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:** | ***2018.009S*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **3 new species (*Rabovirus B, Rabovirus C, Rabovirus D*) in the genus *Rabovirus*** | | | |
|  | | | |
| **Author(s):** | | | |
| Roland Zell, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, Steve Oberste, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Caroline Tapparel, Katja 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:** **2018.009S.N.v1.Rabovirus\_3sp** |

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 3 new species (*Rabovirus B*, *Rabovirus C*, *Rabovirus D*) in the genus *Rabovirus***

The genus *Rabovirus* presently consists of 1 species, *Rabovirus A* (host: Norway rat, *Rattus norvegicus*). Three novel, rabovirus-like picornaviruses have been detected in faecal specimens of various organisms. These are: marmot sapelovirus 1 [HT5] from the Himalayan marmot (*Marmota himalayana*), the murine picornavirus MPV/NYC/2014/M005/0074 from the house mouse (*Mus musculus*), and virus RtMp-PicoV/YN2014 from an unspecified rodent.

**Relation to other picornaviruses:**

- Genome layout of the novel rabo-like viruses:

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

(compare Fig. 1 of supporting material)

- the novel rabo-like viruses have typical hallmarks of picornaviruses:

- presence of a L protein, the sizes range from 68 to 117 amino acids

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

- 2Apro: **G**x**CG**x14**G**x**H** sequence motif,

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

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

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

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

- Phylogenetic analyses indicate clustering with *Rabovirus A* (compare Figs. 2-5 of supporting material).

**Distinguishing features of the novel rabo-like viruses compared to *Rabovirus A*:**

1. Host range: the novel rabo-like viruses were detected in faecal samples of Himalayan marmots, house mouse and an unspecified rodent; the known raboviruses A were detected in specimens from Norway rats.

2. **Sequence divergences** (uncorrected p-distances) of all relevant genome regions suggest 3 species:

- P1: aa divergence <0.53;

- 2Chel: aa divergence <0.43;

- 3Cpro: aa divergence <0.49;

- 3Dpol: aa divergence <0.33 (compare Table 1)

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

**Rabovirus A1 [Berlin/Jan2011/0572]**

**P1 2Chel 3Cpro 3Dpol**

*Rabovirus A*, rabovirus A2 [RPV/NYC-B10] 0.138 0.032 0.037 0.015

*Rabovirus A*, rabovirus A2 [RtRn-PicoV/GD2015] 0.158 0.037 0.027 0.022

Rabovirus B [RtMp-PicoV/YN2014]\*\* 0.513 0.421 0.481 0.325

*Rabovirus C*, marmot sapelovirus 1 [HT5]\*\* 0.504 0.368 0.444 0.322

*Rabovirus D*, murine picornavirus [MPV/NYC/2014/M005/0074] 0.528 0.402 0.428 0.296

unassigned isolate RtMruf-PicoV/JL2014-3 0.553 0.479 0.561 0.407

unassigned isolate RtNn-PicoV/HuB2015-3 0.565 0.464 0.567 0.411

*Avian sapelovirus*, duck picornavirus [TW90A] 0.602 0.602 0.569 0.435

*Sapelovirus A*, porcine sapelovirus [V13] 0.580 0.589 0.533 0.467

*Sapelovirus B*, simian sapelovirus [2383] 0.592 0.508 0.527 0.442

*Enterovirus A*, enterovirus A71 [BrCr] 0.624 0.571 0.560 0.468

*Enterovirus B*, coxsackievirus B3 [Japan] 0.628 0.604 0.566 0.451

*Enterovirus C*, human poliovirus 1 [Mahoney] 0.631 0.571 0.599 0.444

*Enterovirus D*, enterovirus D68 [Fermon] 0.618 0.613 0.577 0.448

Enterovirus E, enterovirus E1 [LC-R4] 0.623 0.564 0.588 0.470

Enterovirus F, enterovirus F1 [BEV-261] 0.603 0.588 0.593 0.453

Enterovirus G, enterovirus G1 [UKG/410/73] 0.644 0.641 0.582 0.437

Enterovirus H, enterovirus H1 [A-2 plaque virus] 0.602 0.617 0.610 0.465

Enterovirus I, enterovirus I1 [19CC] 0.602 0.591 0.610 0.442

Enterovirus J, enterovirus J1 [1631] 0.614 0.583 0.549 0.420

Enterovirus K, enterovirus K1 [rodent/Ee/PicoV/NX2015] 0.599 0.588 0.586 0.497

Enterovirus L, enterovirus L1 [SEV-gx] 0.612 0.551 0.577 0.418

Rhinovirus A, human rhinovirus A9 [ATCC VR-489] 0.650 0.550 0.615 0.468

Rhinovirus B, human rhinovirus B3 [FEB] 0.645 0.595 0.657 0.455

Rhinovirus C, human rhinovirus C3 [HRV-QPM] 0.643 0.584 0.659 0.480

\* number of amino acid differences per site

\*\* to be proposed

**Exemplar:**

***Rabovirus A*:** Berlin/Jan2011/0572, GenBank acc. no. KP233897

***Rabovirus B***: RtMp-PicoV/YN2014, GenBank acc. no. KY432926

***Rabovirus C*:** HT5, GenBank acc. no. KY855432

***Rabovirus D*:** MPV/NYC/2014/M005/0074, GenBank acc. no. MF175072

**Species demarcation criteria:**

Based on available sequence data, preliminary species demarcation criteria were defined.

Members of a species of genus *Rabovirus*:

- share a common genome organization,

- share greater than 70% aa identity in the polyprotein,

- share greater than 70% aa identity in the P1,

- share greater than 75% aa identity in the non-structural proteins 2C + 3CD.

| **References:** |
| --- |
| ***Rabovirus A* (rat picornavirus):**  Firth et al. 2014. Detection of zoonotic pathogens and characterization of novel viruses carried by commensal *Rattus norvegicus* in New York City. mBio 5(5):e01933-14.  Ng et al. 2015. *Rabovirus*: a proposed new picornavirus genus that is phylogenetically basal to enteroviruses and sapeloviruses. Arch Virol 160:2569-2575.  ***Rabovirus B* (rodent picornavirus):**  Du J, Wu Z, Lu L, Jin Q. unpublished.  ***Rabovirus C* (marmot sapelovirus):**  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  ***Rabovirus D* (murine picornavirus):**  Williams SH, Che X, Garcia JA, Klena JD, Lee B, Muller D, Ulrich W, Corrigan RM, Nichol S, Jain K, Lipkin WI. 2018. Viral diversity of house mice in New York City. mBio 9:e01354-17. |



**Figure 1:** Schematic depiction of the genome organisation of raboviruses. The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by ▼. The 1AB processing site is indicated by a diamond (◊), the putative 2Apro cleavage site by a #. 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-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) 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*** and—if available—types and 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 13,000,000 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-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) 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*** and—if available—types and 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 16,000,000 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-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) 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*** and—if available—types and 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 14,000,000 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-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) 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*** and—if available—types and 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 21,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.