This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

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| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.012M*** | | | | (to be completed by ICTV officers) |
| **Short title: Taxonomic expansion and reorganization of the order *Bunyavirales*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Piet Maes  Sergey Alkhovsky  Martin Beer  Thomas Briese  Michael J. Buchmeier  Charles H. Calisher  Rémi Charrel  Il Ryong Choi  Christopher S. Clegg  Juan Carlos de la Torre  Jospeh L. DeRisi  Michele Digiaro  Hideki Ebihara  Sébastien Emonet  Toufic Elbeaino  Jean-Paul Gonzalez  Anne-Lise Haenni  Rakesh Jain  Gilda Jonson  Sandra Junglen  Richard Kormelink  Amy Lambert  Igor S. Lukashevich  Giovanni P. Martelli  Nicole Mielke-Ehret  Hans-Peter Muehlbach  Marcio R. T. Nunes  Clarence J. Peters  Alexander Plyusnin  Sheli R. Radoshitzky  Victor Romanowski  Maria S. Salvato  Takahide Sasaya  Connie Schmaljohn  Yukio Shirako  Mark D. Stenglein  Robert B. Tesh  Taiyun Wei  Shyi-Dong Yeh  Yongzhen Zhang  Xueping Zhou  Jens H. Kuhn | | | | | |
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| Piet Maes, [piet.maes@kuleuven.be](mailto:piet.maes@kuleuven.be)  Jens H. Kuhn, [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov) | | | | | |
| **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 *Arenaviridae*, *Bunyaviridae*, *Emaravirus*, *Tenuivirus*, and *Tospovirus* Study Groups** | | |
| The ICTV *Arenaviridae*, *Bunyaviridae*, *Emaravirus*, *Tenuivirus*, and *Tospovirus* Study Groups and the additional authors of this TaxoProp have seen and discussed this proposal and agreed to its submission to the ICTV Executive Committee based on majority votes of support by individual Study Group members or the absence of (dissenting) votes. | | | | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| N/A | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | | August 11, 2017 | |

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| **ICTV-EC comments and response of the proposer:** |
| EC49 decision:  Uc: Add genome maps (or links); provide derivation of genus names; consider use of "-associated" in some species names. |

**Part 2**: **PROPOSED TAXONOMY**

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| --- |
| In 2016, the ICTV *Bunyaviridae*, *Emaravirus*, and *Tenuivirus* Study Groups have taken initial steps to taxonomically reorganize/reclassify bunyaviruses and bunya-like viruses using a global DEmARC analysis/Bayesian MCMC phylogeny (TaxoProp 2016.030a-vM “Create a new order, *Bunyavirales*, to accommodate nine families (eight new, one renamed) comprising thirteen genera)”. This effort led to the official establishment of the order *Bunyavirales* by the ICTV/IUMS in March 2017 (Adams *et al*.).  Since the beginning of these efforts, numerous bunya-like viruses have been discovered in invertebrates (Li *et al*., Makhsous *et al*., Shi *et al*.). The majority of these viruses has not been isolated in tissue culture, nor is much information available about them other than complete, coding-complete, or fragmented genomic sequences. The ICTV recently decided that viruses are classifiable based on coding-complete/complete genomic sequences alone (Simmonds *et al*.). Thus, we repeated the DEmARC/Bayesian MCMC analysis of 2016 with all those new viruses included for which complete or coding-complete alignable genome sequences have been deposited into GenBank (see accompanying Excel spreadsheet). Briefly, Bayesian phylogenetic analyses were inferred in BEAST 1.8.2 employing 20 independent MCMC runs with a chain length of 25,000,000 generations. Tree and log files of independent runs of BEAST were combined using LogCombiner 1.8.2, employing a Burn in period of 10%. The Markov chain Monte Carlo analyses were run until effective sample sizes above 200 were obtained. The consensus tree was built with TreeAnnotator 1.8.2 using the maximum clade credibility method and visualized in Figtree (<http://tree.bio.ed.ac.uk/software/figtree/>).  The results of this analysis are shown in Figures 1 and 2. They indicate that overall the taxonomic decisions of 2016 (establishment of the order and several new families, including emaraviruses and tenuiviruses) hold up. However, the resolution of the phylogeny increased significantly and several major taxonomic amendments are required:   * three monogeneric families (*Feraviridae*, *Jonviridae*, and *Tospoviridae*) need to be abandoned and their genera need to be moved into existing families * three new families need to be established for highly divergent Chinese viruses * the family *Arenaviridae* needs to be included in the order *Bunyavirales* * 19 new genera need to be established   These results are also in line with analyses published by others (Gutteres *et al*., Li *et al*., Shi *et al*.) and are confirmed by a global RNA virus RdRp analysis (co-submitted proposal to establish a phylum for negative-sense RNA viruses).  C:\Users\kuhnjens\Desktop\Capture1.JPG  **Figure 1**. The figure shows a Bayesian MCMC tree estimated using a Bayesian Markov Chain Monte Carlo method implemented in BEAST, using the WAG amino acid model of amino acid substitutions. Maximum clade credibility trees were determined using TreeAnnotator with a burn-in of 10% of the sampled trees. The Markov chain Monte Carlo analyses were run until effective sample sizes above 200 were obtained. The dataset used consists of full length products of coding regions of the S, M, and L segments (nucleocapsid protein, glycoprotein precursor, and RNA-dependent RNA polymerase, respectively) or in the case of arenavirus S and L segments and concatenated in one multiple alignment. The dashed boxes show the proposed family delineation as calculated with DEmARC version 1.0. The DEmARC method is an approach for partitioning the genetic diversity of a virus family /genus within a hierarchically organized framework. The developed approach can provide quantitative support for both the delineated classification levels and the inferred taxa by objectively devising the number and values of thresholds on family genetic divergence at each level in a rational and family/genus-wide manner. Genetic divergence is quantified by pairwise evolutionary distances (PEDs) estimated by maximum likelihood inference on a multiple alignment of proteins. Numbers over each main node represents the Bayesian Posterior probabilities. The number below the bar (0.6) corresponds to the amino acid distance between sequences.  C:\Users\kuhnjens\Desktop\Capture2.JPG  **Figure 2**: Intra-order genetic divergence in three-level hierarchical clustering of bunyaviruses by DEmARC (version 1.0). Levels are defined by the three strongest PED thresholds. The number of viruses in the identified clusters are shown in brackets. All identified clusters correspond to monophyletic groups. Box-and-whisker graphs were used to plot distributions of distances between viruses from the same genus (orange), and between viruses from different species but the same genus (blue), and between viruses from different genera but the same family (blue). The boxes span from the first to the third quartile and include the median (bold line), and the whiskers (dashed lines) extend to the extreme values. The corresponding part of the PED distribution is shown below. |
| **Name of accompanying spreadsheet: 2017.012M.N.v1.Bunyavirales\_rev** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

