

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

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| **Code assigned:** | **2020.008S** |  |
| **Short title:** Create one new species (*Pemapivirus B*) in the genus *Pemapivirus* (*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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| 2020.008S.R.Pemapivirus\_1nsp.xlsx |

**Abstract**

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| The *Pemapivirus* genus presently comprises only one species, *Pemapivirus A*. A second pemapivirus-like virus has been detected in an organ pool of Chinese broad-headed pond turtle (*Mauremys megalocephala*) in China. The virus has an identical genome layout (5′-UTR[L/1AB-1C-1D/2A1-2A2H-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3′UTR) and significant sequence similarity (69.4% amino acid identity of the polyprotein) to justify assignment to the genus *Pemapivirus*, but to a new species, *Pemapivirus B*. Within-genus sequence diversities are 32.3% for P1, 15.0% for 2Chel, 41.4% for 3Cpro and 19.3% for 3Dpol in comparisons with the respective pemapivirus A1 sequences. Divergences to sequences of other picornavirus genera are >73.6% for P1, >63.3% for 2Chel, 70.0% for 3Cpro and 50.4% for 3Dpol. |

**Text of proposal**

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| |  | | --- | | **Create a new species, *Pemapivirus B*, in the genus *Pemapivirus***  The *Pemapivirus* genus presently comprises only one species, *Pemapivirus A*. The prototype virus, Chinese softshell turtle picornavirus, was detected in an organ pool (gut, liver, lungs) of *Pelodiscus sinensis* in China (Shi et al. 2018). No viable virus was isolated. A second virus from the Chinese broad-headed pond turtle (*Mauremys megalocephala*) was originally considered as pemapivirus A2. However, despite significant similarities to pemapivirus A1, the Chinese broad-headed pond turtle picornavirus exhibits differences which justify assignment to a new species.  **Relation to other picornaviruses:**  1. The Chinese broad-headed pond turtle picornavirus has a typical picornavirus genome layout:  5′-UTR[L/1AB-1C-1D/2A1-2A2H-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3′UTR  (compare Fig. 1 of supporting material)  2. The Chinese broad-headed pond turtle 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** motifs  3. **Phylogenetic analyses** indicate clustering with the sequences of pemapivirus A1 (Chinese softshell turtle 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 Chinese broad-headed pond turtle picornavirus and pemapivirus A1 (Chinese softshell turtle picornavirus) show 30.6% diversity suggesting a new pemapivirus species, *Pemapivirus B*, with 1 type, pemapivirus B1 (GenBank acc. nos. MG600108).  **Distinguishing features of the Chinese broad-headed pond turtle picornavirus compared to other viruses of picornavirus supergroup 2:**  1. Pemapiviruses have **two 2A proteins**; the 2A1 protein is unique and has unknown function; 2A2 has a H-box/NC sequence motif (compare Fig. 1).  2. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 39 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from73.6 to 86.4% for P1,63.3-78.9% for 2Chel, 70.0-89.2% for 3Cpro and 50.4-67.2% for 3Dpol in comparisons with other picornaviruses of super group 2 (compare Table 1).  3. **Divergence** to pemapivirus A1 is 32.3% for P1, 15.0% for 2Chel, 41.4% for 3Cpro and 19.3% for 3Dpol (compare Table 1).  **Species demarcation criteria:**  Members of a species of genus *Pemapivirus*:  - share a common genome organization,  - are less than 30% divergent in the polyprotein sequence,  - are less than 35% divergent in the P1 aa sequence,  - are less than 20% divergent in the 2C+3CD aa sequence.  **Exemplar virus of species:**  ***Pemapivirus B***, pemapivirus B1 (Chinese broad-headed pond turtle picornavirus) strain WHWGC151314, GenBank acc. no. MG600108. | |

**Supporting evidence**

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

**Pemapivirus B1 (Chinese broad-headed pond turtle picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Pemapivirus Pemapivirus A* 32.3% 15.0% 41.4% 19.3%

*Kobuvirus Aichivirus A* 77.1% 73.3% 85.3% 55.4%

*Aichivirus B* 78.7% 76.0% 84.9% 54.0%

*Aichivirus C* 77.1% 75.7% 85.5% 54.8%

*Aichivirus D* 79.4% 75.6% 83.8% 57.1%

*Aichivirus E* 80.1% 73.0% 84.3% 57.9%

*Aichivirus F* 79.8% 73.5% 84.8% 54.9%

*grey squirrel kobuvirus* 78.5% 72.6% 87.6% 57.5%

*Dicipivirus Cadicivirus A* 76.7% 74.5% 75.1% 58.2%

*Cadicivirus B* 77.9% 71.5% 76.7% 54.9%

*Gallivirus Gallivirus A* 84.7% 74.4% 85.6% 54.4%

*Hemipivirus Hemipivirus A* 73.6% 70.5% 76.6% 57.9%

*Livupivirus Livupivirus A* 77.3% 71.2% 85.8% 52.7%

*Ludopivirus Ludopivirus A* 79.0% 70.1% 84.0% 57.1%

*Megrivirus Megrivirus A* 83.3% 66.3% 71.2% 60.1%

*Megrivirus B* 81.4% 63.7% 70.0% 57.3%

*Megrivirus C* 83.0% 67.0% 73.7% 60.3%

*Megrivirus D* 82.7% 66.1% 74.6% 57.0%

*Megrivirus E* 83.4% 65.6% 71.6% 57.7%

*Myrropivirus Myrropivirus A* 76.6% 69.3% 72.0% 54.3%

*Oscivirus Oscivirus A* 81.0% 70.2% 85.7% 52.4%

*Passerivirus Passerivirus A* 81.7% 73.8% 81.5% 53.9%

*Passerivirus B* 82.2% 72.9% 83.7% 56.1%

*Poecivirus Poecivirus A* 82.2% 71.8% 75.4% 60.1%

*Rafivirus Rafivirus A* 77.6% 70.1% 81.3% 54.7%

*Rafivirus B* 78.1% 70.3% 82.4% 54.0%

*Rafivirus C* 78.2% 69.8% 79.9% 55.8%

*Rosavirus Rosavirus A* 77.0% 66.6% 75.1% 50.8%

*Rosavirus B* 77.4% 66.7% 75.1% 52.1%

*Rosavirus C* 78.3% 65.3% 76.2% 53.1%

*Sakobuvirus Sakobuvirus A* 80.3% 72.5% 89.2% 56.3%

*Salivirus Salivirus A* 79.6% 74.2% 82.0% 60.8%

*Sicinivirus Sicinivirus A* 82.0% 73.1% 88.6% 56.7%

*Symapivirus Symapivirus A* 82.5% 75.0% 79.9% 58.9%

*Tropivirus Tropivirus A* 81.6% 63.3% 73.6% 51.9%

Yili teratoscincus roborowskii picornavirus 1 80.8% 67.0% 73.5% 50.4%

unassigned Wenling sharpspine skate picornavirus 86.4% 78.9% 86.7% 56.8%

unassigned pingu picornavirus 83.4% 71.0% 85.2% 67.2%

unassigned zebrafish picornavirus 85.6% 76.8% 79.6% 63.0%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of pemapiviruses (schematic depiction). The genome of the Chinese broad-headed pond turtle picornavirus 1 is compared to the genome of the Chinese softshell turtle picornavirus 1, the exemplar virus of *Pemapivirus 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