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:** | ***2019.013S*** | |  |
| **Short title:** Create 1 new genus (*Parabovirus*) with 3 species (*Parabovirus A, Parabovirus B* and *Parabovirus C*) | | | |
|  | | | |
| **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:** |
| Minor changes suggested to the format of Table 1.  Response: the suggested changes were made. |

**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:** 2019.013S.A.v1.1newgen\_Parabovirus\_A-C.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, *Parabovirus*, with three species, *Parabovirus A, Parabovirus B* and *Parabovirus C***

Novel picornaviruses, paraboviruses, have been identified in faecal samples of Norwegian rats and striped field mice collected in China (W.-P. Guo & Y.-Z. Zhang, unpublished). Similar viruses were identified in pharyngeal and anal swabs of various rodents captured in China (Wu et al., 2018). These picornaviruses differ significantly from the known rodent picornaviruses but show similarity to the raboviruses. They represent six types of three novel species in a novel genus. No virus was isolated yet.

|  |  |  |  |
| --- | --- | --- | --- |
| **Virus name [strain]** | **Host** | **GenBank acc. no.** | **Sampling place/year** |
| **parabovirus A1**  (Rattus norwegicus picornavirus\*)  [Longwan-Rn37] | Brown rat  *(Rattus norvegicus)* | MF352412 | Zhejiang/2012 |
| **parabovirus A2**  (Apodemus agrarius picornavirus)  [Longquan-R132] | striped field mouse  (*Apodemus agrarius*) | MF352414 | Guizhou/2013 |
| **parabovirus A3**  [RtNn-PicoV/HuB2015-3] | Confucian niviventer  (*Niviventer confucianus*) | KY432935 | Hubei/2015 |
| **parabovirus A4**  [RtMruf-PicoV/JL2014-3] | Gray red-backed vole  (*Myodes rufocanus*) | KY432932 | Jilin/2014 |
| **parabovirus A4**  [RtAc-PicoV/GZ2016] | Chevrier's field mouse  (*Apodemus chevrieri*) | KY432940 (partial) | Guizhou/201& |
| **parabovirus B1**  [RtCb-PicoV/HeB2014] | Striped dwarf hamster  (*Cricetulus barabensis*) | KY432927 | Hebei/2014 |
| **parabovirus C1**  [RtNn-PicoV/HuB2015-1] | Confucian niviventer (*Niviventer confucianus*) | KY432933 | Hubei/2015 |

\* Guo & Zhang suggested the name "Apodemus agrarius picornavirus"

**Relation to other picornaviruses:**

- Genome layout of paraboviruses:

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

(compare Fig. 1 of supporting material)

- Paraboviruses have typical hallmarks of picornaviruses:

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

- **2Apro** with **GxCG** motif of chymotrypsin-like cystein proteinases.

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

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

- **3Cpro** : rabovirus A1 to A4: **GxCGx10AxH** motif,

rabovirus B1 and C1: **GxCGx11AxH** motif,

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

- Like raboviruses, paraboviruses have been detected only in **rodent hosts**.

**Distinguishing features:**

- **2A protein** with presumed proteinase activity; characteristic of supergroup 3 picornaviruses (*Anativirus/Enterovirus/Rabivirus/Sapelovirus* supergroup).

- Despite an identical genome layout and some sequence similarity, paraboviruses do not cluster with the raboviruses, felipiviruses and boosepiviruses in **phylogenetic analyses** (compare Figs. 2 & 3 of supporting material). Paraboviruses comprise a **distinct clade** of supergroup 3. Three species with 6 types can be distinguished.

- **Sequence divergence** (uncorrected p-distances) of the polyprotein, P1 and 2C+3CD suggest creation of a novel genus with three species (compare Table 1 A, B, C). Comparison of VP1 sequences indicate four *Parabovirus A* types and each one type of *Parabovirus B* and *C* (Table 1 D). p-Distances of the polyprotein sequences <30% indicate members of a species, whereas the members of the genus *Parabovirus* show p-distances <50% (Table 1A). The P1 polypeptides of the paraboviruses show divergences <20% in within-species comparisons and 39-45% in between-species comparisons (Table 1B). Comparisons of the parabovirus 2C+3CD proteins yield p-distances <30% in within-species comparisons, 34-40% in between-species comparisons and >44% in comparisons with other genera (Table 1C). Members of the same parabovirus type show p-disctances of VP1 <15%. Between-type divergences of the known parabovirus types range from 17-32% (Table 1D).

