

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

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| **Code assigned:** | **2020.009S** |  |
| **Short title:** Create one new species (*Tropivirus B*) in the genus *Tropivirus* (*Picornavirales*: *Picornaviridae*) |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
| 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**

|  |
| --- |
| 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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| 2020.009S.A.v1.Tropivirus\_1nsp.xlsx |

**Abstract**

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| The *Tropivirus* genus presently comprises only one species, *Tropivirus A*. A second tropivirus-like virus has been detected in an organ pool of geckos, *Teratoscincus roborowskii*, from northwestern China. The virus has an identical genome layout (5'-UTR[L/1AB-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) and significant sequence similarity (53.1% amino acid identity of the polyprotein) to justify assignment to the genus *Tropivirus*, but to a new species, *Tropivirus B*. Within-genus sequence diversities are 51.7% for P1, 42.9% for 2Chel, 43.2% for 3Cpro and 31.2% for 3Dpol in comparisons with the respective tropivirus A1 sequences. Divergences to sequences of other picornavirus genera are >77.4% for P1, >62.3% for 2Chel, 68.6% for 3Cpro and 49.1% for 3Dpol. |

**Text of proposal**

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| **Create a new species, *Tropivirus B*, in the genus *Tropivirus***The *Tropivirus* genus presently comprises only one species, *Tropivirus A*. This virus was detected in an organ pool of the Chinese water skink (*Tropidophorus sinicus*) in the Guangdong province in China (Shi et al. 2018). The same authors also reported a new picornavirus from an organ pool of *Teratoscincus roborowskii*, a small gecko which is endemic in Xinjiang Uygur Autonomous Region, northwestern China. No viable virus was isolated. Despite significant similarities to the known tropivirus A1, the Yili teratoscincus roborowskii picornavirus 1 exhibits differences which justify assignment to a new species.**Relation to other picornaviruses:**1. The Yili teratoscincus roborowskii picornavirus 1 has a typical picornavirus genome layout: 5'-UTR[L/1AB-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR (compare Fig. 1 of supporting material)2. The Yili teratoscincus roborowskii picornavirus 1 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 a distinct branch that clusters with the sequences of tropivirus A1 (Guangdong Chinese waterskink picornavirus) and the sequences of the picornavirus supergroup 2 (*Dicipivirus/Hemipivirus/Gallivirus/Kobuvirus/Livupivirus/ Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/Passerivirus/Pemapivirus/Poecivirus/ Rafivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus/Symapivirus/Tropivirus*) in the P1 and 3D trees (compare Figs. 2 & 3 of supporting material).4. **Divergence:** The polyproteins of Yili teratoscincus roborowskii picornavirus 1 (2375 aa) and tropivirus A1 (Guangdong Chinese waterskink picornavirus) show 46.9% diversity suggesting a new tropivirus species, *Tropivirus B*, with 1 type, tropivirus B1 (GenBank acc. nos. MG600083).**Distinguishing features of the Yili teratoscincus roborowskii picornavirus 1 compared to other viruses of picornavirus supergroup 2:** 1. The Yili teratoscincus roborowskii picornavirus 1 has characteristic features of the **1AB, 1C, 2B** and **3A** proteins (compare Fig. 1): - the 1AB protein is 31 aa shorter and exhibits significant differences at the N-terminus (corresponding to the VP4 polypeptide);- the 1C protein is 20 aa shorter and displays a different C-terminus;- the 2B protein exhibits a different N-terminus;- the 3A protein is 23 aa longer.2. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 38 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from77.4 to 88.0% for P1,62.3-76.9% for 2Chel, 68.6-84.2% for 3Cpro and49.1-64.9% for 3Dpol in comparisons to other picornaviruses of super group 2 (compare Table 1). Divergence to tropivirus A1 is 51.7% for P1, 42.9% for 2Chel, 43.2% for 3Cpro and 31.2% for 3Dpol.**Species demarcation criteria:**Members of a species of genus *Tropivirus*:- share a common genome organization,- are less than 45% divergent in polyprotein sequence,- are less than 50% divergent in the P1 aa sequence,- are less than 35% divergent in the 2C+3CD aa sequence.**Exemplar virus of species:** ***Tropivirus B***, tropivirus B1 (Yili teratoscincus roborowskii picornavirus) strain LPWC175499, GenBank acc. no. MG600083 |

