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:** | ***2019.005S*** |  |
| **Short title:** Create 1 new genus (*Diresapivirus*) with 2 species (*Diresapivirus A* and *Diresapivirus B*) |
|  |
| **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:** |
| Table 1 list host species not hosts.Response: table heading has been changed to ‘host species’. |

**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:** 2019.005S.A.v1.1newgen\_Diresapivirus\_A-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 genus, *Diresapivirus*, with two species, *Diresapivirus A* and *Diresapivirus B***

Various picornaviruses from pharyngeal or anal swabs of bats captured in China have been described by Wu et al. (2016). Samples of 4440 bat individuals of 40 species were analyzed. Four novel viruses (Table 1) are distantly related to entero- and sapeloviruses and comprise members of two species of a new picornavirus genus. These viruses were provisionally named diresapiviruses.

**Table 1: Bat picornavirus isolates**

**Virus strain host species GenBank acc. no.**

diresapivirus A1 BtRf-PicoV-1/YN2012 Rhinolophus ferrumequinum KJ641685 (complete genome)

diresapivirus A1 BtRlep-PicoV/FJ2012 Rhinolophus lepidus KJ641688 (partial genome)

diresapivirus A1 BtRa-PicoV/JS2013 Rhinolophus affinis KJ641692 (partial genome)

diresapivirus B1 BtNv-PicoV/SC2013 Nyctalus velutinus KJ641697 (complete genome)

**Relation to other picornaviruses:**

- Genome layout of diresapiviruses:

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

 (compare Fig. 1 of supporting material)

- Diresapviruses 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. The presumed catalytic

 tryad comprises the conserved **H65-D95-GxC166G** residues.

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

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

 - **3Cpro** with **GxCGx10GxH** motif,

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

- Diresapiviruses comprise a **distinct clade** of the *Anativirus/Enterovirus/Rabovirus/Sapelovirus* supergroup (supergroup 3) in phylogenetic analyses (compare Figs. 2 & 3 of supporting material).

**Distinguishing features:**

- Diresapiviruses lack a **L protein**.

- **Sequence divergence** (uncorrected p-distance) of **complete polyprotein** suggest two diresapivirus species: 31.9-32.8% divergence of polyprotein in *between-species* comparisons; *within-species* comparisons indicate 1 diresapivirus A1 type (compare Table 2).

**Table 2. Estimates of evolutionary divergence between diresapivirus sequences**

 [ 1 2 3 4 ]

[1] KJ641685, diresapivirus A1 BtRf-PicoV-1/YN2012

[2] KJ641688, diresapivirus A1 BtRlep-PicoV/FJ2012 0.011

[3] KJ641692, diresapivirus A1 BtRa-PicoV/JS2013 0.011 0.005

[4] KJ641697, diresapivirus B1 BtNv-PicoV/SC2013 0.319 0.327 0.328

- **Sequence divergences** (uncorrected p-distances) of orthologous proteins in pairwise comparisons of diresapiviruses with representative sequences of all acknowledged and proposed species of picornavirus supergroup 3 (*Anativirus/Enterovirus/Rabivirus/Sapelovirus*) support creation of one genus with two species (compare Table 3).

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

diresapivirus A1 (KJ641685) vs. member of ... P1 2Chel 3Cpro 3Dpol

*within-genus* comparisons:

*Diresapivirus*† *Diresapivirus A*† (diresapivirus A1, KJ641688) 1.3% 0.9% 0.5% 0.4%

 *Diresapivirus B*† (diresapivirus B1) 31.0% 17.8% 35.3% 24.7%

*between-genus* comparisons:

