

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.004S** |  |
| **Short title:** Create one new species (*Grusopivirus C*) in the genus *Grusopivirus* (*Picornavirales*: *Picornaviridae*) |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Picornaviridae* Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 02/06/2020 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.004S.A.v1.Grusopivirus\_1nsp.xlsx |

**Abstract**

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| The *Grusopivirus* genus presently comprises two species, *Grusopivirus A* and *Grusopivirus B*. Another grusopivirus-like virus has been detected in faecal samples of the rainbow lorikeet (*Trichoglossus moluccanus*) in China. The virus has a genome layout identical to that of grusopivirus A1 (5'-UTR[1AB-1C-1D/2A1npgp-2A2npgp-2A3npgp-2A4H-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) and significant sequence similarity (65.4% amino acid identity of the polyprotein) which justifies assignment to the genus *Grusopivirus*, but to a new species, *Grusopivirus C*. Within-genus sequence diversities are 65.5% and 54.3% for P1, 7% and 45.0% for 2Chel, 23.2 % and 43.1% for 3Cpro and 14.6% and 48%% for 3Dpol in comparisons with the respective grusopivirus A1 and B1 sequences. Divergences to sequences of other picornavirus genera are >65.9% for P1, >43.9% for 2Chel, >49.4% for 3Cpro and 50.4% for 3Dpol. |

**Text of proposal**

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| **Create a new species, *Grusopivirus C*, in the genus *Grusopivirus***The *Grusopivirus* genus presently comprises two species, *Grusopivirus A* and *Grusopivirus B*. The grusopiviruses have been detected in faecal samples of red-crowned cranes in China (Y. Wang et al. 2019). No viable viruses were isolated. Another grusopivirus-like virus was detected in faecal samples of the rainbow lorikeet (*Trichoglossus moluccanus*) (H. Wang et al. 2019). Despite significant similarities to grusopivirus A1, the lorikeet picornavirus exhibits differences which justify assignment to a new species.**Relation to other picornaviruses:**1. The lorikeet picornavirus has a typical picornavirus genome layout: 5'-UTR[1AB-1C-1D/2A1npgp-2A2npgp-2A3npgp-2A4H-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR (compare Fig. 1 of supporting material)2. The lorikeet picornavirus possesses typical hallmarks of picornaviruses:  **capsid proteins:** 1AB, 1C, 1D have **rhv** domains with drug-binding site,  **2Chel:** **G**xx**G**x**GKS** motif of helicases, **3BVPg:** **Y-3** residue, **3Cpro:** **C**x**CG**x14**G**x**H** motif, **3Dpol:** **KDE**, **PSG**, **YGDD**, **FLKR** motifs3. **Phylogenetic analyses** indicate clustering with the sequences of the picornavirus supergroup 4 (*Aalivirus, Aquamavirus, Avihepatovirus, Avisivirus, Crohivirus, Grusopivirus, Kunsagivirus, Limnipivirus, Orivirus, Parechovirus, Pasivirus, Potamipivirus, Shanbavirus*) in the P1 and 3D trees (compare Figs. 2 & 3 of supporting material). Closest relative is the grusopivirus A1.4. **Divergence:** The polyproteins of lorikeet picornavirus and grusopivirus A1 (crane picornavirus 5) show 34.6% diversity suggesting a new grusopivirus species, *Grusopivirus C*, with 1 type, grusopivirus C1 (GenBank acc. nos. MK443503).**Distinguishing features of grusopivirus C (lorikeet picornavirus) compared to other viruses of picornavirus supergroup 4:** 1. Grusopiviruses A and C have **four 2A proteins**; the 2A1, 2A2 and 2A3 proteins have a NPGP sequence motif, whereas 2A4 has a H-box/NC sequence motif (compare Fig. 1).2. **Within-genus divergence** (uncorrected p-distances) in comparisons with grusopivirus A1 and B1 are 65.5% and 54.3% for P1, 7% and 45.0% for 2Chel, 23.2 % and 43.1% for 3Cpro and 14.6% and 48% for 3Dpol (compare Table 1).3. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 40 acknowledged and proposed species of picornavirus supergroup 4. The amino acid divergences range from 65.9 to 81.9% for P1, 43.9-76.9% for 2Chel, 49.4-86.8% for 3Cpro and 50.4-71.0% for 3Dpol (compare Table 1). **Species demarcation criteria:**Members of a species of the genus *Grusopivirus*:-are less than 66% divergent in P1 aa sequence,-are less than 50% divergent in 2C+3CD aa sequence,- cluster in phylogenetic analyses of the P1, 3C, 3D proteins.**Exemplar virus of species:** ***Grusopivirus C***, grusopivirus C1 (lorikeet picornavirus) strain LoPV-1, GenBank acc. no. MK443503. |

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**Supporting evidence**

**Table 1: Diversities of orthologous proteins\***

**Grusopivirus C1 (lorikeet picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Grusopivirus Grusopivirus A* 65.5% 7.6% 23.2% 14.6%