**Table 1. Estimates of evolutionary divergence between parabovirus and rabovirus protein sequences**

[ 1] MF352412, Parabovirus A1 (Rattus norwegicus picornavirus) [Longwan-Rn37]

[ 2] MF352414, Parabovirus A2 (Apodemus agrarius picornavirus) [Longquan-Rl32]

[ 3] KY432935, Parabovirus A3 [RtNn-PicoV/HuB2015-3]

[ 4] KY432932, Parabovirus A4 [RtMruf-PicoV/JL2014-3]

[ 5] KY432927, Parabovirus B1 [RtCb-PicoV/HeB2014]

[ 6] KY432933, Parabovirus C1 [RtNn-PicoV/HuB2015-1]

[ 7] KP233897, Rabovirus A1 [Berlin/Jan2011/0572]

[ 8] MF352425, Rabovirus A2 [Wencheng-Rn449]

[ 9] KJ950883, Rabovirus A3 (rat picornavirus) [RPV/NYC-B10]

[10] KY432936, Rabovirus A3 [RtRn-PicoV/GD2015]

[11] MF352417, Rabovirus A4 [Wencheng-Rt38-1]

[12] MF352408, Rabovirus A5 [Ruian-Rn93-2]

[13] KY432926, Rabovirus B1 [RtMp-PicoV/YN2014]

[14] KY855432, Rabovirus C1 (marmot rabovirus) [HT5]

[15] MF175072, Rabovirus D1 (murine picornavirus) [MPV/NYC/2014/M005/0074]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

**A. Polyprotein**

[ 1]

[ 2] 0.101

[ 3] 0.180 0.171

[ 4] 0.292 0.291 0.296

[ 5] 0.440 0.441 0.440 0.436

[ 6] 0.474 0.473 0.476 0.481 0.452

[ 7] 0.548 0.544 0.552 0.557 0.545 0.538

[ 8] 0.552 0.548 0.555 0.561 0.548 0.541 0.076

[ 9] 0.553 0.547 0.555 0.562 0.547 0.538 0.083 0.062

[10] 0.553 0.548 0.553 0.558 0.544 0.535 0.072 0.075 0.073

[11] 0.550 0.543 0.551 0.558 0.547 0.535 0.178 0.185 0.180 0.182

[12] 0.552 0.545 0.548 0.558 0.545 0.534 0.259 0.265 0.259 0.259 0.286

[13] 0.538 0.538 0.542 0.544 0.517 0.530 0.480 0.477 0.476 0.478 0.477 0.479

[14] 0.533 0.534 0.538 0.535 0.526 0.530 0.461 0.459 0.461 0.457 0.451 0.452 0.412

[15] 0.536 0.537 0.544 0.540 0.523 0.532 0.471 0.471 0.471 0.473 0.475 0.463 0.346 0.390

**B. P1 polypeptide**

[ 1]

[ 2] 0.112

[ 3] 0.141 0.117

[ 4] 0.199 0.188 0.184

[ 5] 0.400 0.405 0.404 0.391

[ 6] 0.443 0.438 0.437 0.431 0.437

[ 7] 0.557 0.559 0.563 0.556 0.550 0.538

[ 8] 0.569 0.569 0.571 0.564 0.549 0.545 0.120

[ 9] 0.559 0.558 0.566 0.561 0.554 0.542 0.138 0.134

[10] 0.566 0.559 0.571 0.566 0.556 0.532 0.158 0.149 0.104

[11] 0.551 0.545 0.550 0.548 0.545 0.523 0.335 0.337 0.332 0.325

[12] 0.561 0.556 0.564 0.561 0.566 0.532 0.415 0.426 0.425 0.423 0.417

[13] 0.531 0.527 0.529 0.526 0.502 0.515 0.511 0.510 0.501 0.501 0.497 0.505

[14] 0.515 0.513 0.519 0.508 0.488 0.492 0.502 0.501 0.499 0.501 0.463 0.492 0.406