*Anativirus* *Anativirus A* (duck picornavirus) 61.7% 57.2% 64.2% 42.6%

 *Anativirus B* (phacovirus) 62.7% 61.0% 69.8% 50.9%

 *Anativirus B* (quail picornavirus) 62.6% 61.7% 64.2% 51.7%

*Boosepivirus*† *Boosepivirus A*† (boosepivirus A1) 62.8% 52.3% 54.2% 44.9%

 *Boosepivirus B*† (boosepivirus B1) 61.6% 52.9% 60.9% 46.6%

 *Boosepivirus C*†(boosepivirus C1) 60.7% 56.7% 58.1% 46.4%

*Enterovirus* *Enterovirus A* (enterovirus A71) 67.7% 57.4% 61.3% 47.6%

 *Enterovirus B* (enterovirus B1) 67.6% 54.9% 60.8% 47.9%

 *Enterovirus C* (poliovirus 1) 67.8% 59.3% 60.8% 45.6%

 *Enterovirus D* (enterovirus D68) 66.7% 57.7% 61.3% 46.5%

 *Enterovirus E* (enterovirus E1) 67.9% 59.7% 61.3% 47.9%

 *Enterovirus F* (enterovirus F1) 66.2% 58.3% 61.9% 45.3%

 *Enterovirus G* (enterovirus G1) 68.4% 60.8% 61.9% 45.5%

 *Enterovirus H* (enterovirus H1) 67.3% 57.4% 62.4% 47.4%

 *Enterovirus I* (enterovirus I1) 67.4% 58.6% 63.0% 44.9%

 *Enterovirus J* (enterovirus J1) 66.8% 54.7% 60.2% 43.2%

 *Enterovirus K* (enterovirus K1) 64.7% 56.7% 62.0% 49.6%

 *Enterovirus L* (enterovirus L1) 66.3% 58.5% 57.5% 45.9%

 *Rhinovirus A* (human rhinovirus A9) 68.1% 63.0% 61.9% 46.8%

 *Rhinovirus B* (human rhinovirus B3) 68.3% 58.2% 62.8% 44.7%

 *Rhinovirus C* (human rhinovirus C1) 69.0% 60.0% 60.2% 47.0%

*Felipivirus*† *Felipivirus A*† (felipivirus A1) 59.8% 51.1% 55.2% 42.6%

*Parabovirus*† *Parabovirus A*† (parabovirus A1) 59.6% 53.2% 54.9% 43.5%

 Parabovirus B† (parabovirus B1) 59.7% 45.8% 57.1% 43.9%

 Parabovirus C† (parabovirus C1) 59.5% 50.2% 60.1% 41.1%

*Rabovirus Rabovirus A* (rabovirus A1) 61.9% 56.4% 62.5% 45.9%

 *Rabovirus B* (rabovirus B1) 62.8% 51.5% 65.2% 49.0%

 *Rabovirus C* (rabovirus C1) 60.1% 54.7% 63.6% 45.5%

 *Rabovirus D* (rabovirus D1) 60.5% 53.9% 64.1% 46.6%

*Sapelovirus Sapelovirus A* (porcine sapelovirus ) 58.1% 53.5% 64.1% 47.1%

 *Sapelovirus B* (simian sapelovirus) 57.4% 48.2% 59.7% 41.7%

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

***Diresapivirus A***, diresapivirus A1 strain BtRf-PicoV-1/YN2012, GenBank acc. no. KJ641685

**Exemplar:**

*Diresapivirus A*, diresapivirus A1 strain BtRf-PicoV-1/YN2012, GenBank acc. no. KJ641685

*Diresapivirus B*, diresapivirus B1 strain BtNv-PicoV-1/SC2013, GenBank acc. no. KJ641697

**Species demarcation criteria:**

Members of a species of the genus *Diresapivirus*:

- 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:**

**diresapivirus**: derived from acronym "**di**stant relatives of **r**abo-, **e**ntero-, **s**apelo-, **a**nativiruses" and **pi**corna**virus**

| **References:** |
| --- |
| 1. Wu et al. 2016. Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. ISME J 10:609-620. |

**Supporting Material**



**Figure 1:** Genome of diresapiviruses (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. The exact location of the 1D/2A cleavage site is unknown (indicated by a ?).



**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.