

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

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| **Code assigned:** | **2020.003S** |  |
| **Short title:** Create one new species (*Fipivirus F*) in the genus *Fipivirus* (*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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| 2020.003S.R.Fipivirus\_1nsp.xlsx |

**Abstract**

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| The *Fipivirus* genus presently comprises five species, *Fipivirus A* to *E*. Another fipivirus-like virus has been detected in a gut/liver/gill organ pool of a perch (*Chelidoperca sp.*) in China. The virus has a typical picornavirus genome layout (5'-UTR[1A-1B-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) and significant sequence similarities to fipiviruses (divergences >60% for the polyprotein, >52% for P1 and >58% for 2C+3CD) which justifies assignment to the genus *Fipivirus*, but to a new species, *Fipivirus F*. Divergences to sequences of other picornavirus genera are >69% for P1, >71% for 2Chel, >77% for 3Cpro and >70% for 3Dpol. |

**Text of proposal**

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| |  | | --- | | **Create one new species, *Fipivirus F*, in the genus *Fipivirus***  The *Fipivirus* genus presently comprises five species, *Fipivirus A* to *E*. The known fipiviruses have been detected in organ pools (gut, liver, gill) of fishes but no viable virus has been isolated yet. Another fipivirus-like virus was detected in organ pools (gut, liver, gill) of an unclassified perch (*Chelidoperca sp.*) in China (Shi et al. 2018). The Wenling chelidoperca picornavirus exhibits a significant genetic diversity which justifies assignment to a new *Fipivirus* species.  **Relation to other picornaviruses:**  1. The Wenling chelidoperca picornavirus has a typical picornavirus genome layout:  5'-UTR[1A-1B-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR  (compare Fig. 1 of supporting material)  2. The Wenling chelidoperca picornavirus possesses typical hallmarks of picornaviruses:  **capsid proteins:** 1B, 1C, 1D have **rhv** domains with drug-binding site,  **2Chel:** **G**xx**G**x**GKS/T** 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 the picornavirus supergroup 5 (*Crahelivirus, Fipivirus, Hepatovirus, Gruhelivirus, Rohelivirus, Tremovirus*) in the P1 and 3D trees (compare Figs. 2 & 3 of supporting material). Closest relatives are fipiviruses.  **Distinguishing features of fipivirus F1 (Wenling chelidoperca picornavirus) compared to other fipiviruses:**  1. **Within-genus divergence** (uncorrected p-distances) in comparisons with other fipiviruses are >60% for the polyprotein, >52% for P1 and >58% for 2C+3CD (compare Table 1). The **divergence data** suggest a new fipivirus species, *Fipivirus F*, with one type, fipivirus F1 (GenBank acc. nos. MG600074).  2. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 19 acknowledged and proposed species of picornavirus supergroup 5. The amino acid divergences range from 69.1–74.5% for P1, 71.1–77.8% for 2Chel, 77.2–87.0% for 3Cpro and 70.9–75.2% for 3Dpol (compare Table 2).  **Species demarcation criteria**  Preliminary species demarcation criteria have been defined. Members of a species of the genus *Fipivirus* ...  1. ... share a common genome organization,  2. ... are less than 40% divergent in polyprotein aa sequence,  3. ... are less than 50% divergent in P1 aa sequence,  4. ... are less than 50% divergent in 2C+3CD aa sequence,  5. ... share a natural host range.  **Exemplar virus of species:**  ***Fipivirus F***, fipivirus F1 (Wenling chelidoperca picornavirus) strain LXMC188591, GenBank acc. no. MG600074. | |

**Supporting evidence**

**Table 1: Diversities**

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| --- | --- | --- | --- | --- | --- | --- |
|  | **FiV-A1** | **FiV-B1** | **FiV-C1** | **FiV-D1** | **FiV-E1** | **FiV-F1** |
| **Polyprotein** | | | | | | |
| **FiV-A1** | - |  |  |  |  |  |
| **FiV-B1** | 0.640 | - |  |  |  |  |
| **FiV-C1** | 0.681 | 0.672 | - |  |  |  |
| **FiV-D1** | 0.668 | 0.670 | 0.662 | - |  |  |
| **FiV-E1** | 0.715 | 0.700 | 0.694 | 0.695 | - |  |
| **FiV-F1** | 0.699 | 0.687 | 0.686 | 0.678 | 0.602 |  |
| **P1 protein** | | | | | | |
| **FiV-A1** |  |  |  |  |  |  |
| **FiV-B1** | 0.567 | - |  |  |  |  |
| **FiV-C1** | 0.616 | 0.613 | - |  |  |  |
| **FiV-D1** | 0.602 | 0.626 | 0.597 | - |  |  |
| **FiV-E1** | 0.650 | 0.664 | 0.647 | 0.647 | - |  |
| **FiV-F1** | 0.627 | 0.624 | 0.634 | 0.642 | 0.525 | - |
| **2C+3CD protein** | | | | | | |
| **FiV-A1** | - |  |  |  |  |  |
| **FiV-B1** | 0.656 | - |  |  |  |  |
| **FiV-C1** | 0.680 | 0.661 | - |  |  |  |
| **FiV-D1** | 0.667 | 0.644 | 0.651 | - |  |  |
| **FiV-E1** | 0.719 | 0.662 | 0.675 | 0.660 | - |  |
| **FiV-F1** | 0.697 | 0.667 | 0.662 | 0.636 | 0.580 | - |

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

**Fipivirus F1 (Wenling chelidoperca picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Fipivirus Fipivirus A* 62.1% 71.5% 77.5% 66.7%

*Fipivirus B* 63.5% 73.4% 75.9% 59.2%

*Fipivirus C* 65.3% 68.4% 72.6% 62.8%

Fipivirus D 62.8% 71.6% 64.7% 56.4%

Fipivirus E 52.2% 59.8% 54.6% 58.3%

*Crahelivirus Crahelivirus A* 71.4% 73.0% 83.8% 75.0%

*Gruhelivirus Gruhelivirus A* 72.8% 77.8% 78.8% 74.7%

*Hepatovirus Hepatovirus A* 69.3% 72.4% 79.4% 75.2%

*Hepatovirus B* 69.1% 74.9% 80.5% 74.4%

*Hepatovirus C* 70.5% 71.1% 79.5% 73.0%

*Hepatovirus D* 70.0% 73.0% 79.5% 71.9%

*Hepatovirus E* 69.5% 73.4% 82.3% 74.6%

*Hepatovirus F* 69.4% 73.6% 78.0% 72.9%

*Hepatovirus G* 70.5% 72.2% 81.0% 73.8%

*Hepatovirus H* 70.5% 72.2% 79.5% 74.8%

*Hepatovirus I* 69.9% 72.1% 81.5% 74.1%

*Rohelivirus Rohelivirus A* 74.5% 76.1% 87.0% 73.3%

*Tremovirus Tremovirus A* 69.1% 72.8% 77.2% 75.2%

*Tremovirus B* 70.0% 73.3% 76.8% 74.2%

unassigned Guangdong fish caecilians picornavirus 71.6% 72.5% 79.7% 70.9%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of fipiviruses (schematic depiction). The genomes of fipiviruses A1, B1, C1, D1, E1 are compared to the genome of the Wenling chelidoperca picornavirus, the exemplar virus of *Fipivirus F*. 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’-UTRs 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.