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**

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| --- | --- | --- | --- |
| **Code assigned:** | ***2018.018M*** | |  |
| **Short title:** Reorganize the family *Birnaviridae* | | | |
|  | | | |
| **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 | |
| Delmas B | | Bernard.delmas@inra.fr | |
| **Corresponding author** | | | |
| Delmas, Bernard; [Bernard.delmas@inra.fr](mailto:Bernard.delmas@inra.fr) | | | |
| **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) | | ICTV *Birnaviridae* and *Picobirnaviridae* Study Group | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 19, 2019 |
| Date of this revision (if different to above): | | |  |

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

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

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| **Name of accompanying Excel module:** 2018.018M.A.v1.Birnaviridae |

**Supporting material:**

***Only fully sequenced birnaviruses are proposed to define new species and/or type species for a new genus.***

Figures 1 and 2 show phylogenetic trees based on the amino acid sequences alignments of the capsid protein VP2 and of the RdRp VP1, respectively. Phylogenetic trees have been constructed using the web site “ <http://phylogeny.lirmm.fr/phylo_cgi/simple_phylogeny.cgi> “ with predefined parameters.

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**Propositions:**

**To create a virus species: *Mosquito X virus (MXV)* integrated to the existing *Entomobirnavirus* genus**

**with the virus name exemplar: mosquito X virus**

Complete sequence: Accession numbers: AFU34333, AFU34334

Reference: Huang et al., 2013. Presence of entomobirnavirus in Chinese mosquitoes in the absence of Dengue virus co-infection. J Gen Virol **PMID 23175239**

MXV was identified by RNA high-throughput sequencing of ***Anopheles sinensis*** and display **77% amino acid identity to *Drosophila X virus*** (DXV, the type species of the genus *Entomobirnavirus*) VP1 (the RdRp encoded by segment B). See **Table 1** for amino acids identity scores in RdRp pairwise alignments and **Table 2** for capsid proteins (VP2) pairwise alignments.

**To create a virus species: *Lates calcarifer birnavirus* (LCBV) integrated to the existing *Blosnavirus* genus**

**with the virus name exemplar: *Lates calcarifer* birnavirus**

Complete sequence: Accession numbers: QCQ84349, QCQ84350

Reference: Chen et al., 2019. Detection and characterization of a novel marine birnavirus isolated from Asian seabass in Singapore. Virology Journal **PMID 31138237**

LCBV was identified in a tropical fish (*Lates calcarifer).* Phylogenetic analyses on VP1 and VP2 proteins show the phylogenetic proximity of LCBV and BSNV (about 60% amino acid identity between the two RdRps and the two capsid proteins). See **Table 1** for identity score in RdRp pairwise alignments.

Furthermore, a specific polypeptide (not found in *Aquabirnavirus* and *Avibirnavirus* species) is predicted between the pVP2 (the capsid precursor) and the VP4 (the viral protease) for LCBV, like previously evidenced in BSNV, the prototype species of *Blosnavirus* (Da Costa et al., 2003).

**To create a new genus: *Dronavirus* with the type species: *Drosophila B birnavirus* (DBV)**

**with the virus name exemplar: Drosophila birnavirus**

Complete sequence: Accession numbers: ACU32790, ACU32792

Reference: Wu et al., 2010. Virus discovery by deep sequencing and assembly of virus-derived small silencing RNAs. Proc Natl Acad Sci U S A. **PMID: 20080648**

*Dronavirus* genus will be defined by a single birnavirus, DBV. Pairwise amino acid sequence alignment of the DBV RdRp shows between **21 to 38 %** identity with others birnavirus RdRp, and only 30 to 32% identity with members of the *Entomobirnavirus* genus. See **Table 1** for identity score in RdRp pairwise alignments.

*Dronavirus* genus is proposed to be defined by viruses with more than 60% amino acid identity with the RdRp of DBV.

**To create a new genus: *Ronavirus* with the type species: *Rotifer birnavirus***

**with the virus name exemplar: Rotifer birnavirus (RBV)**

Complete sequence: Accession number: FM995220, FM995221

Reference: Gibrat et al., 2013. Analyses of the radiation of birnaviruses from diverse host phyla and of their evolutionary affinities with other double-stranded RNA and positive strand RNA viruses using robust structure-based multiple sequence alignments and advanced phylogenetic methods. BMC Evol Biol. **PMID: 23865988**

*Ronavirus* genus will be defined by a single birnavirus, RBV which was previously an unassigned birnavirus. Pairwise amino acid sequence alignment of RBV RdRp shows between **19 to 41 %** identity with others birnavirus RdRp. See **Table 1** for identity score in RdRp pairwise alignments.

*Ronavirus* genus is proposed to be defined by viruses with more than 60% amino acid identity with the RdRp of RBV.

**To create a new genus: *Telnavirus* with the type species: *Tellina virus 1* (TV-1)**

**with the virus name exemplar: Tellina virus 1**

Complete sequence: Accession number: AJ920335, AJ920336

Reference: Nobiron et al., 2008. Genome and polypeptides characterization of Tellina virus 1 reveals a fifth genetic cluster in the *Birnaviridae* family. Virology. **PMID: 17976679**

*Telnavirus* genus will be defined by a single birnavirus, TV-1 which was previously an unassigned birnavirus. TV-1 was isolated from a tellina, a bivalve. Pairwise amino acid sequence alignment of TV-1 RdRp shows between **21 to 55 %** identity with others birnavirus RdRp. See **Table 1** for identity score in RdRp alignments.

*Telnavirus* genus is proposed to be defined by viruses with more than 60% amino acid identity with the RdRp of TV-1.

| **References:** |
| --- |
| Da Costa et al., 2003. Blotched snakehead virus is a new aquatic birnavirus that is slightly more related to *Avibirnavirus* than to *Aquabirnavirus.* J. Virol. **PMID:**  Gibrat et al., 2013. Analyses of the radiation of birnaviruses from diverse host phyla and of their evolutionary affinities with other double-stranded RNA and positive strand RNA viruses using robust structure-based multiple sequence alignments and advanced phylogenetic methods. BMC Evol Biol. **PMID: 23865988**  Huang et al., 2013. Presence of entomobirnaviruses in Chinese mosquitoes in the absence of Dengue virus co-infection. J. Gen Virol. **PMID: 23175239**  Nobiron et al., 2008. Genome and polypeptides characterization of Tellina virus 1 reveals a fifth genetic cluster in the Birnaviridae family. Virology. **PMID: 17976679**  Wu et al., 2010. Virus discovery by deep sequencing and assembly of virus-derived small silencing RNAs. Proc Natl Acad Sci U S A. **PMID: 20080648** |

Table 1: Identity score in amino acid alignment between RdRp (below)



Table 2: Identity score in amino acid alignment between capsid proteins (VP2)

