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**

|  |  |  |  |
| --- | --- | --- | --- |
|  | **2019.008S** | |  |
| **Short title:**  Create 1 new genus (*Grusopivirus*) with 2 species (*Grusopivirus A* and *Grusopivirus* *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:** |
| KY312543 (proposed species *Grusopivirus C*) labelled as CG but only partial coding seq?  Response: The proposal for *Grusopivirus C* has been removed. |

**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:** 2019.008S.A.v1.1newgen\_Grusopivirus\_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 (*Grusopivirus*) with 2 species (*Grusopivirus A* and *Grusopivirus B*)**

Six novel picornaviruses have been detected in faecal samples of red-crowned cranes (*Grus japonensis*) collected in China, 2014, four of which--grusopivirus A1, A2, B1 and crane picornavirus 4--show similarity to members of picornavirus supergroup 4 (Wang et al., 2018).

**Relation of grusopiviruses to other picornaviruses:**

- Genome layout of grusopiviruses A1 and A2:

5'-UTR[1AB-1C-1D-2A1npgp/2A2npgp/2A3npgp/2A4H-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'-UTR

Genome layout of grusopiviruses B1:

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

(compare Fig. 1 of supporting material)

- Grusopiviruses have typical hallmarks of picornaviruses:

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

- grusopivirus A1 and A2: **2A1, 2A2 and 2A3** have a **NPGP**-motif, **2A4** has a **H-box/NC**

motiv,

grusopivirus B1: **2A** with unknown function

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

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

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

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

- ***Grusopivirus*** comprises a distinct clade in P1 and 3CD trees of picornavirus supergroup 4 (compare Figs. 2, 3 of supporting material).

**Distinguishing features of grusopiviruses compared to picornavirus supergroup 4:**

- Grusopiviruses A1 and A2 have three **2Anpgp** proteins plus **2A4H-box/NC**, whereas grusopivirus B1 and crane picornavirus 4 have a 2A protein with unknown function.

- **Sequence divergence** (uncorrected p-distance) of complete genomes suggests three grusopivirus species, ***Grusopivirus A*** and ***Grusopivirus B***: genetic distances of *between-species* comparisons range from 44.1 to 48.0% (compare Table 1):

**Table 1. Estimates of evolutionary divergence between grusopivirus sequences**

[1] KY312544, grusopivirus A1 (crane picornavirus 5) isolate yc-5

[2] KY312542, grusopivirus A2 (crane picornavirus 3) isolate yc-3

[3] KY312545, grusopivirus B1 (crane picornavirus 6) isolate yc-6

[4] KY312543, crane picornavirus 4, isolate yc-4

[ 1 2 3 4 ]

[1]

[2] 28.5%

[3] 48.0% 45.2%

[4] 47.7% 45.1% 44.1%

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins in pairwise comparisons of grusopiviruses with representatives of all acknowledged and proposed species of picornavirus supergroup 4 viruses (*Aalivirus/Aquamavirus/Avihepatovirus/ Avisivirus/Crohivirus/Kunsagivirus/Limnipivirus/Orivirus/Parechovirus/Pasivirus/ Potamipivirus/Shanbavirus*) justifies creation of a **new genus with 2 species** (compare Table 2).

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

grusopivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol

*Within-genus* comparisons:

*Grusopivirus*† *Grusopivirus A*† *(grusopivirus A2)* 64.7% 2.1% 2.2% 5.1%

*Grusopivirus B*† 66.1% 43.5% 43.6% 47.5%

unassignedcrane picornavirus 4 67.6% 41.0% 42.0% 41.4%

*Between-genus* comparisons:

