

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

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| **Code assigned:** | **2021.039M** |  |
| **Short title:** Create ten new genera, create eight new species, abolish one species, and rename all six remaining species (*Mononegavirales*: *Xinmoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Paraskevopoulou S |

**List the ICTV Study Group(s) that have seen this proposal**

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| There is currently no Study Group for this family. |

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

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| N/A |

**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

**Submission dates**

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| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 16, 2021 |

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

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| * Please add the missing (“pending”) GenBank accession numbers – if not possible by deadline then please delete the rows from the Excel sheets.   Response: GenBank accession numbers remain pending, unfortunately, for four species. Hence, these entries/species were removed from the Excel and the Word modules.  Edit Word module etymology section; references are not quoted in text; suggest adding the virus name abbreviation in the spreadsheet when necessary.  Response: Etymology section was clarified; references are now quoted in the text; virus abbreviations have been added to the Excel module.   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

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

**Name of accompanying Excel module**

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| 2021.039M.A.v1.Xinmoviridae\_11ngen\_8nsp |

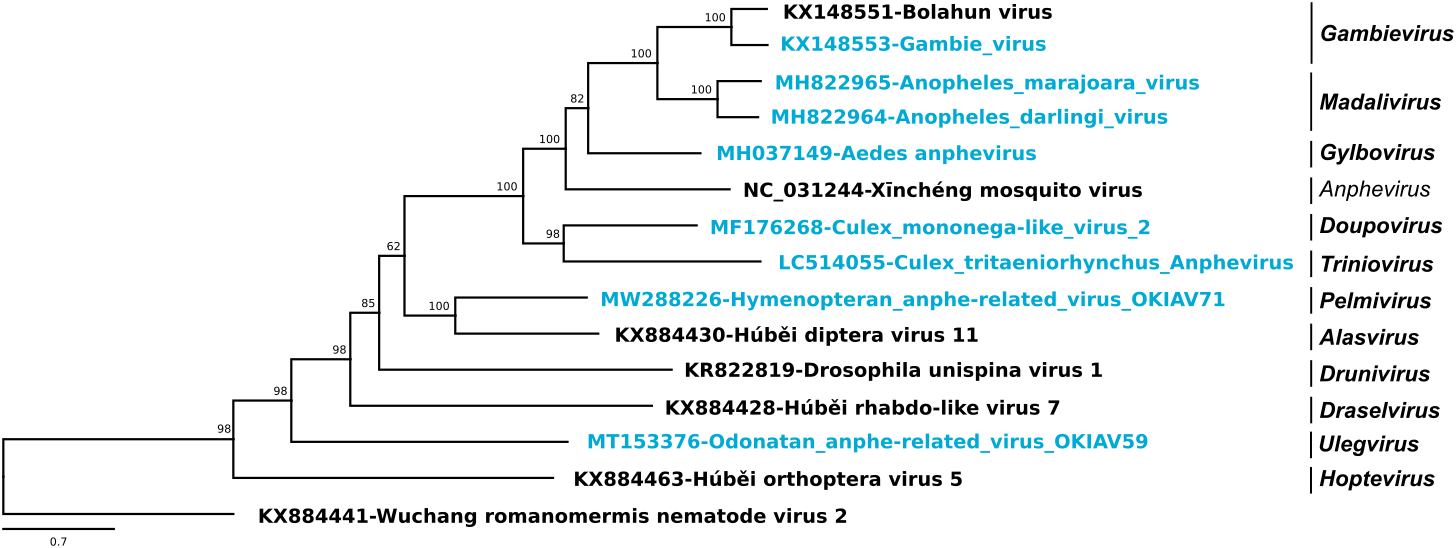
**Abstract**

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| We propose the creation of ten new genera to be included in mononegaviral family *Xinmoviridae.* Genus (and species) demarcation is proposed to be based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparisons similar to established genus/species demarcation criteria for other mononegaviral families. |

