

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

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| **Code assigned:** | **2020.026M** |  |
| **Short title:** Reorganize the order to include four new families, 18 new genera, and 22 new species *(Jingchuvirales*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Jingchuvirales* Study Group |

**ICTV study group comments and response of proposer**

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| N/A (Study Group authored the proposal) |

**Submission dates**

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| Date first submitted to SC Chair | July 31, 2020 |
| Date of this revision (if different to above) | December 6, 2020 |

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

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| The ICTV Executive Committee (EC) requested major revisions to this TaxoProp: As all viruses analyzed in this TaxoProp are known only from metagenomic sequences, the EC requested re-evaluation and re-interpretation of all involved sequence data to exclude obviously incomplete genome sequences and/or bad assemblies, resulting in a dataset consistent with the available scientific knowledge of (-)ssRNA virus replication and transcription. Specifically, the EC requested to:   * identify and remove viruses for which genome sequences are obviously poorly assembled and/or are not coding-complete; * identify and remove viruses for which GenBank accession numbers are not yet available (or to instead obtain the accession numbers); * align the demarcation of taxa with genome organization, and if possible the structure of encoded glycoproteins and host/source associations of the viruses (i.e., the ecological context of their evolution); and * to remove/fix errors in the accompanying Excel sheet in regard to genus *Taceavirus* (missing parent) and genus *Muscavirus* (missing parent and genus name already exists and should be renamed).   Consequently, we have:   * removed all viruses from the analysis for which genome sequences were poorly assembled and/or are not coding-complete (“coding-complete” is now defined as complete N+L coding sequences rather than L alone); * have added all missing GenBank number; * aligned the demarcation of taxa qith genome organization (but did not take glycoprotein structure into account as many viruses do not seem to encode glycoprotein and abstained for now from taking host/source association into account as in the case of most viruses it is unclear whether they were found in a particular host, on a particular host, or were part of an alleged host’s diet); and * fixed the Excel sheet errors by renaming genus *Muscavirus* and assigning all genera to correct parents.   We would like to thank the ICTV Proposal Secretary, Peter Walker, for sharing detailed analyses with us and engaging in in-depth discussions to improve the TaxoProp according to the EC revision requests. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.026M.R.Jingchuvirales.xlxs |

**Abstract**

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| *Jingchuvirales* is a monjiviricete order that currently includes a single family, *Chuviridae*, for numerous novel viruses currently only known from sequence data. Here, we propose four new families, 18 new chuvirid genera, and a total of 22 novel chuvirid species in the order to better reflect the phylogenetic relationships between these viruses. In addition to providing a genomic “framework” for future updates of the order, all existing member species names are proposed to be harmonized to a standard format and reorganized according to amino acid percent identity and phylogenetic estimations derived from shared large protein (L) sequences encoding an RNA-directed RNA polymerase domain and genome organization. The inclusion of species into the order depended on the presence of complete L and nucleoprotein (N) genes and genomic organizations reminiscent of other members of the phylum *Negarnaviricota*, the parent of class *Monjiviricetes*. |