[15] 0.535 0.527 0.533 0.525 0.505 0.516 0.524 0.527 0.513 0.517 0.506 0.540 0.368 0.381

**C. 2C+3CD protein**

[ 1]

[ 2] 0.068

[ 3] 0.146 0.145

[ 4] 0.259 0.252 0.272

[ 5] 0.350 0.350 0.351 0.346

[ 6] 0.385 0.380 0.394 0.396 0.350

[ 7] 0.452 0.449 0.459 0.462 0.449 0.455

[ 8] 0.453 0.447 0.459 0.459 0.451 0.448 0.029

[ 9] 0.450 0.449 0.458 0.461 0.448 0.451 0.025 0.029

[10] 0.456 0.453 0.459 0.465 0.449 0.456 0.028 0.021 0.027

[11] 0.462 0.459 0.458 0.464 0.451 0.462 0.175 0.175 0.181 0.175

[12] 0.452 0.449 0.457 0.460 0.446 0.454 0.035 0.027 0.036 0.034 0.171

[13] 0.448 0.448 0.455 0.461 0.423 0.447 0.386 0.386 0.380 0.386 0.390 0.386

[14] 0.459 0.468 0.470 0.455 0.435 0.452 0.361 0.355 0.354 0.359 0.369 0.353 0.347

[15] 0.449 0.446 0.457 0.453 0.431 0.445 0.355 0.363 0.360 0.359 0.361 0.360 0.289 0.320

**D. Capsid protein VP1**

[ 1]

[ 2] 0.176

[ 3] 0.227 0.157

[ 4] 0.311 0.284 0.285

[ 5] 0.568 0.568 0.570 0.560

[ 6] 0.587 0.583 0.573 0.592 0.575

[ 7] 0.652 0.655 0.679 0.663 0.647 0.638

[ 8] 0.668 0.660 0.679 0.671 0.632 0.650 0.183

[ 9] 0.667 0.655 0.675 0.660 0.629 0.631 0.219 0.201

[10] 0.678 0.663 0.690 0.675 0.634 0.620 0.229 0.211 0.119

[11] 0.680 0.675 0.670 0.687 0.664 0.633 0.417 0.412 0.419 0.404

[12] 0.659 0.651 0.668 0.648 0.668 0.650 0.468 0.483 0.476 0.490 0.512

[13] 0.691 0.693 0.699 0.695 0.600 0.639 0.626 0.628 0.615 0.616 0.660 0.603

[14] 0.674 0.683 0.693 0.670 0.615 0.649 0.597 0.599 0.582 0.596 0.616 0.590 0.526

[15] 0.692 0.681 0.679 0.678 0.604 0.659 0.611 0.627 0.599 0.608 0.662 0.675 0.473 0.471

within type comparison, between types/within species comparison,

between species/within genus comparison, between genera comparison

- **Sequence divergences** (uncorrected p-distances) of orthologous proteins in pairwise comparisons with representative sequences of all acknowledged and proposed species of picornavirus supergroup 3 support creation of one genus with three species (compare Table 2).

**Table 2: Amino acid divergence\***

parabovirus A1 (MF352412) vs. member of ... P1 2Chel 3Cpro 3Dpol

*within-genus* comparisons:

*Parabovirus*† *Parabovirus B*† (parabovirus B1) 40.4% 45.2% 37.7% 26.9%

*Parabovirus C*†(parabovirus C1) 44.2% 45.9% 50.3% 28.4%

*between-genus* comparisons:

*Anativirus* *Anativirus A* (duck picornavirus) 58.2% 61.4% 60.6% 38.5%

*Anativirus B*† (phacovirus) 60.1% 63.0% 61.1% 51.1%

Boosepivirus† Boosepivirus A† (boosepivirus A1) 50.7% 44.5% 51.7% 34.7%

Boosepivirus B† (boosepivirus B1) 51.1% 45.4% 50.6% 38.4%

Boosepivirus C† (boosepivirus C1) 51.6% 49.5% 50.6% 40.1%

*Diresapivirus*† *Diresapivirus A*† (diresapivirus A1, KJ641688) 59.6% 53.2% 54.9% 43.5%

