

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

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| **Code assigned:** | **2020.006S** |  |
| **Short title:** Create one new genus (*Marsupivirus*) including one new species (*Picornavirales*: *Picornaviridae*) |
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**Author(s) and email address(es)**

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| Zell R, Gorbalenya AE, Hovi T, Knowles NJ, Lindberg AM, Oberste MS, Palmenberg AC, Reuter G, Simmonds P, Skern T, Tapparel C, Wolthers KC, Woo PCY | 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)**

|  |
| --- |
| 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**

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| Roland Zell (roland.zell@med.uni-jena.de) |

**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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| 2020.006S.A.v1.Marsupivirus\_1ngen1nsp.xlsx |

**Abstract**

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| A novel picornavirus has been identified in a collection of poly-A selected RNA-seq libraries of ocular tissue sampled from koalas (*Phascolarctus cinereus*) by a recent metagenomics study. No viable virus was obtained. The virus was named Burpengary virus after the sampling place with the highest prevalence, Burpengary, Queensland, Australia. Burpengary virus constitutes the prototype of the proposed species *Marsupivirus A* of the new genus *Marsupivirus*. The genome of Burpengary virus has a length of 6821 nucleotides; the open reading frame (orf) encodes a single polyprotein of 2069 amino acids (aa). The virus exhibits a genome layout of a typical picornavirus (i.e., 5'-UTRIRES[1A-1B-1C-1D-2Anpg↓p-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) and shows sequence diversities of the orthologous proteins P1, 2C, 3C and 3D of greater 65.8%, 59.9%, 69.9% and 50.3%, respectively. The P1 and 3CD sequences of this virus constitute distinct branches in phylogenetic trees.  |

**Text of proposal**

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| **Create a new genus, *Marsupivirus*, with one species *Marsupivirus A***A novel picornavirus has been identified in poly-A selected RNA-seq libraries of ocular tissue sampled from koalas (*Phascolarctus cinereus*) in New South Wales and Queensland, Australia. Four complete open reading frames and nine partial genomes of a novel picornavirus were assembled from 26 tested libraries. The genome has a length of 6821 nucleotides; the open reading frame (orf) encodes a single polyprotein of 2069 amino acids (aa). The virus was named Burpengary virus after the sampling place with the highest prevalence. No viable virus was obtained. Phylogenetic analysis revealed a highly divergent picornavirus.**Relation to other picornaviruses:**- The Burpengary virus has a typical picornavirus genome layout: 5'-UTRIRES[1A-1B-1C-1D-2Anpg↓p-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR (compare Fig. 1 of supporting material)- The Burpengary virus possesses typical hallmarks of picornaviruses:  **capsid proteins:** 1B, 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** motifs Burpengary virus lacks a L protein and has a short 2A protein with NPG↓P motif.- **Phylogenetic analyses** indicate a distinct branch that clusters with sequences of the picornavirus supergroup 1 (*Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/ Erbovirus/Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Mupivirus*/*Senecavirus/ Teschovirus/Torchivirus/Tottorivirus*) in the P1 and 3CD trees (compare Figs. 2 & 3 of supporting material).**Distinguishing features of the Burpengary virus compared to other viruses of picornavirus supergroup 1:** - **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 37 acknowledged and proposed species of picornavirus supergroup 1. The amino acid divergences range from 65.8 to 73.7% for P1, 59.9-69.0% for 2Chel,69.9-83.4% for 3Cpro and 50.3-60.6% for 3Dpol (compare Table 1). These values justify the creation of a new genus in compliance with the *Picornaviridae* genus demarcation rules.**Type species of the genus:** ***Marsupivirus A***, marsupivirus A1 (Burpengary virus) strain Koala/Australia/2015-16, GenBank acc. no. MK882499**Species demarcation criteria:**not applicable**Origin of name:****marsupivirus**: derived from ***Marsupialia*** (mammalian infraclass including koalas; ***marsupium***, the technical term for the abdominal pouch of female marsupials). |

