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:** | ***2017.016M*** | | | | (to be completed by ICTV officers) |
| **Short title: Taxonomic expansion and reorganization of the order *Mononegavirales*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
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| **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 *Bornaviridae*, *Filoviridae*, *Mononegavirales*, *Nyamiviridae*, *Paramyxoviridae*, and *Rhabdoviridae,* Study Groups** | | |
| **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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|  |
| **Name of accompanying spreadsheet: 2016.016M.N.v1.Mononegavirales\_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

As of 2017, the order *Mononegavirales* includes eight families and five unassigned genera (Adams *et al*., Amarasinghe *et al*.). From 2015 on, numerous mononega-like viruses (including the so-called “chŭviruses”) have been discovered in invertebrates, fungi, and plants (Fauver *et al*., Li *et al*., Longdon *et al*., Marzano *et al*., Shi *et al*.). The majority of these viruses have 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 performed DEmARC/Bayesian MCMC analysis of all classified and unclassified mononegaviruses for which complete or coding-complete alignable genome sequences have been deposited into GenBank (see accompanying Excel spreadsheet). A dataset of all mononegavirus sequences was constructed with using complete RNA-dependent RNA polymerase (L) amino acid sequences and these sequences were aligned with MAFFT v7.123. Bayesian phylogenetic relationships were inferred in BEAST2 employing 10 independent MCMC runs with a chain length of 50,000,000 generations using full amino acid polymerase sequences. Tree and log files of independent runs of BEAST were combined using LogCombiner 2.4.5, employing a Burn-in period of 10%. Markov chain Monte Carlo analyses were run until effective sample sizes above 200 were obtained. A consensus tree was built with TreeAnnotator 2.4.5 using the maximum clade credibility method and visualized in FigTree v1.4.0. A DEmARC-mediated analysis of genomic variation (version 1.0) was used to set order-wide demarcation criteria for the different ranks. Only PED thresholds with a clustering cost of zero, CC=0 and monophyletic clustering under these thresholds in the Bayesian maximum clade credibility summary tree were retained.

The primary results of this analysis are shown in Figure 1 and confirmed a global RNA virus RdRp palm domain analysis (see co-submitted Phylum TaxoProp). They indicate that overall the past taxonomic decisions (establishment of the order with eight families) hold up. However, the resolution of the phylogeny increased significantly and several major taxonomic amendments are required:

* four new families need to be established. One of those families (“chŭviruses”) is proposed to also constitute a new order (“*Jingchuvirales*”, see co-submitted Phylum TaxoProp) because the genomic organization of “chŭviruses” is fundamentally different from all other viruses in the order *Mononegavirales* (all of which have genomes with the core structure 3´-N-P-M-G-L-5´);
* All five free-floating mononegaviral genera (*Anphevirus*, *Arlivirus*, *Chengtivirus*, *Crustavirus*, and *Wastrivirus*) can be assigned to families and some of them need to be merged; and
* the nyamiviral genus *Peropuvirus* needs to be moved into a new family.

Higher-resolution trees for the individual families are shown in Figures 2–7. We proposed each new family to be monogeneric including several novel species.