**Text of proposal**

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| |  | | --- | | **Introduction**  The recent formation of the realm *Riboviria* was based on the observation that most RNA viruses could be unified and classified at the highest echelons and extremes of diversity [17]. Within the realm, a phylum for negative-sense RNA viruses (*Negarnaviricota*) including two subyphyla (*Haploviricotina* and *Polyploviricotina*) was established in 2017 [17, 18]. This step included the creation of the monjiviricete order *Jingchuvirales* as a sister taxon to the order *Mononegavirales*, and a single jingchuviral family, *Chuviridae*. Arising from the discovery of several viruses described in China 2015, *Chuviridae* was named after the historic ‘Chǔ’ (楚) region, which refers to a large area in the middle and lower sections of the Yangzi River [19]. A single genus, *Mivirus*, was established within the *Chuviridae* family for viruses characterized by a range of hosts (*e.g.*, ticks, nematodes, fish, and snakes), multiple genomic organizations (*i.e.*, circular, circular and segmented, and linear), and global prevalence [[2-4](#ENREF_2), [8](#ENREF_8), [9](#ENREF_9), [11-14](#ENREF_11), [17](#ENREF_17), [19-25](#ENREF_19), [27](#ENREF_27), [29](#ENREF_29), [30](#ENREF_30)]. Within the genus, sequences also show a range of sequence diversity down to 13% amino acid identity (data available upon request).  **Species**  Chuvirid species demarcation criteria have not yet been established. Here we propose to consider establishment of a new species if amino acid identity between two complete L protein sequences of chuvirids is <90%. A new chuvirid species may only be established if a coding-complete L protein sequence is available for the virus to be classified. Additionally, the inclusion of species depends on the presence of a complete nucleoprotein (N) gene. Finally, the genomic organization should have homology to other mononegaviruses and be free of any obvious assembly errors.  In consideration of currently ICTV-accepted miviruses and their relevant % identities, 22 new jingchuviral species should be created with many of them included into several additional new genera and families (Figure 1, data available upon request).  **Higher taxa**  In consideration of chuvirid percentage of identities (Figure 1), we propose the creation of four new families within the order. Based on the distribution of amino acid identity within the order, we propose to consider establishment of new families when amino acid identity between complete L sequences is <21%. In accordance, we propose the creation of 18 new genera. We propose to consider establishment of new genera when amino acid identity between complete L sequences is <31%. This classification agrees with our phylogenetic analysis (Figure 2). All new families and genera that include more than one species are clustered together with well-supported nodes. In contrast, all families and genera that currently include a single species are more often than not only poorly supported, or long branches and their phylogenetic position is likely to change when more jingchuvirals are discovered and included in the analysis. Several ICTV-accepted species are proposed to be moved and renamed as a result of this novel classification.  **Etymology**  1. *Bosco* — From Late Latin busca, \*buscus or boscus, from Proto-Germanic \*buskaz (whence also came Old High German busk and English bush). Compare Spanish and Portuguese bosque, French bois, Friulian bosc, Dalmatian buasc, Occitan boscs.  2. *Myria* — is a now obsolete decimal metric prefix denoting a factor of 104 (ten thousand). It originates from the Greek μύριοι (mýrioi) (myriad)  3. Demaptera — Modern Latin (plural), from Greek derma ‘skin’ + pteron ‘wing’.  4. *Crustacea* — from [Latin](https://en.wikipedia.org/wiki/Latin) [crusta](https://en.wiktionary.org/wiki/crusta#Latin) (“shell”) +‎ [-acea](https://en.wiktionary.org/wiki/-acea#Translingual)  5. *Alius* — alius (feminine [alia](https://en.wiktionary.org/wiki/alia#Latin), neuter [aliud](https://en.wiktionary.org/wiki/aliud#Latin)), means “other, another”. From [Proto-Indo-European](https://en.wikipedia.org/wiki/Proto-Indo-European_language) [\*h*₂*élyos](https://en.wiktionary.org/wiki/Reconstruction:Proto-Indo-European/h%2525E2%252582%252582%2525C3%2525A9lyos), from [\*h*₂*el-](https://en.wiktionary.org/wiki/Reconstruction:Proto-Indo-European/h%2525E2%252582%252582el-) (“beyond, other”). Cognates include [Ancient Greek](https://en.wikipedia.org/wiki/Ancient_Greek) [ἄλλος](https://en.wiktionary.org/wiki/%2525E1%2525BC%252584%2525CE%2525BB%2525CE%2525BB%2525CE%2525BF%2525CF%252582#Ancient_Greek) (állos) (Modern [Greek](https://en.wikipedia.org/wiki/Greek_language) [αλλιώς](https://en.wiktionary.org/wiki/%2525CE%2525B1%2525CE%2525BB%2525CE%2525BB%2525CE%2525B9%2525CF%25258E%2525CF%252582#Greek) (alliós)), [αἶλος](https://en.wiktionary.org/w/index.php?title=%2525CE%2525B1%2525E1%2525BC%2525B6%2525CE%2525BB%2525CE%2525BF%2525CF%252582&action=edit&redlink=1) (aîlos) ([Arcadocypriot](https://en.wikipedia.org/wiki/Arcadocypriot_Greek)), [Old Armenian](https://en.wikipedia.org/wiki/Classical_Armenian) [այլ](https://en.wiktionary.org/wiki/%2525D5%2525A1%2525D5%2525B5%2525D5%2525AC#Old_Armenian) (ayl), [Proto-Celtic](https://en.wikipedia.org/wiki/Proto-Celtic_language) [\*alyos](https://en.wiktionary.org/wiki/Reconstruction:Proto-Celtic/alyos), [Proto-Germanic](https://en.wikipedia.org/wiki/Proto-Germanic_language) [\*aljaz](https://en.wiktionary.org/wiki/Reconstruction:Proto-Germanic/aljaz). Other forms from [Proto-Indo-European](https://en.wikipedia.org/wiki/Proto-Indo-European_language) [\*h*₂*el-](https://en.wiktionary.org/wiki/Reconstruction:Proto-Indo-European/h%2525E2%252582%252582el-) include [Latin](https://en.wikipedia.org/wiki/Latin) [ille](https://en.wiktionary.org/wiki/ille#Latin) and [uls](https://en.wiktionary.org/wiki/uls#Latin)  6. *Natare* — inflection of nato, means “swim, float”  7. *Crepuscu* — from Latin [crepusculum](https://www.wordsense.eu/crepusculum/#Latin), means “twilight, dim”  8. *Odonata* — from [Ancient Greek](https://en.wikipedia.org/wiki/Ancient_Greek) [ὀδούς](https://en.wiktionary.org/wiki/%2525E1%2525BD%252580%2525CE%2525B4%2525CE%2525BF%2525CF%25258D%2525CF%252582#Ancient_Greek) (odoús, “tooth”)  9. *Melongena* — from mēlongēna f (genitive [mēlongēnae](https://en.wiktionary.org/wiki/melongenae#Latin)), means “aubergine, eggplant” Medieval Latin, compare [Italian](https://en.wikipedia.org/wiki/Italian_language) [melanzana](https://en.wiktionary.org/wiki/melanzana#Italian). From [Byzantine Greek](https://en.wikipedia.org/wiki/Medieval_Greek) [μελιτζάνα](https://en.wiktionary.org/wiki/%2525CE%2525BC%2525CE%2525B5%2525CE%2525BB%2525CE%2525B9%2525CF%252584%2525CE%2525B6%2525CE%2525AC%2525CE%2525BD%2525CE%2525B1#Ancient_Greek) (melitzána), from [Arabic](https://en.wikipedia.org/wiki/Arabic) [بَاذِنْجَان](https://en.wiktionary.org/wiki/%2525D8%2525A8%2525D8%2525A7%2525D8%2525B0%2525D9%252586%2525D8%2525AC%2525D8%2525A7%2525D9%252586#Arabic)‎ (bāḏinjān), from [Persian](https://en.wikipedia.org/wiki/Persian_language) [بادنجان](https://en.wiktionary.org/wiki/%2525D8%2525A8%2525D8%2525A7%2525D8%2525AF%2525D9%252586%2525D8%2525AC%2525D8%2525A7%2525D9%252586#Persian)‎ (bâdinjân)  10. *Culicida* — from culicid, originating from Culex (“midge, gnat”)  11. *Doliu* — from [Latin](https://en.wikipedia.org/wiki/Latin) [dōlium](https://en.wiktionary.org/wiki/dolium#Latin) (large [earthenware](https://en.wiktionary.org/wiki/earthenware) [vessel](https://en.wiktionary.org/wiki/vessel), [hogshead](https://en.wiktionary.org/wiki/hogshead), [cask](https://en.wiktionary.org/wiki/cask)). According to Pokorny, from [Proto-Indo-European](https://en.wikipedia.org/wiki/Proto-Indo-European_language)  12. *Morsus* —perfect passive participle of [Proto-Italic](https://en.wikipedia.org/wiki/Proto-Italic_language) [\*mordeō](https://en.wiktionary.org/wiki/Reconstruction:Proto-Italic/morde%2525C5%25258D), (“I bite”). From [Proto-Indo-European](https://en.wikipedia.org/wiki/Proto-Indo-European_language) [\*(s)merd-](https://en.wiktionary.org/wiki/Reconstruction:Proto-Indo-European/(s)merd-) (“to bite, sting”)  12. *Pedia* — from [Ancient Greek](https://en.wikipedia.org/wiki/Ancient_Greek) [πεδίον](https://en.wiktionary.org/wiki/%2525CF%252580%2525CE%2525B5%2525CE%2525B4%2525CE%2525AF%2525CE%2525BF%2525CE%2525BD#Ancient_Greek) (pedíon, “plain, field”)  13. *Tacea* — from [Latin](https://en.wikipedia.org/wiki/Latin) [tacēre](https://en.wiktionary.org/wiki/tacere#Latin), present active infinitive of [taceō](https://en.wiktionary.org/wiki/taceo#Latin), from [Proto-Italic](https://en.wikipedia.org/wiki/Proto-Italic_language) [\*takēō](https://en.wiktionary.org/wiki/Reconstruction:Proto-Italic/tak%25C4%2593%25C5%258D), possibly from [Proto-Indo-European](https://en.wikipedia.org/wiki/Proto-Indo-European_language) [\*tak-](https://en.wiktionary.org/w/index.php?title=Reconstruction:Proto-Indo-European/tak-&action=edit&redlink=1) or [\*tHk-](https://en.wiktionary.org/w/index.php?title=Reconstruction:Proto-Indo-European/tHk-&action=edit&redlink=1).  14. *Ollus* — from estonian *ollus*, means “[substance](https://en.wiktionary.org/wiki/substance), [matter](https://en.wiktionary.org/wiki/matter), [material](https://en.wiktionary.org/wiki/material)”, from Old Latin [ollus](https://www.wordsense.eu/ello/)‎ ("he, that")  15. *Obscuru* — from obscurus (Latin) means “dark, dusky, shadowy”  16. *Charybdi* — Charybdis was a sea monster in Greek mythology, which dwelt in the Strait of Messina  17. *Aqualaru* — from [Latin](https://en.wikipedia.org/wiki/Latin) [aqua](https://en.wiktionary.org/wiki/aqua#Latin), means “water”, and from Latin *larua*, means “ghost, evil spirit, demon”. | |

