This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.007S*** |  |
| **Short title:** Create one new genus (*Fipivirus*) with 5 species (*Fipivirus A*, *Fipivirus B*, *Fipivirus C*, *Fipivirus D* and *Fipivirus E*) |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Zell R, Gorbalenya AE, Hovi T, Knowles NJ, Lindberg M, Oberste S, Palmenberg AC, Reuter G, Simmonds P, Skern T, Tapparel C, Wolthers K, Woo P | 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):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| 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:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ***Picornaviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 21/05/2019 |
| Date of this revision (if different to above): |       |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|       |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module: 2019.007S.N.v1.1newgen\_Fipivirus\_A-E.xlsx** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

Create one new genus(***Fipivirus***)with 5 species (***Fipivirus A***, ***Fipivirus B***, ***Fipivirus C***, ***Fipivirus D*** and ***Fipivirus E***)

Seven novel picornaviruses have been detected in organ pools comprising tissue of gut/liver/gill of various captured fresh water and sea water fish (Shi et al., 2018):

|  |  |  |
| --- | --- | --- |
| **Virus name** | **Host** | **Proposed species/type** |
| Wuhan sharpbelly picornavirus 2 | *Hemiculter leucisculus*(sharpbelly, wild carp) | ***Fipivirus A***/fipivirus A1 |
| Wuhan sharpbelly picornavirus 3 | *Hemiculter leucisculus*(sharpbelly, wild carp) | ***Fipivirus B***/fipivirus B1 |
| Wenling crossorhombus picornavirus | *Crossorhombus spec.*(lefteye flounder) | ***Fipivirus C***/fipivirus C1 |
| Wenling jack mackerels picornavirus | *Trachurus spec.*(Jack mackerel, saurel) | ***Fipivirus D***/fipivirus D1 |
| Wenling banjofish picornavirus 1 | *Banjos banjos*(banjofish) | ***Fipivirus E***/fipivirus E1 |
| Wenling banjofish picornavirus 2 | *Banjos banjos*(banjofish) | tentative fipivirus, partial sequence |
| Beihai wrasse picornavirus | *Hologymnosus spec.*(wrasse) | tentative fipivirus, partial sequence |

**Relation to other picornaviruses:**

- Fipiviruses have a typical picornavirus genome layout:

 5'-UTR[1A-1B-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

 (compare Figure 1 in Supporting Material)

- Fipiviruses possess typical hallmarks of picornaviruses:

 **Capsid proteins:** 1B, 1C, 1D have **rhv** domains with drug-binding site,

 **2A:** H-box/NC sequence motif,

 **2Chel:** **G**xx**G**x**GKS/T** motif of helicases,

 **3BVPg:** **Y-3** residue,

 **3Cpro:** **C**x**CG**x15**G**x**H** motif,

 **3Dpol:** **KDE**, **PSG**, **YGDD**, **FLKR** motifs.

- **Phylogenetic analysis** indicates a distinct branch in the P1 and 3CD trees that clusters with sequences of picornavirus supergroup 5 (*Hepatovirus/Tremovirus*) and some unclassified viruses (compare Figs. 2 & 3 of supporting material). Assuming less than 30% divergence of complete genome sequences for species demarcation, available sequence divergence data of 5 complete genome sequences indicate 5 fipivirus species; 2 partial sequences (P2P3) suggest the existence of 1 or 2 additional species. Fipiviruses show monophyly in phylogenetic trees (P1, 3CD).

**Distinguishing features of fipiviruses compared to other viruses of picornavirus supergroup 5:**

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise *within-genus* comparisons. The amino acid divergences range from 64.1-71.4% for the complete genome, 56.6 to 64.0% for P1, 65.0-71.8% for 2Chel, 70.6-75.7% for 3Cpro and 62.6-69.7% for 3Dpol (compare Table 1).

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise *between-genus* comparisons with 15 acknowledged and proposed species of picornavirus supergroup 5. The amino acid divergences range from 70.7 to 75.8% for P1, 70.9-73.9% for 2Chel, 76.0-84.5% for 3Cpro and 71.6-77.5% for 3Dpol (compare Table 1). Divergence to sequences of other picornavirus supergroups is even greater.