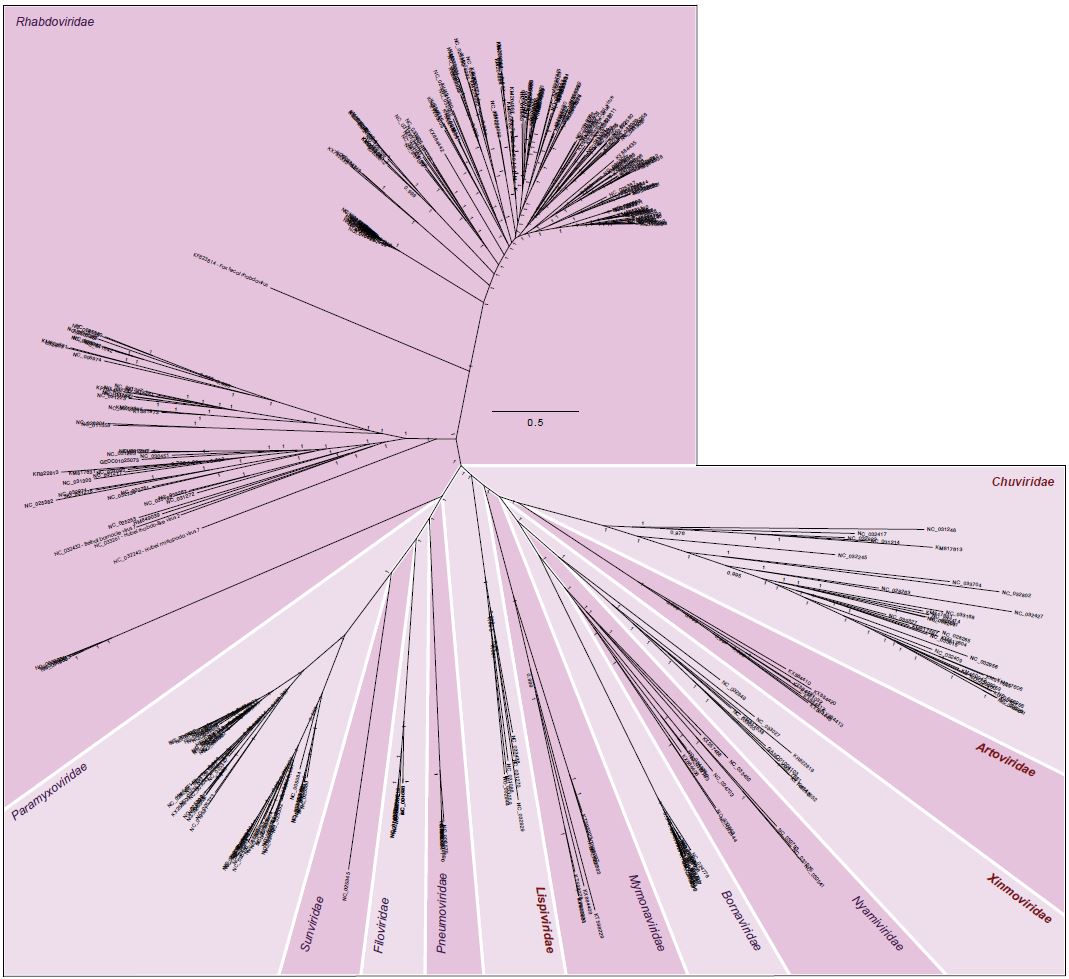


Figure 1. The order *Mononegavirales* and its sister order encompassing “chŭviruses”. New family-level taxa are depicted in red.