*Aalivirus Aalivirus* A 67.0% 48.2% 50.8% 49.6%

*Aquamavirus Aquamavirus A* 76.3% 73.3% 80.3% 71.6%

*Avihepatovirus Avihepatovirus A*  67.8% 45.6% 48.9% 50.6%

*Avisivirus Avisivirus A*  69.2% 56.1% 64.4% 59.7%

*Avisivirus B* 68.3% 60.4% 61.4% 56.0%

*Avisivirus C* 67.3% 58.3% 61.4% 59.1%

*Crohivirus Crohivirus A*  78.6% 66.0% 76.2% 64.5%

*Crohivirus B*  75.3% 67.9% 77.8% 63.9%

*Kunsagivirus Kunsagivirus A*  81.5% 73.2% 84.1% 69.3%

*Kunsagivirus B*  82.6% 70.1% 81.3% 69.1%

*Kunsagivirus C*  80.9% 68.2% 81.2% 69.3%

*Limnipivirus Limnipivirus A*  81.0% 76.9% 81.8% 66.1%

*Limnipivirus B*  79.9% 75.7% 82.1% 66.9%

*Limnipivirus C*  80.2% 76.2% 81.4% 66.5%

*Orivirus Orivirus A*  73.4% 59.4% 72.6% 55.6%

*Parechovirus Parechovirus A*  74.6% 67.3% 76.0% 67.9%

*Parechovirus B*  76.9% 67.0% 73.5% 62.2%

*Parechovirus C*  76.3% 63.2% 75.0% 61.9%

*Parechovirus D*  75.6% 67.6% 76.1% 62.4%

*Parechovirus E*† 75.8% 67.7% 77.2% 65.2%

*Parechovirus F*† 76.2% 69.6% 79.4% 63.6%

*Pasivirus Pasivirus A*  77.7% 69.2% 77.0% 68.7%

*Potamipivirus Potamipivirus A* 78.0% 68.0% 81.4% 63.1%

*Potamipivirus B*† 75.4% 67.1% 82.0% 65.4%

*Shanbavirus Shanbavirus A*  80.4% 57.6% 70.5% 65.1%

\* number of amino acid differences per site

† proposed taxa

- There is evidence of **interspecies recombination**. The presumed recombinant, **crane picornavirus 3**, exhibits an overall polyprotein divergence of 28.5% to its closest relative, grusopivirus A1 (Table 1). The P1 polyprotein, however, shows divergences >54% with all known grusopiviruses, whereas 2Chel, 3Cpro and 3Dpol display great similarity to grusopivirus A1 (diversity only 2-5%) but great divergence to grusopivirus B1 and C1 (>40%) (compare Table 3). Thus, crane picornavirus 3 could be a recombinant of a member of *Grusopivirus A* with a member of a yet unrecognized grusopivirus species; it is tentatively named **grusopivirus A2**.

Table 3. Estimates of Evolutionary Divergence between Sequences

[1] KY312542, grusopivirus A2 (crane picornavirus 3) isolate yc-3

[2] KY312544, grusopivirus A1 (crane picornavirus 5) isolate yc-5

[3] KY312545, grusopivirus B1 (crane picornavirus 6) isolate yc-6

[4] KY312543, crane picornavirus 4 isolate yc-4

**A. P1**

[ 1 2 3 4 ]

[ 1]

[ 2] 0.647

[ 3] 0.566 0.661

[ 4] 0.544 0.676 0.493

**B. 2Chel**

[ 1]

[ 2] 0.021

[ 3] 0.435 0.435

[ 4] 0.407 0.410 0.460

**C. 3Cpro**

[ 1]

[ 2] 0.022

[ 3] 0.436 0.436

[ 4] 0.420 0.420 0.387

**D. 3Dpol**

[ 1]

[ 2] 0.051

[ 3] 0.462 0.475

[ 4] 0.416 0.414 0.392

**Type species of genus:**

*Grusopivirus A*, grusopivirus A1 (crane picornavirus 5) strain yc-5, KY312544

**Exemplar:**

*Grusopivirus A*, grusopivirus A1 (crane picornavirus 5) strain yc-5, KY312544

*Grusopivirus B*, grusopivirus B1 (crane picornavirus 6) strain yc-6, KY312545

**Species demarcation criteria:**

Members of a species of the genus *Grusopivirus*:

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

-are less than 30% divergent in P1 aa sequence,

-are less than 20% divergent in 2C+3CD aa sequence,

- share a common genome organization,

| **References:** |
| --- |
| 1. Wang Y, Yang S, Liu D, Zhou C, Li W, Lin Y, Wang X, Shen Q, Wang H, Li C, Zong M, Ding Y, Song Q, Deng X, Qi D, Zhang W, Delwart E. The fecal virome of red-crowned cranes. Arch Virol. 2018 Sep 17. doi: 10.1007/s00705-018-4037-x. |

**Supporting Material**



**Figure 1:** Genome organization of grusopiviruses A1 and B1 (schematic depiction). The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated 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 UTRs may be incomplete.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Forty-five picornavirus sequences of the *Aalivirus/Aquamavirus/Avihepatovirus/Avisivirus/Crohivirus/ Kunsagivirus/Limnipivirus/Orivirus/Parechovirus/Pasivirus/Potamipivirus/Shanbavirus* 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 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). Forty-six picornavirus sequences of the *Aalivirus/Aquamavirus/Avihepatovirus/Avisivirus/ Crohivirus/Kunsagivirus/Limnipivirus/Orivirus/Parechovirus/Pasivirus/Potamipivirus/Shanbavirus* 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 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.