new species (*Mosavirus B*) in the genus *Mosavirus* |
|  |
| **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:** **2019.011S.N.v1.1newsp\_Mosavirus\_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 (*Mosavirus B*) in the genus *Mosavirus***

The genus *Mosavirus* presently consists of only one species, *Mosavirus A*, with two types. A novel, mosavirus-like picornavirus was detected in the intestinal contents of captured Himalayan marmots (*Marmota himalayana*) from the Qinghai-Tibetan Plateau, China (Luo et al., 2018).

**Relation to mosavirus and other picornaviruses:**

- Genome layout of marmot mosavirus:

 5'-UTRIRES-II[L-1A-1B-1C-1D-2Anpgp/2B-2Chel/3A-3B1VPg-3B2VPg-3Cpro-3Dpol]3'-UTR

 (compare Fig. 1 of supporting material)

- Marmot mosavirus has typical hallmarks of picornaviruses:

 - long **L protein** possibly with proteinase activity,

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

 - **2A** has a **NPGP**-motif,

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

 - two **3BVPg** peptides with **Y-3** residue,

 - **3Cpro** with **GxCGx14GxH** motif,

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

- Marmot mosavirus P1 and 3CD sequences cluster with the mosavirus sequences in phylogenetic analyses (compare Figs. 2 & 3 of supporting material).

**Distinguishing features of marmot mosavirus compared to mosavirus A1 and A2:**

- Marmot mosavirus has a shorter **L protein** (385 aa vs. 452 aa of mosavirus 2; 5'-end of mosavirus A1 may be incomplete; its **L protein** has a length of 192 aa, N-terminus is missing). The protein sequences show little similarity to each other and to the aphthovirus and erbovirus L proteins.

- **Sequence divergence** (uncorrected p-distance) of complete genome suggests a distinct mosavirus species: mosavirus B1 vs. mosavirus A1 56.2%

 mosavirus B1 vs. mosavirus A2 58.9%

- **Sequence divergences** (uncorrected p-distances) of orthologous proteins in pairwise comparisons of mosaviruses with representative picornavirus supergroup 1 viruses (*Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Malagasi-virus/Mischivirus/Senecavirus/Teschovirus/Torchivirus/Tottorivirus*/unclassified siropiviruses) justify creation of a new species (compare Table 1).

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

mosavirus B1 (marmot mosavirus) vs. member of ... P1 VP1 2Chel 3Cpro 3Dpol

within-genus comparisons:

*Mosavirus* mosavirus A1 0.500 0.638 0.505 0.653 0.441

 mosavirus A2 0.507 0.628 0.508 0.657 0.454

between-genus comparisons:

*Ailurivirus* ailurivirus A1 0.661 0.720 0.654 0.754 0.611

*Aphthovirus* foot-and-mouth disease virus O1 0.717 0.789 0.696 0.768 0.639

*Bopivirus* bopivirus A1 0.682 0.864 0.664 0.793 0.645

*Cardiovirus* cardiovirus A1 0.623 0.718 0.632 0.755 0.616

*Cosavirus* human cosavirus A1 0.683 0.749 0.646 0.768 0.654

*Erbovirus* erbovirus A1 0.641 0.760 0.675 0.795 0.628

*Hunnivirus* hunnivirus A1 0.709 0.829 0.671 0.765 0.628

*Malagasivirus* malagasivirus A1 0.693 0.778 0.655 0.785 0.643

*Mischivirus* mischivirus A1 0.674 0.757 0.609 0.738 0.597

*Senecavirus* senecavirus A1 0.685 0.780 0.635 0.778 0.618

*Mupivirus*† mupivirus A1 0.622 0.726 0.614 0.811 0.621

 mupivirus A2 0.615 0.735 0.615 0.806 0.623

*Teschovirus* teschovirus A1 0.708 0.802 0.695 0.778 0.636

*Torchivirus* torchivirus A1 0.622 0.736 0.685 0.705 0.544

*Tottorivirus* tottorivirus A1 0.700 0.782 0.689 0.789 0.631

\* number of amino acid differences per site

† proposed genus

**Exemplar:**

*Mosavirus B*, mosavirus B1 (marmot mosavirus) strain HT8, GenBank acc. no. KY855435

**Species demarcation criteria:**

Members of a species of the genus *Mosavirus*:

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

-are less than 35% divergent in P1 aa sequence,

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

- share a common genome organization,

| **References:** |
| --- |
| 1. Luo XL, Lu S, Jin D, Yang J, Wu SS, Xu J. 2018. *Marmota himalayana* in the Qinghai-Tibetan plateau as a special host for bi-segmented and unsegmented picobirnaviruses. Emerg Microbes Infections 7:20 |

**Supporting Material**



**Figure 1:** Genome of mosaviruses (schematic depiction). The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by a ▼, the VP0 processing site 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'-UTR may be incomplete. The 1D/2A cleavage site of mosaviruses in unclear.



**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. The proposed name is 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. 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.