 *Grusopivirus B* 54.3% 45.0% 43.1% 48.0%

*Aalivirus Aalivirus A* 69.9% 48.5% 52.5% 50.4%

*Aquamavirus Aquamavirus A* 77.6% 73.3% 81.3% 70.1%

*Avihepatovirus Avihepatovirus A* 65.9% 43.9% 62.1% 50.1%

*Avisivirus Avisivirus A* 72.6% 54.9% 61.4% 59.5%

 *Avisivirus B* 68.0% 60.6% 60.2% 56.5%

 *Avisivirus C* 68.8% 57.9% 49.4% 60.9%

*Crohivirus Crohivirus A* 77.8% 67.3% 74.6% 62.6%

 *Crohivirus B* 75.8% 69.8% 76.8% 62.9%

*Kunsagivirus Kunsagivirus A* 80.5% 71.4% 81.6% 70.2%

 *Kunsagivirus B* 80.0% 69.6% 80.8% 69.8%

 *Kunsagivirus C* 78.6% 68.4% 81.4% 71.0%

*Limnipivirus Limnipivirus A* 81.9% 76.9% 82.5% 66.0%

 *Limnipivirus B* 81.3% 76.6% 85.1% 67.6%

 *Limnipivirus C* 81.6% 75.9% 83.2% 67.1%

*Orivirus Orivirus A* 71.0% 59.9% 67.8% 58.9%

*Parechovirus Parechovirus A* 74.3% 69.5% 73.3% 65.2%

 *Parechovirus B* 73.7% 67.9% 71.8% 62.4%

 *Parechovirus C* 74.9% 64.4% 75.7% 62.4%

 *Parechovirus D* 75.0% 67.9% 75.1% 62.6%

 *Parechovirus E* 73.7% 67.0% 75.7% 65.7%

 *Parechovirus F* 74.5% 69.9% 76.8% 63.6%

*Pasivirus Pasivirus A* 76.8% 71.9% 76.5% 67.8%

*Potamipivirus Potamipivirus A* 79.4% 68.9% 78.0% 63.6%

 *Potamipivirus B* 80.0% 67.2% 80.9% 64.2%

*Shanbavirus Shanbavirus A* 80.7% 71.0% 67.0% 66.0%

unassigned Beihai conger picornavirus 77.6% 68.2% 79.4% 64.8%

unassigned Guangdong spotted longbarbel catfish picornavirus 80.6% 74.1% 84.9% 65.1%

unassigned Wenling bighead beaked sandfish picornavirus 81.5% 74.5% 84.5% 65.9%

unassigned Wenling brown-lined puffer picornavirus 77.3% 68.9% 82.8% 64.9%

unassigned Wenling fish picornavirus 79.1% 73.9% 78.8% 65.0%

unassigned Wenling hoplichthys picornavirus 78.2% 70.6% 83.4% 64.6%

unassigned Wenling lepidotrigla picornavirus 78.2% 70.7% 80.5% 64.0%

unassigned Wenling rattails picornavirus 77.5% 69.1% 82.3% 62.9%

unassigned Wenling scaldfish picornavirus 1 77.8% 68.6% 84.9% 63.0%

unassigned Wenling scaldfish picornavirus 2 78.2% 72.2% 78.7% 65.3%

unassigned Wenling thamnaconus septentrionalis picornavirus 80.3% 76.5% 86.8% 67.6%

unassigned Western African lungfish picornavirus 75.7% 73.6% 82.4% 69.0%

unassigned Wuhan carp picornavirus 76.1% 69.4% 83.3% 62.2%

unassigned Wuhan sharpbelly picornavirus 1 74.7% 70.3% 77.7% 64.1%

unassigned Yancheng osbecks grenadier anchovy picornavirus 78.4% 71.4% 85.3% 66.7%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of grusopiviruses (schematic depiction). The genome of the lorikeet picornavirus 1 is compared to the genomes of crane picornavirus 5, the exemplar virus of *Grusopivirus A* and crane picornavirus 6, the exemplar virus *of Grusopivirus B*. The open reading frame is indicated by a box. Position of putative 3Cpro cleavage sites are indicated by a ▼. The names and lengths of the deduced proteins are presented. The 5’-UTR may be incomplete.



**Figure 2:** Phylogenetic analysis of picornavirus P1 protein using Bayesian tree inference (MrBayes 3.2). Sixty-one picornavirus sequences of the *Aalivirus/Aquamavirus/Avihepatovirus/Avisivirus/ Crohivirus/Grusopivirus/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, species names, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Genus names are presented at the right. 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.



**Figure 3:** Phylogenetic analysis of picornavirus 3D protein using Bayesian tree inference (MrBayes 3.2). Sixty picornavirus sequences of the *Aalivirus/Aquamavirus/Avihepatovirus/Avisivirus/ Crohivirus/Grusopivirus/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, species names, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Genus names are presented at the right. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Asterisks (\*) indicate incomplete genomes. 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.

**References**

 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. 2019. The fecal virome of red-crowned cranes. Arch Virol 164:3-16. PMID: 30225519; PMCID: PMC7086969; DOI: 10.1007/s00705-018-4037-x.

 Wang H, Yang S, Shan T, Wang X, Deng X, Delwart E, Zhang W. 2019. A novel picornavirus in feces of a rainbow lorikeet (*Trichoglossus moluccanus*) shows a close relationship to members of the genus *Avihepatovirus*. Arch Virol 164:1911-1914. PMID: 30982088; DOI: 10.1007/s00705-019-04246-5.