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**Supporting evidence**

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

**Burpengary virus vs. P1 2Chel 3Cpro 3Dpol**

*Ailurivirus* *Ailurivirus A* 70.1% 66.5% 69.9% 52.7%

*Aphthovirus* *Bovine rhinitis A virus* 72.5% 65.0% 79.8% 56.0%

 *Bovine rhinitis B virus* 72.0% 65.0% 79.3% 54.4%

 *Equine rhinitis A virus* 71.0% 66.3% 75.0% 56.2%

 *Foot-and-mouth disease virus* 72.5% 63.1% 75.3% 56.4%

*Bopivirus* *Bopivirus A* 71.1% 64.4% 81.7% 58.8%

*Cardiovirus* *Cardiovirus A* 69.2% 64.0% 73.0% 54.5%

 *Cardiovirus B* 70.3% 63.5% 75.8% 53.6%

 *Cardiovirus C* 67.0% 63.5% 76.6% 50.3%

 *Cardiovirus D* 70.4% 61.9% 74.2% 55.0%

 *Cardiovirus E* 69.9% 67.0% 76.8% 53.6%

 *Cardiovirus F* 70.9% 66.2% 76.8% 56.0%

*Cosavirus* *Cosavirus A* 71.4% 65.2% 76.0% 57.0%

 *Cosavirus B* 72.1% 63.2% 74.9% 58.1%

 *Cosavirus D* 72.8% 65.2% 74.0% 59.6%

 *Cosavirus E* 71.4% 63.9% 76.0% 58.3%

 *Cosavirus F* 71.8% 64.5% 78.6% 58.7%

*Erbovirus* *Erbovirus A* 69.8% 65.4% 77.4% 58.7%

*Hunnivirus* *Hunnivirus A* 68.5% 65.2% 83.4% 59.6%

*Malagasivirus* *Malagasivirus A* 67.6% 66.5% 81.2% 58.5%

 *Malagasivirus B* 65.8% 68.5% 81.1% 59.4%

*Mischivirus* *Mischivirus A* 71.3% 63.0% 75.6% 54.4%

 *Mischivirus B* 70.3% 62.7% 76.1% 54.7%

 *Mischivirus C* 70.5% 61.3% 75.4% 55.0%

 *Mischivirus D* 70.7% 64.1% 76.5% 53.2%

*Mosavirus* *Mosavirus A* 68.8% 62.8% 74.9% 57.6%

 *Mosavirus B* 70.1% 64.8% 79.6% 60.6%

Mupivirus *Mupivirus A1* 68.9% 59.9% 76.8% 51.5%

*Senecavirus* *Senecavirus A* 72.4% 66.0% 72.5% 54.2%

*Teschovirus* *Teschovirus A* 73.7% 67.4% 74.1% 58.7%

 *Teschovirus B* 72.3% 68.1% 75.1% 58.7%

*Torchivirus* *Torchivirus A* 70.7% 67.6% 73.4% 56.8%

*Tottorivirus* *Tottorivirus A* 69.7% 67.2% 80.3% 55.6%

unassigned Suncus murinus mischivirus 71.0% 65.0% 77.0% 52.8%

unassigned Hainan black-spectacled toad picornavirus 70.6% 63.6% 74.5% 56.6%

unassigned Zheijiang banded bullfrog picornavirus 73.3% 69.0% 78.4% 59.9%

\* number of amino acid differences per site

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**Figure 1:** Schematic depiction of the marsupivirus A1 (Burpengary virus) genome organisation. The open reading frame is indicated by a box. Position of putative 3Cpro cleavage sites are indicated by a ▼, the NPGP motif by #, and the VP0 processing site 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). Seventy-six picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/ Cosavirus/Erbovirus/Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Mupivirus/Senecavirus/ Teschovirus/Torchivirus/Tottorivirus* 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 (●). \* indicates 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.



**Figure 3:** Phylogenetic analysis of picornavirus 3CD protein using Bayesian tree inference (MrBayes 3.2). Seventy-six picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/ Cosavirus/Erbovirus/Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Mupivirus/Senecavirus/ Teschovirus/Torchivirus/Tottorivirus* 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 (●). \* indicates 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**

Harvey E, Madden D, Polkinghorne A, Holmes EC. 2019. Identification of a novel picorna-like virus, Burpengary virus, that is negatively associated with chlamydial disease in the Koala. Viruses 11(3): 211. PMID: 30832350; PMCID: PMC6466430; DOI: 10.3390/v11030211.