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**Supporting evidence**

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

**Tropivirus B1 (Yili teratoscincus roborowskii picornavirus 1) vs. P1 2Chel 3Cpro 3Dpol**

*Tropivirus Tropivirus A* 51.7% 42.9% 43.2% 31.2%

*Kobuvirus Aichivirus A* 77.7% 71.1% 77.0% 57.4%

 *Aichivirus B* 79.5% 72.0% 80.4% 56.6%

 *Aichivirus C* 79.0% 72.6% 81.1% 54.8%

 *Aichivirus D* 79.9% 72.8% 79.3% 59.9%

 *Aichivirus E* 79.2% 69.0% 78.1% 54.3%

 *Aichivirus F* 77.8% 68.8% 78.7% 55.8%

 *grey squirrel kobuvirus* 77.4% 67.6% 83.2% 56.3%

*Dicipivirus Cadicivirus A* 80.6% 71.6% 70.5% 61.9%

 *Cadicivirus B* 81.1% 69.3% 68.9% 59.3%

*Gallivirus Gallivirus A* 85.2% 70.7% 85.9% 56.7%

*Hemipivirus Hemipivirus A* 78.7% 66.3% 79.5% 54.9%

*Livupivirus Livupivirus A* 78.9% 69.0% 79.5% 55.7%

*Ludopivirus Ludopivirus A* 78.4% 68.1% 80.2% 58.0%

*Megrivirus Megrivirus A* 82.7% 67.0% 75.9% 60.0%

 *Megrivirus B* 84.3% 67.4% 73.1% 57.6%

 *Megrivirus C* 83.2% 64.5% 76.9% 59.3%

 *Megrivirus D* 82.8% 68.3% 73.6% 57.1%

 *Megrivirus E* 82.5% 66.1% 72.7% 56.1%

*Myrropivirus Myrropivirus A* 81.1% 67.8% 74.2% 58.6%

*Oscivirus Oscivirus A* 82.8% 67.2% 77.0% 52.7%

*Passerivirus Passerivirus A* 81.6% 71.0% 81.1% 57.3%

 *Passerivirus B* 83.6% 71.7% 80.0% 57.0%

*Pemapivirus Pemapivirus A* 79.5% 67.4% 77.7% 49.1%

 *Chinese broad-headed pond turtle picornavirus 1* 80.8% 67.0% 73.5% 50.4%

*Poecivirus Poecivirus A* 83.8% 73.1% 71.1% 59.8%

*Rafivirus Rafivirus A* 77.5% 69.3% 81.6% 59.3%

 *Rafivirus B* 77.9% 69.8% 81.1% 58.5%

 *Rafivirus C* 78.1% 68.1% 79.2% 58.6%

*Rosavirus Rosavirus A* 79.1% 65.6% 73.3% 54.6%

 *Rosavirus B* 79.7% 63.1% 68.6% 55.7%

 *Rosavirus C* 78.1% 62.3% 69.1% 56.2%

*Sakobuvirus Sakobuvirus A* 79.5% 70.4% 81.0% 56.6%

*Salivirus Salivirus A* 78.6% 70.9% 80.4% 63.1%

*Sicinivirus Sicinivirus A* 84.6% 69.6% 81.2% 56.0%

*Symapivirus Symapivirus A* 83.4% 74.3% 74.2% 60.2%

*unassigned Wenling sharpspine skate picornavirus* 88.0% 76.9% 84.2% 56.6%

*unassigned pingu picornavirus*  82.0% 68.8% 82.6% 64.9%

*unassigned zebrafish picornavirus*  83.1% 73.3% 84.6% 62.8%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of tropiviruses (schematic depiction). The genome of Yili teratoscincus roborowskii picornavirus 1 is compared to the genome of the Guangdong Chinese waterskink picornavirus, the exemplar virus of *Tropivirus A*. 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). Eighty-three picornavirus sequences of the *Dicipivirus/Hemipivirus/Gallivirus/Kobuvirus/ Livupivirus/Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/Passerivirus/Pemapivirus/Poecivirus/ Rafivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus/Symapivirus/Tropivirus* 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). Eighty-three picornavirus sequences of the *Dicipivirus/Hemipivirus/Gallivirus/Kobuvirus/ Livupivirus/Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/Passerivirus/Pemapivirus/Poecivirus/ Rafivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus/Symapivirus/Tropivirus* 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**

 Shi M, Lin XD, Chen X, Tian JH, Chen LJ, Li K, Wang W, Eden JS, Shen JJ, Liu L, Holmes EC, Zhang YZ. 2018. The evolutionary history of vertebrate RNA viruses. Nature 556:197-202. PMID: 29618816; DOI: 10.1038/s41586-018-0012-7