**Supporting evidence**

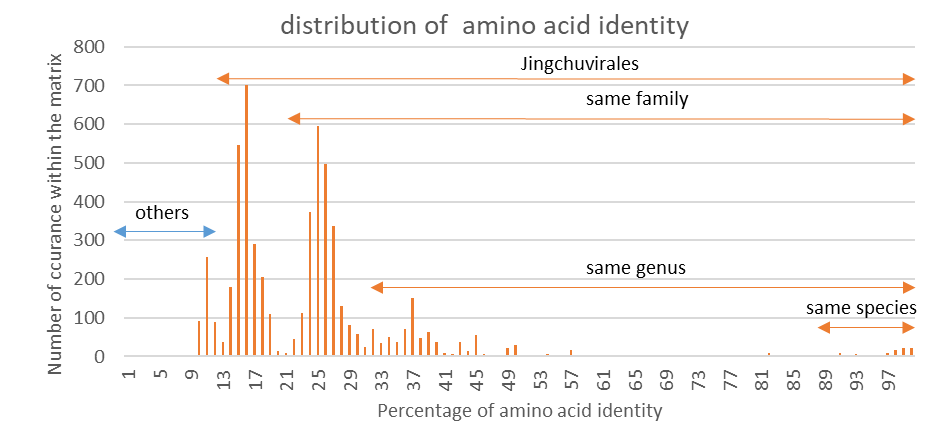


Figure 1: Distribution of amino acid identities between viruses representing proposed species.