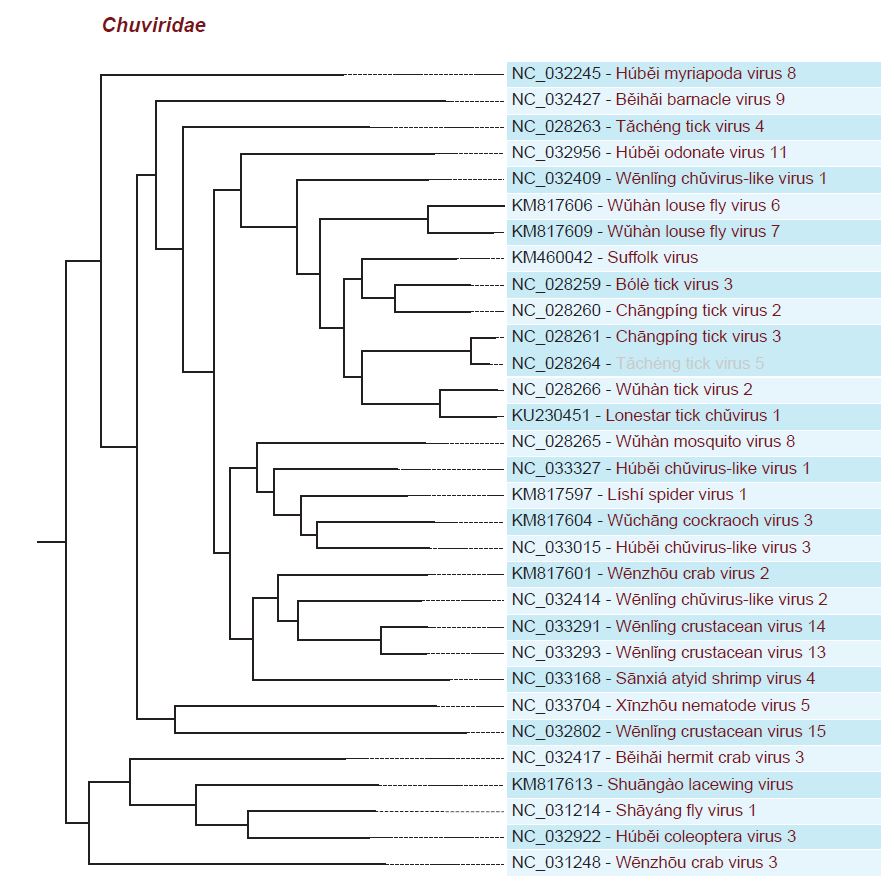


Figure 2. Proposed monogeneric family “*Chuviridae*” (included in the proposed order “*Jingchuvirales*”, see also co-submitted Phylum TaxoProp). Viruses that should be assigned to novel species are depicted red.



Figure 3. Proposed monogeneric family “*Artoviridae*” including the genus *Peropuvirus* (formerly *Nyamiviridae*). Viruses that should be assigned to novel species are depicted red.



Figure 4. Existing monogeneric family *Mymonaviridae*. Viruses that should be assigned to novel species are depicted red.

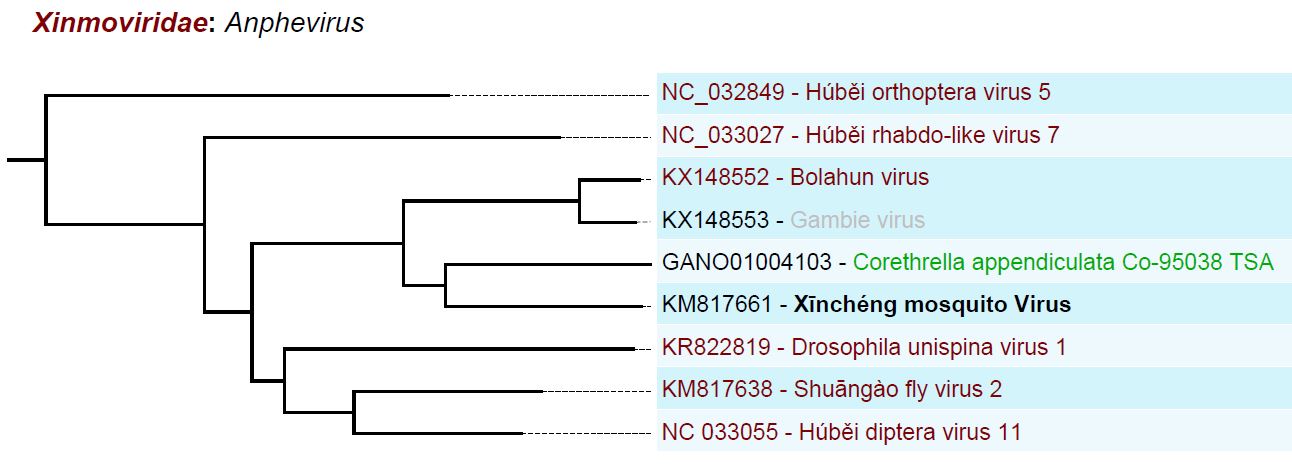


Figure 5. Proposed monogeneric family “*Xinmoviridae*” absorbing the previously free-floating genus *Anphevirus*. Viruses that should be assigned to novel species are depicted red. Green: “xīnmoviral” sequence from a transcriptional shotgun assembly (TSA) not yet proposed to represent a novel species (whether TSA-derived sequences are classifiable has yet to be discussed).

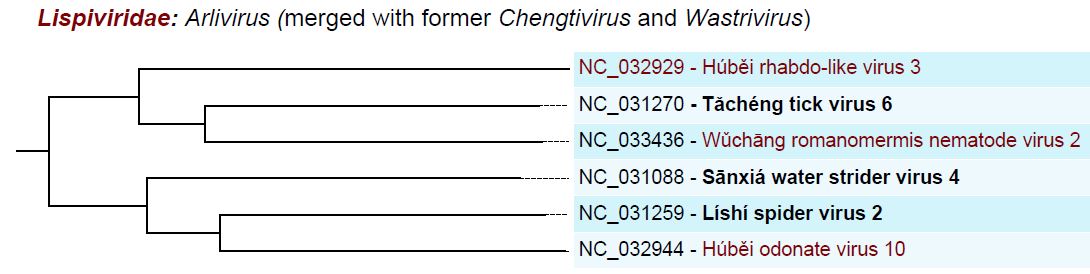


Figure 6. Proposed monogeneric family “*Lispiviridae*”, absorbing the previously free-floating genera *Chengtivirus* and *Wastrivirus*. Viruses that should be assigned to novel species are depicted red.