**Text of proposal**

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| |  | | --- | | *Xinmoviridae* is a monogeneric family of the haploviricotine order *Mononegavirales*. The family is currently monogeneric family, including only genus *Anphevirus* with seven species. Here, we propose that virus classification criteria for this family should include:   * a coding/near-complete genome * at least 20% amino acid identity of the RNA-directed RNA polymerase (RdRp) sequence   The above criteria were chosen to be similar to those used for other mononegaviral families. We consequently propose the abolishment of species *Shuangao anphevirus* due to the lack of a coding/near-complete genome of its member virus.  Additionally, we propose that the xinmovirid genus demarcation criterion should be RdRp amino acid identity of 60% or lower, and that the species demarcation criterion should be an RdRp amino acid identity of 60% or higher. Using xinmovirid sequences deposited in GenBank and/or described in various publications (references 1-5), and based on the phylogenetic analysis of these sequences shown in **Figure 1**, we propose the demarcation of ten new genera and eight new species.  Also, in March 2021, the ICTV ratified TaxoProp 2018.001G.R.binomial\_species, which requires all species names to follow a new codified rule:  "A species name shall consist of only two distinct word components separated by a space. The first word component shall begin with a capital letter and be identical in spelling to the name of the genus to which the species belongs. The second word component shall not contain any suffixes specific for taxa of higher ranks. The entire species name (both word components) shall be italicized."  This rule requires most established species names to be changed. Here, we propose to change the names of the established xinmovirid species to follow this rule by adopting a binomial species name, and such names are also proposed for newly proposed species.  Etymologies:   * *Gambievirus bolahunense* for Bolahun virus discovered by HTS in *Anopheles gambiae* mosquitos sampled in Burkina Faso. The species epithet is derived from the virus name (Bolahun, Liberia). The genus name is derived from the virus name “Gambie virus” (see below). * *Gambievirus senegalense* for Gambie virus discovered by HTS in *Anopheles gambiae* mosquitos sampled in Senegal (hence the species epithet). * *Madalivirus amapaense* for Anopheles marajoara virus discovered by HTS in *Anopheles marajoara* mosquitos sampled in Amapá state, Brazil. The genus is named after a syllable combination from the *Anopheles* species epithets *marajoara* and *darlingi* (mosquitoes of both species yielded madaliviruses; see below). * *Madalivirus amazonaense* for Anopheles darlingi virus discovered by HTS in *Anopheles darlingi* mosquitos sampled in Amapá and Amazonas states, Brazil. * *Gylbovirus aagae* for Aedes anphevirus discovered initially by HTS in *Aedes aegypti* mosquitos and then in the Aag2 *Aedes* *albopictus* cell line. The genus is named after a syllable combination from the words aegypti and albopictus. * *Anphevirus xinchengense* for Xīnchéng anphevirus discovered by HTS in *Anopheles sinensis* mosquitos sampled in Xincheng, China. The species was renamed from *Xincheng anphevirus.* * *Doupovirus australiaense* for Culex mononega-like virus 2 discovered by HTS in *Culex australicus* mosquitos sampled in Point Douro, Australia. The genus is named after a contraction of Point Douro. * *Triniovirus yonagoense* for Culex tritaeniorhynchus anphevirus discovered by HTS in *Culex tritaeniorhynchus* mosquitos sampled in Yonago, Japan. The genus is named after a syllable combination from the word *tritaeniorhynchus*. * *Pelmivirus eymattense* for hymenopteran anphe-related virus OKIAV71 discovered by HTS in *Heteropelma amictum* parasitoid wasps sampled in Eymatt, Bern, Switzerland. The genus is named after a syllable combination from the host species *Heteropelma amictum*. * *Alasvirus muscae* for dipteran anphevirus discovered by HTS in a Diptera sp. pool sampled in Hubei, China. The genus is named using the Latin word “alas” which means wings (Diptera is an insect order for insects that have only two wings). The species is named using the singular genitive of musca, the Latin word for fly. * *Drunivirus chambonense* for drosophilid anphevirus in *Drosophila unispina* sampled in Chambon, France. The genus is named after a syllable combination from the host species *Drosophila unispina*. * *Draselvirus dentati* for odonate anphevirus discovered by HTS in an Odonata sp. pool sampled in Hubei, China. The genus is named after a syllable combination from the common names of Odonata, dragonflies and damselflies. The species is named using the singular genitive of dentatum, the Latin word for toothed (odonate is derived from the Greek word for tooth (ὀδούς)). * *Ulegvirus freckenfeldense* for odonatan anphe-related virus OKIAV59 discovered by HTS in *Cordulegaster boltonii* dragonflies sampled in Freckenfeld, Rhineland-Palatinate, Germany. The genus is named after a syllable combination from the host genera *Libellula* and *Cordulegaster*. * *Hoptevirus orthopteris* for orthopteran anphevirus discovered by HTS in an Orthoptera sp. pool sampled in Hubei, China. The genus is named after a syllable combination from the word Orthoptera. The species is named using the likely singular genitive of the order name Orthoptera. | |

**Supporting evidence**

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**Figure 1:** Phylogenetic relationships of xinmovirids. The phylogenetic tree is based on a MAFFT-alignment of the RdRp amino acid sequences using the E-INS-i algorithm and was inferred using IQtree and the LG substitution model. Numbers on branch nodes represent transfer bootstrap expectation values (1,000 replicates). Proposed new xinmovirid genera are shown in bold at the right; viruses proposed to be classified into new species are shown in blue. The tree is rooted to *Wuchang arlivirus* from the genus *Arlivirus* of the *Lispiviridae* family.

**References**

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5. Käfer S, Paraskevopoulou S, Zirkel F et al (2019) Re-assessing the diversity of negative strand RNA viruses in insects. PLOS Pathogens, 15(12): e1008224. <https://doi.org/10.1371/journal.ppat.1008224>