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:** | ***2019.002S*** | |  |
| **Short title:** Create one new genus (*Boosepivirus*) with three species (*Boosepivirus A, Boosepivirus B* and *Boosepivirus 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): | | |  |

|  |
| --- |
| **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: 2019.002S.N.v1.1newgen\_Boosepivirus\_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, *Boosepivirus*, with three species, *Boosepivirus A, Boosepivirus B* and *Boosepivirus C***

Novel picornaviruses, boosepiviruses, have been identified in faecal samples of diarrhoeic cattle in the Hokkaido Prefecture, Japan, and in unspecified samples of sheep (Nagai et al., 2015; Forth et al., 2019). These viruses represent four types of three novel species in a novel genus. No virus was isolated yet.

**Relation to other picornaviruses:**

- Genome layout of boosepiviruses:

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

(compare Fig. 1 of supporting material)

- Boosepiviruses have typical hallmarks of picornaviruses:

- **type I IRES**

- 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** with **GxCGx10A/GxH** motif,

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

- Boosepiviruses comprise a **distinct clade** of the *Anativirus/Enterovirus/Rabovirus/Sapelovirus* supergroup (supergroup 3) in phylogenetic analyses (compare Figs. 2 & 3 of supporting material). Three species with 4 types can be distinguished (compare Table 1).

**Distinguishing features:**

- **2A protein** with presumed proteinase activity; characteristic of supergroup 3 picornaviruses.

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons of boosepiviruses with representative sequences of all acknowledged and proposed species of picornavirus supergroup 3 (*Anativirus/Enterovirus/Rabivirus/Sapelovirus*) (compare Table 1).

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

boosepivirus A1 (LC006971) vs. member of ... P1 2Chel 3Cpro 3Dpol

*within-genus* comparisons:

*Boosepivirus*† *Boosepivirus B*† (boosepivirus B1) 43.7% 39.8% 43.9% 37.1%

*Boosepivirus C*†(boosepivirus C1) 43.1% 47.6% 32.8% 36.6%

*between-genus* comparisons:

*Anativirus* *Anativirus A* (duck picornavirus) 58.5% 57.5% 63.5% 39.2%

*Anativirus B*† (phacovirus) 61.2% 57.7% 61.2% 51.6%

*Diresapivirus*† *Diresapivirus A*† (diresapivirus A1, KJ641688) 62.8% 52.3% 54.2% 44.9%

*Diresapivirus B*† (diresapivirus B1) 64.8% 52.7% 52.0% 42.0%

*Enterovirus* *Enterovirus A* (enterovirus A71) 61.0% 60.1% 62.2% 47.6%

*Enterovirus B* (enterovirus B1) 63.6% 60.2% 57.8% 42.5%

*Enterovirus C* (poliovirus 1) 62.2% 58.3% 61.1% 44.7%

*Enterovirus D* (enterovirus D68) 65.3% 59.4% 61.1% 45.7%

*Enterovirus E* (enterovirus E1) 62.4% 55.2% 61.1% 46.3%

*Enterovirus F* (enterovirus F1) 61.4% 58.2% 58.3% 43.6%

*Enterovirus G* (enterovirus G1) 62.5% 61.6% 58.3% 44.7%

*Enterovirus H* (enterovirus H1) 63.0% 59.6% 64.4% 45.5%

*Enterovirus I* (enterovirus I1) 61.3% 57.6% 58.9% 43.6%

*Enterovirus J* (enterovirus J1) 62.9% 61.8% 57.2% 44.1%

*Enterovirus K* (enterovirus K1) 60.6% 58.1% 62.9% 46.7%

*Enterovirus L* (enterovirus L1) 60.0% 57.3% 56.7% 44.5%

*Rhinovirus A* (human rhinovirus A9) 63.7% 57.8% 61.1% 45.3%

*Rhinovirus B* (human rhinovirus B3) 63.3% 56.9% 61.5% 43.6%

*Rhinovirus C* (human rhinovirus C1) 65.2% 60.3% 63.3% 44.8%

*Felipivirus*† *Felipivirus A*†(felipivirus A1) 48.1% 43.6% 46.1% 37.5%

*Parabovirus*† *Parabovirus A*†(parabovirus A1) 50.7% 44.5% 51.7% 34.7%

*Parabovirus B*† (parabovirus B1) 47.8% 43.9% 48.6% 35.6%

*Parabovirus C*† (parabovirus C1) 51.1% 44.7% 54.1% 36.9%

*Rabovirus Rabovirus A* (rabovirus A1) 55.8% 45.8% 58.3% 43.4%

*Rabovirus B* (rabovirus B1) 55.1% 49.4% 57.8% 42.5%

*Rabovirus C* (rabovirus C1) 55.6% 47.4% 60.6% 39.8%

*Rabovirus D* (rabovirus D1) 55.1% 49.1% 54.4% 43.6%

*Sapelovirus Sapelovirus A* (porcine sapelovirus ) 57.3% 55.0% 56.7% 43.3%

*Sapelovirus B* (simian sapelovirus) 57.2% 50.6% 53.9% 37.6%

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

***Boosepivirus A***, boosepivirus A1 strain Bo-11-39/2009/JPN, GenBank acc. no. LC006971

**Exemplar:**

***Boosepivirus A***, boosepivirus A1 strain Bo-11-39/2009/JPN, GenBank acc. no. LC006971

***Boosepivirus B***, boosepivirus B1 strain Bo-12-39/2009/JPN, GenBank acc. no. LC006979

***Boosepivirus C***, boosepivirus C1 strain NA, GenBank acc. no. LR216006

**Species demarcation criteria:**

Members of a species of the genus *Boosapivirus*:

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

- are less than 40% divergent in P1 aa sequence,

- are less than 35% divergent in 2C+3CD aa sequence,

- share a common genome organization,

**Origin of name:**

**boosepivirus**: derived from **bo**vine, **o**vine **s**apelo-**e**ntero-like **pi**corna**virus**

| **References:** |
| --- |
| 1. Nagai, M., Omatsu, T., Aoki, H., Kaku, Y., Belsham, G.J., Haga, K., Naoi, Y., Sano, K., Umetsu, M., Shiokawa, M., Tsuchiaka, S., Furuya, T., Okazaki, S., Katayama, Y., Oba, M., Shirai, J., Katayama, K. and Mizutani, T. (2015). Identification and complete genome analysis of novel picornavirus in bovine in Japan. Virus Res. 2015 Aug 7. pii: S0168-1702(15)30033-2.  2. Forth LF, Scholes SFE, Pesavento PA, Jackson K, Mackintosh A, Carson A, Howie F, Schlottau K, Wernike K, Pohlmann A, Höper D, Beer M. (2019). Novel picornavirus in lambs with severe encephalomyelitis. Emerging Infectious Diseases 25(5), May 2019. |

**Supporting Material**



**Figure 1:** Genome of boosepiviruses (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.