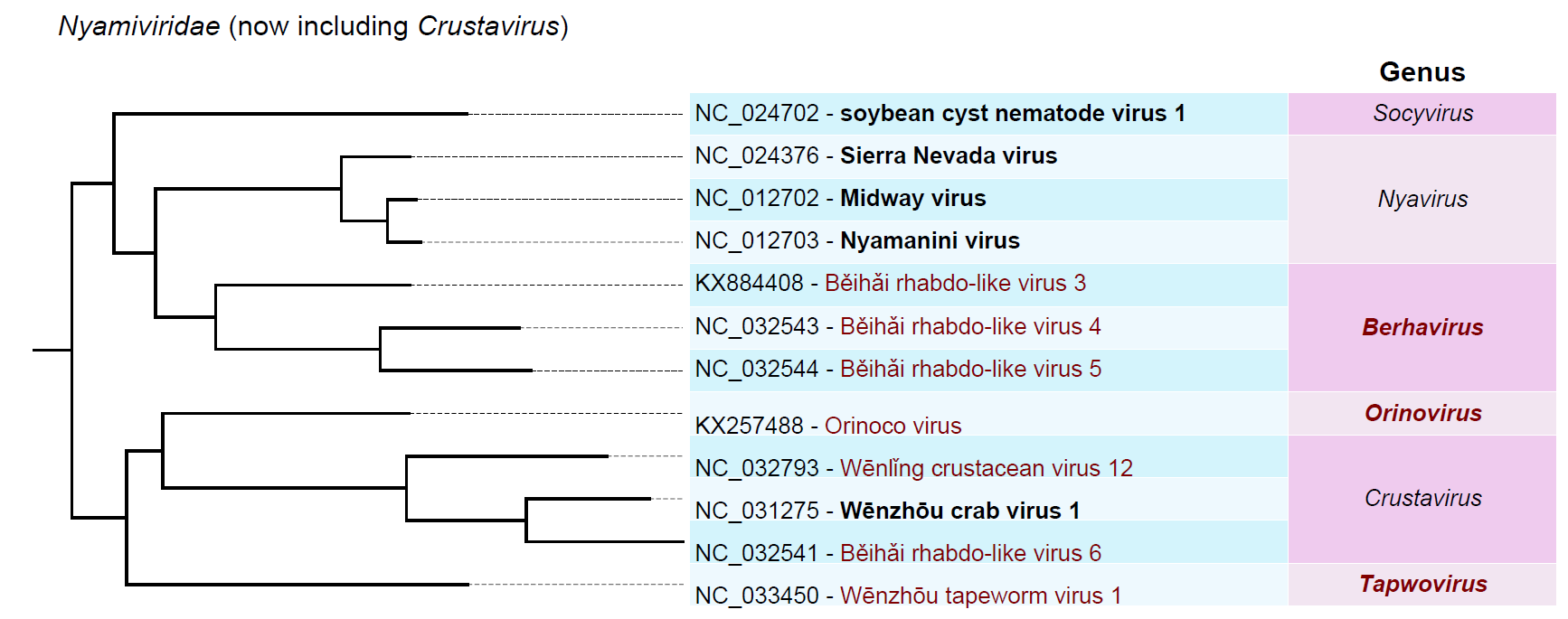


Figure 7. Existing family *Nyamiviridae*, absorbing the previously free-floating genus *Crustavirus*, expanded by three new genera (bold red), and reduced by one genus (*Peropuvirus*, moved into “*Artoviridae*”). Viruses that should be assigned to novel species are depicted red.

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**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:**

* *Orinovirus*: *Orino*: derived from Orinoco virus; *virus*: suffix for a genus
* *Tapwovirus*: *Tapwo*: sigil of Wēnzhōu tapeworm virus 1; *virus*: suffix for a genus
* *Berhavirus*: *Berha*: sigil of Běihǎi rhabdo-like virus 3; *virus*: suffix for a genus
* *Xinmoviridae*: *Xinmo*: sigil of Xīnchéng mosquito virus; *viridae*: suffix for a family
* *Lispiviridae*: *Lispi*: sigil of Lĭshì spider virus 2; *viridae*: suffix for a family
* *Artoviridae*: *Arto*: sigil of arthropod; *viridae*: suffix for a family

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