**Table 1: Amino acid divergence\***

**fipivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol**

*within-genus* comparisons:

*Fipivirus*† *Fipivirus B*†  0.566 0.650 0.706 0.645

 *Fipivirus C*† 0.631 0.681 0.734 0.626

 *Fipivirus D*† 0.609 0.680 0.731 0.626

 *Fipivirus E*† 0.640 0.718 0.757 0.697

*between-genus* comparisons:

*Crahelivirus*† *Crahelivirus A*† 0.735 0.714 0.768 0.755

*Hepatovirus Hepatovirus A* 0.728 0.709 0.801 0.770

 *Hepatovirus B*  0.715 0.715 0.802 0.764

 *Hepatovirus C* 0.731 0.722 0.807 0.763

 *Hepatovirus D* 0.719 0.718 0.792 0.754

 *Hepatovirus E* 0.717 0.719 0.831 0.760

 *Hepatovirus F* 0.718 0.709 0.821 0.762

 *Hepatovirus G* 0.727 0.709 0.797 0.775

 *Hepatovirus H* 0.722 0.709 0.821 0.775

 *Hepatovirus I* 0.721 0.717 0.797 0.788

*Gruhelivirus*† *Gruhelivirus A*†  0.734 0.739 0.803 0.716

*Rohelivirus*† *Rohelivirus A*† 0.758 0.723 0.816 0.727

*Tremovirus* *Tremovirus A* 0.707 0.738 0.760 0.745

 *Tremovirus B*† 0.718 0.718 0.845 0.738

 *unassigned*  Guangdong fish caecilians picornavirus 0.738 0.731 0.820 0.760

\* number of amino acid differences per site

† proposed taxa

- Unusual **3A-3B cleavage sites** of fipiviruses B1, D1 and E1 challenge the hypothesis of a conserved Y3-residue of 3BVPg. In these cases, alternative E/G and E/A cleavage sites, respectively, would yield a Y5-residue. However, E/G and E/A cleavage site are conserved among picornaviruses.

 Presumed cleavage site Alternative cleavage site

 Fipivirus B1: QKT**EG**K↓RAY1565 QKT**E**↓**G**KRAY1565

 Fipivirus D1: PDT**EA**T↓RAY1651 PDT**E**↓**A**TRAY1651

 Fipivirus E1: DPV**EA**S↓SPY1669 DPV**E**↓**A**SSPY1669

- Based on sequence similarity to other fipiviruses, it is assumed that fipivirus C1 has an **AUG start codon** at nt position 579. The deduced 1A protein (VP4) has a length of 25 amino acids. An alternative in-frame start codon at nt 461 would yield a 1A protein of 62 aa but its significance is unclear.

**Type species of genus:**

***Fipivirus A***, fipivirus A1 (Wuhan sharpbelly picornavirus 2) strain DSYC36136, GenBank acc. no. MG600068

**Exemplar:**

***Fipivirus A***: fipivirus A1 (Wuhan sharpbelly picornavirus 2) strain DSYC36136, GenBank acc. no. MG600068

***Fipivirus B***: fipivirus B1 (Wuhan sharpbelly picornavirus 3) strain DSYC47507, GenBank acc. no. MG600069

***Fipivirus C***: fipivirus C1 (Wenling crossorhombus picornavirus) strain XDXMC21480, GenBank acc. no. MG600095

***Fipivirus D***: fipivirus D1 (Wenling Jack mackarels picornavirus) strain LXMC375591, GenBank acc. no. MG600075

***Fipivirus E***: fipivirus E1 (Wenling banjofish picornavirus 1) strain LXMC34076, GenBank acc. no. MG600070

**Species demarcation criteria:**

Preliminary species demarcation criteria have been defined.

Members of a species of the genus *Fipivirus*:

- are less than 40% divergent in polyprotein aa sequence,

- are less than 50% divergent in P1 aa sequence,

- are less than 50% divergent in 2C+3CD aa sequence,

- share a common genome organization,

- share a natural host range.

**Origin of name:**

**Fipivirus**: derived from **fi**sh **pi**corna**virus**

| **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. |

**Supporting material:**



**Figure 1:** Genome of the fipiviruses (schematic depiction). The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by a ▼. The VP0 processing site is indicated by a hash (#). The names and lengths of the deduced proteins are presented. The 5'-UTR may be incomplete.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Thirty-five picornavirus sequences of the *Hepatovirus/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, ***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 names are 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.



**Legend to Figure 3:**  Phylogenetic analysis of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Thirty-seven picornavirus sequences of the *Hepatovirus/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, ***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 (●). 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.