*Diresapivirus B*† (diresapivirus B1) 61.6% 51.5% 50.5% 40.1%

*Enterovirus* *Enterovirus A* (enterovirus A71) 60.8% 58.3% 51.6% 43.4%

*Enterovirus B* (enterovirus B1) 60.8% 57.9% 54.4% 41.6%

*Enterovirus C* (poliovirus 1) 64.3% 57.0% 59.3% 40.3%

*Enterovirus D* (enterovirus D68) 63.7% 61.0% 58.2% 43.4%

*Enterovirus E* (enterovirus E1) 62.5% 58.8% 56.6% 42.3%

*Enterovirus F* (enterovirus F1) 61.0% 60.2% 57.1% 42.1%

*Enterovirus G* (enterovirus G1) 62.1% 63.6% 53.8% 41.4%

*Enterovirus H* (enterovirus H1) 61.9% 60.7% 63.7% 40.8%

*Enterovirus I* (enterovirus I1) 61.2% 55.9% 57.1% 41.4%

*Enterovirus J* (enterovirus J1) 62.0% 59.0% 54.9% 41.2%

*Enterovirus K* (enterovirus K1) 59.6% 53.9% 65.0% 45.8%

*Enterovirus L* (enterovirus L1) 60.2% 58.5% 56.6% 41.2%

*Rhinovirus A* (human rhinovirus A9) 64.5% 57.0% 61-0% 45.2%

*Rhinovirus B* (human rhinovirus B3) 64.0% 57.6% 62.4% 42.8%

*Rhinovirus C* (human rhinovirus C1) 65.2% 59.9% 62.6% 43.4%

*Felipivirus*† *Felipivirus A*† (felipivirus A1) 49.0% 43.8% 44.5% 33.2%

*Rabovirus Rabovirus A* (rabovirus A1) 56.1% 45.5% 55.1% 40.6%

*Rabovirus B* (rabovirus B1) 53.4% 44.7% 50.3% 42.6%

*Rabovirus C* (rabovirus C1) 51.5% 46.2% 59.4% 40.4%

*Rabovirus D* (rabovirus D1) 53.4% 46.5% 52.4% 40.2%

*Sapelovirus Sapelovirus A* (porcine sapelovirus ) 54.0% 58.5% 54.8% 39.7%

*Sapelovirus B* (simian sapelovirus) 56.7% 52.0% 47.8% 31.2%

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

***Parabovirus A***, parabovirus A1 strain Longwan-Rn37, GenBank acc. no. MF352412

**Exemplar:**

***Parabovirus A***, parabovirus A1 strain Longwan-Rn37, GenBank acc. no. MF352412

***Parabovirus B***, parabovirus B1 strain RtCb-PicoV/HeB2014, GenBank acc. no. KY432927

***Parabovirus C***, parabovirus C1 strain RtNn-PicoV/HuB2015-1, GenBank acc. no. KY432933

**Species demarcation criteria:**

Members of a species of the genus *Parabovirus*:

- 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,

- share a rodent host.

**Origin of name:**

**parabovirus**: derived from **para** (Greek παρά, beside, by) and **rabovirus**.

| **References:** |
| --- |
| 1. 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. Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome. 2018 Oct 3;6(1):178.  2. W.-P. Guo & Y.-Z. Zhang. Picornaviruses in small mammals, China. Unpublished. |

**Supporting Material**



**Figure 1:** Genome of paraboviruses (schematic depiction). The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by a ▼, the putative 2Apro cleavage site by a diamond (◊), and the VP0 processing site by a ¶. The names and lengths of the deduced proteins are presented. The 5'-UTRs may be incomplete.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Eighty-nine picornavirus sequences of the *Anativirus/Enterovirus/Rabovirus/Sapelovirus* 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.



**Legend to Figure 3:**  Phylogenetic analysis of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Ninty-two picornavirus sequences of the *Anativirus/Enterovirus/Rabovirus/Sapelovirus* 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 15,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.