**For genome maps of most viruses proposed to be classified here see Li *et al*. (**<https://elifesciences.org/articles/05378>**) and Shi *et al*.**

**Etymology of proposed genus and family names:**

* *Banyangvirus*: *Banyang*: sigil of Bhanja virus and Huaiyangshan virus; *virus*: suffix for a genus
* *Beidivirus*: *Beidi*: sigil of Húběi diptera virus 3; *virus*: suffix for a genus
* *Cruliviridae*: *Cruli*: sigil of *Crustacean lincruvirus*; *viridae*: suffix for a family
* *Horwuvirus*: *Horwu*: sigil of Wǔhàn horsefly virus; *virus*: suffix for a genus
* *Hubavirus*: *Huba*: sigil of Húběi myriapoda virus 5; *virus*: suffix for a genus
* *Hudivirus*: *Hudi*: sigil of Húběi diptera virus 4; *virus*: suffix for a genus
* *Hudovirus*: *Hudo*: sigil of Húběi lepidoptera virus 1; *virus*: suffix for a genus
* *Inshuvirus*: *Inshu*: sigil of Shuāngào insect virus 2; *virus*: suffix for a genus
* *Lincruvirus*: *Lincru*: sigil of *Wēnlǐng crustacean virus 9*; *virus*: suffix for a genus
* *Loanvirus*: *Loan*: sigil of Lóngquán; *virus*: suffix for a genus
* *Mobatvirus*: *Mobat*: sigil of mole and bat; *virus*: suffix for a genus
* *Mobuvirus*: *Mobu*: sigil of Mothra virus and bunyavirus; *virus*: suffix for a genus
* *Mypoviridae*: *Mypo*: sigil of Húběi myriapoda virus 5; *viridae*: suffix for a family
* *Pidchovirus*: *Pidcho*: derived from Pidgey virus; *virus*: suffix for a genus
* *Shangavirus*: *Shanga*: sigil of Shuāngào insect virus 1; *virus*: suffix for a genus
* *Shaspivirus*: *Shaspi*: sigil of Shāyáng spider virus 1; *virus*: suffix for a genus
* *Striwavirus*: *Striwa*: sigil of Sānxiá water strider virus 1; *virus*: suffix for a genus
* *Thottimvirus*: *Thottim*: derived from Thottopalayam; *virus*: suffix for a genus
* *Wubeivirus*: *Wubei*: sigil of Wǔhàn fly virus 1 and Húběi diptera virus 5; *virus*: suffix for a genus
* *Wuhivirus*: *Wuhi*: sigil of Wǔhàn insect virus 2; *virus*: suffix for a genus
* *Wumivirus*: *Wumi*: sigil of Wǔhàn millipede virus 2; *virus*: suffix for a genus
* *Wupedeviridae*: *Wupede*: sigil of Wǔhàn millipede virus 2; *viridae*: suffix for a family

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