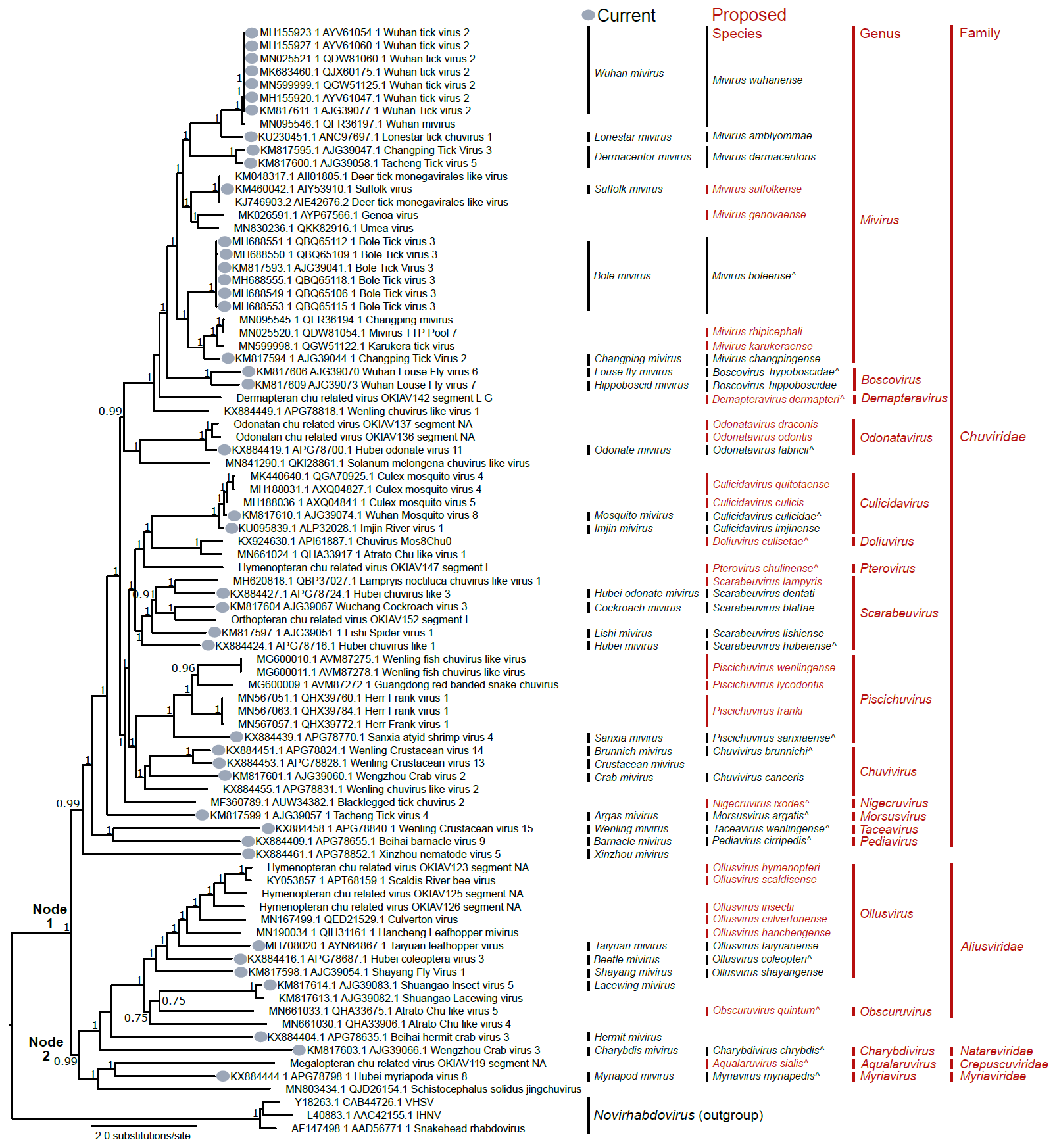


Figure 2. Maximum likelihood phylogenetic tree estimated using 82 complete L protein sequences. Three novirhabdovirus (*Mononegavirales*: *Rhabdoviridae*: *Novirhabdovirus*) sequences were included as a monophyletic outgroup. Sequences were initially aligned using ClustalW [28], refined using Muscle [6], and manually curated in Geneious R9 [15]. Prottest [1] was used to estimate the best amino acid substitution model for the dataset (LG+I+G+F). The tree was estimated using PhyML 3.0 [10], a Subtree Pruning and Regrafting (SPR) topology searching algorithm, and aBayes branches support algorithm. Tree branches are scaled by substitutions per site. Support values are shown as decimal values. Tree tips with a gray circle mark ICTV-accepted *Jingchuvirales* species. Red text shoes newly proposed species and genera. A caret (^) denotes proposed genera member type species.

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