

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

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| **Code assigned:** | **2020.001S** |  |
| **Short title:** Create one new genus (*Caecilivirus*) including one new species (*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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| 2020.001S.A.v1.Caecilivirus\_1ngen1nsp.xlsx |

**Abstract**

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| A novel picornavirus from Banna caecilians (*Ichthyophis bannanicus*), a limbless amphibian from China, was identified in an organ pool (gut, liver, lungs).The virus has a typical picornavirus genome layout (5'-UTR[1A-1B-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) but the 2A gene region is very long encoding 451 amino acids with unknown function. Phylogenetic analyses reveal clustering with viruses of the picornavirus supergroup 5. However, the deduced orthologous protein are highly divergent (>60% for P1, >59% for 2Chel, >66% for 3Cpro and >62% for 3Dpol) in comparisons with other viruses of supergroup 5. The results suggest a new genus named *Caecilivirus* with a single species, *Caecilivirus A*.  |

**Text of proposal**

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| **Create one new genus, *Caecilivirus*, with one species *Caecilivirus A***A novel picornavirus was detected in an organ pool comprising gut, liver and lungs of limbless amphibians, the Banna caecilians (*Ichthyophis bannanicus*), in China (Shi et al. 2018). No viable virus was isolated. The Guangdong fish caecilians picornavirus exhibits a significant genetic diversity which justifies assignment to a new genus, *Caecilivirus*.**Relation to other picornaviruses:**1. The Guangdong fish caecilians picornavirus has a typical picornavirus genome layout: 5'-UTR[1A-1B-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR (compare Fig. 1 of supporting material)2. The Guangdong fish caecilians picornavirus possesses typical hallmarks of picornaviruses:  **capsid proteins:** 1B, 1C, 1D have **rhv** domains with drug-binding site,  **2Chel:** **G**xx**G**x**GKT** motif of helicases, **3BVPg:** **Y-3** residue, **3Cpro:** **C**x**CG**x15**G**x**H** motif, **3Dpol:** **KDE**, **PSG**, **YGDD**, **FLKR** motifs3. **Phylogenetic analyses** indicate clustering with the sequences of the picornavirus supergroup 5 (*Crahelivirus, Fipivirus, Gruhelivirus, Hepatovirus, Rohelivirus, Tremovirus*) in the P1 and 3D trees (compare Figs. 2 & 3 of supporting material). Based on the sequence similarity of the deduced capsid proteins, the Guangdong fish caecilians picornavirus likely has a very short VP4 polypeptide (27 aa) -- in accordance with many other viruses of the supergroup 5.**Distinguishing features of caecilivirus A1 (Guangdong fish caecilians picornavirus) compared to other viruses of picornavirus supergroup 5:** 1. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 20 acknowledged and proposed species of picornavirus supergroup 5. The amino acid divergences are >60% for P1, >59% for 2Chel, >66% for 3Cpro and >62% for 3Dpol (compare Table 2).2. The unique **2A protein** is rather long (451 amino acids) and has unknown function. There are 2 or 3 possible 3Cpro-processing sites with unknown significance.**Species demarcation criteria**not applicable**Exemplar virus of species:** ***Caecilivirus A***, caecilivirus A1 (Guangdong fish caecilians picornavirus) strain GDYYC83005, GenBank acc. no. MG600103.**Origin of name:*****Caecili-*** was derived from **caecili**an, the host of the Guangdong fish caecilians picornavirus (***caecus***, Lat. blind). |

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**Supporting evidence**

**Table 2: Diversities of orthologous proteins\***

**Fipivirus F1 (Guangdong fish caecilians picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Crahelivirus Crahelivirus A* 67.4% 65.4% 67.3% 69.3%

*Fipivirus Fipivirus A* 74.5% 72.5% 82.8% 74.7%

 *Fipivirus B* 76.3% 70.9% 81.9% 75.8%

 *Fipivirus C* 72.7% 73.2% 81.3% 74.3%

 Fipivirus D 73.0% 73.4% 82.8% 72.1%

 Fipivirus E 71.8% 75.7% 82.6% 74.9%

*Gruhelivirus Gruhelivirus A* 65.4% 62.8% 66.7% 68.0%

*Hepatovirus Hepatovirus A* 62.9% 60.9% 67.1% 63.7%

 *Hepatovirus B* 64.0% 61.4% 66.8% 64.6%

 *Hepatovirus C* 63.5% 62.0% 68.7% 65.1%

 *Hepatovirus D* 62.8% 62.7% 66.8% 62.9%

 *Hepatovirus E* 62.0% 61.7% 69.0% 64.2%

 *Hepatovirus F* 62.8% 63.0% 65.9% 64.0%

 *Hepatovirus G* 61.9% 61.7% 68.7% 66.1%

 *Hepatovirus H* 63.6% 59.3% 67.3% 66.3%

 *Hepatovirus I* 60.9% 62.9% 66.8% 63.2%

*Rohelivirus Rohelivirus A* 72.3% 65.4% 73.9% 70.6%

*Tremovirus Tremovirus A* 64.3% 60.6% 66.4% 64.8%

 *Tremovirus B* 63.1% 65.1% 67.1% 62.3%

unassigned Wenling chelidoperca picornavirus 71.6% 73.9% 79.7% 70.9%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of the Guangdong fish caecilians picornavirus (schematic depiction). The open reading frame is indicated by a box. Position of putative 3Cpro cleavage sites are indicated by a ▼ and the 1AB 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). Thirty-seven picornavirus sequences of the *Crahelivirus/Fipivirus/Gruhelivirus/Hepatovirus/ Rohelivirus/Tremovirus* 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). Thirty-nine picornavirus sequences of the *Crahelivirus/Fipivirus/Gruhelivirus/Hepatovirus/ Rohelivirus/Tremovirus* 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**

1. 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.