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:** | **2018.006M** | |  |
| **Short title:** Reorganize taxonomy of the family *Picobirnaviridae* | | | |
|  | | | |
| **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, Attoui H, Ghosh S, Malik Y, Mundt E, Vakharia VN | | [bernard.delmas@inra.fr](mailto:bernard.delmas@inra.fr); [houssam.attoui@vet-alfort.fr](mailto:houssam.attoui@vet-alfort.fr); [sghosh@rossu.fr](mailto:sghosh@rossu.fr); [malikyps@ivri.res.in](mailto:malikyps@ivri.res.in); [egbert.mundt@boehringer-ingelheim.com](mailto:egbert.mundt@boehringer-ingelheim.com); vakharia@umbc.edu | |
| **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]) | |  | | | | |
| **Corresponding author** | | | |
| Bernard Delmas | | | |
| **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) | | ***Picobirnaviridae* ICTV study group** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 6, 2018 |
| Date of this revision (if different to above): | | | May 24, 2019 |

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| **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:** 2018.006M.A.v1.Picobirnaviridae |

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:**

**I- NEW PICOBIRNAVIRUS SPECIES AND GENUS PROPOSITIONS**

**(Lines refer to lines in the Excel document 2018.006M.A.v1.Picobirnaviridae)**

The viruses listed in the two Excel Tables “2018.006M.A.v1.TableRdRpPicobirnaviridae” and “2018.006M.A.v1.TableCapsidPicobirnaviridae” represent all the completely sequenced picobirnaviruses and “picobirna-like” viruses so far (June 2018), namely 21 “conventional” picobirnaviruses and 7 “picobirna-like viruses”, **thus sequenced on their two genomic dsRNA segments, 1 and 2.**

**Virus species: *Human picobirnavirus* (AB186897, AB186898)**

To be still considered as the type species of the genus *Picobirnavirus*, and of its genogroup 1 (see document “2018.006M.A.v1.TableRdRpPicobirnaviridae”).

**Wakuda et al.,** 2005. Complete nucleotide sequences of two RNA segments of human picobirnavirus. Journal of Virological Methods. 126; 165-169.

**Line 4: *Rabbit picobirnavirus (AJ244022)***

Since we know only ½ of its genome, we propose it should not be classified into a virus species as defined before.

**Green et al.,** 1999. Genomic characterization of the large segment of a rabbit picobirnavirus and comparison with the atypical picobirnavirus of *Cryptosporidium parvum*. Arch Virol. 144; 2457-2465.

**Duquerroy et al., 2009**. The picobirnavirus crystal structure provides functional insights into virion assembly and cell entry. EMBO J. 28; 1655-1665.

**Da Costa et al., 2011**. Picobirnaviruses encode a protein with repeats of the ExxRxNxxxE motif. Virus Res. 158: 251-256.

**Line 5:** **Virus species: *Equine picobirnavirus* (KR902507, KR902508)**

Based on the phylogenetic tree carried out with the picobirnavirus RdRp sequences and the document “2018.006M.A.v1.TableRdRpPicobirnaviridae” showing scores or pairwise alignment, we propose to create a new virus species in the genus *Picobirnavirus* to define its genogroup 2.

**Li et al., 2015**. Exploring the virome of diseased horses. J Gen Virol. 96; 2721-2733.

**Line 6: Virus species: *Beihai picobirnavirus* (KX884062, KX884063)**

Seven new viruses isolated from diverse invertebrates and related to picobirnaviruses have been fully sequenced (Shi et al., 2016). They are dsRNA viruses, mono- or bi-segmented viruses.

***Segment 2 encoding the RdRp:***

**Their RdRp show identity scores between 21 and 30% when compared to viruses belonging to the genus *Picobirnavirus*** (see document “2018.006M.A.v1.TableRdRpPicobirnaviridae”). It is here important to note that **the scores in pairwise alignment between picobirnaviruses of genogroups 1 and 2 are found between 21 to 28%, thus providing a strong argument to include this group of viruses in the *Picobirnaviridae* family.** Pairwise alignment carried out with other bisegmented dsRNA viruses such as partitiviruses shows lowest identity scores.

***Segment 1 encoding the capsid protein:***

Capsid sequences of these seven viruses found in invertebrates have no detectable sequence similarity with capsids of picobirnaviruses infecting vertebrates.

No ORF was found upstream the capsid gene, in contrast to (nearly) all picobirnaviruses of the *Picobirnavirus* genus (genogroups 1 & 2) that encode a protein with repeats of the ExxRxNxxxE motif (Da Costa et al., 2011).

Taking in account the high sequence similarity on their RdRp, differences in the capsid proteins and the presence/absence of an upstream ORF encoding repeats of a highly recognizable motif, we propose to create a new genogroup in the *Picobirnaviridae* family called genogroup 3, and we propose as a virus species *Beihai picobirnavirus* with Běihǎi picobirnavirus 7 as an exemplar virus name (accession numbers KX884062, KX884063) in genogroup 3.

**Li et al., 2015**. Exploring the virome of diseased horses. J Gen Virol. 96; 2721-2733.

| 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. |

Two excel documents with identity score between the RdRp and between the capsid amino acid sequences.

2018.006M.A.v1.TableRdRpPicobirnaviridae

2018.006M.A.v1.TableCapsidPicobirnaviridae

2018.006M.A.v1.Picobirna\_Suppl.pdf

| **References:** |
| --- |
| **Da Costa et al.,** 2011. Picobirnaviruses encode a protein with repeats of the ExxRxNxxxE motif. Virus Res. 158: 251-256.  **Duquerroy et al.,** 2009. The picobirnavirus crystal structure provides functional insights into virion assembly and cell entry. EMBO J. 28; 1655-1665.  **Green et al.,** 1999. Genomic characterization of the large segment of a rabbit picobirnavirus and comparison with the atypical picobirnavirus of Cryptosporidium parvum. Arch Virol. 144; 2457-2465.  **Li et al., 2015**. Exploring the virome of diseased horses. J Gen Virol. 96; 2721-2733.  **Shi et al.,** 2016. Redefining the invertebrate RNA virosphere. Nature. 540; 539-543.  **Wakuda et al.,** 2005. Complete nucleotide sequences of two RNA segments of human picobirnavirus. Journal of Virological Methods. 126; 165-169. |