

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

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| **Code assigned:** | ***2022.020M*** |  |
| **Short title:** Two new genera, 10 new species, and 1 moved and renamed species in family *Phenuiviridae* (*Bunyavirales*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Phenuiviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| Approved. |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Phenuiviridae* Study Group | 9 | 0 | 0 |

**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 |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | May 27, 2022 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2022.020M.N.v1.Phenuiviridae\_3ngen\_12nsp\_1rensp.xlsx |

**Abstract**

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| We propose the classification of 10 newly discovered phenuivirids into 1 new species in 1 new monospecific genus and 9 new species in established genera, and the move of one species into a new genus. |

**Text of proposal**

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| |  | | --- | | The bunyaviral family *Phenuiviridae* currently includes 20 genera (*Bandavirus*, *Beidivirus*, *Coguvirus*, *Entovirus*, *Goukovirus*, *Horwuvirus*, *Hudivirus*, *Hudovirus*, *Ixovirus*, *Laulavirus*, *Lentinuvirus, Mobuvirus*, *Phasivirus*, *Phlebovirus*, *Pidchovirus*, *Rubodvirus*, *Tanzavirus*, *Tenuivirus*, *Uukuvirus*, and *Wenrivirus*). In 2021, the ICTV *Phenuiviridae* Study Group  established a species demarcation criterion of <95% identity in the amino acid sequence of the phenuivirid RNA-directed RNA polymerase (RdRp) (TaxoProp 2020.029M). A reanalysis of the dataset used in TaxoProp 2020.029M, complemented with newly described phenuivirid sequences, indicated that 10 viruses should be classified into 1 novel monospecific genus and 9 novel species in established genera, and that 1 species ought to be moved into a novel genus (Supplementary Data, Figure 1):  **Novel monospecific genera:**   * Aphis citricidus bunyavirus (AcBV) was discovered by high-throughput sequencing (HTS) in brown citrus aphids (*Aphis citricidus* (Kirkaldy, 1907)) sampled from an aphid colony at Southwest University ( 西南大学), Chóngqìng (重庆市), China. Analyses place the virus in *Phenuiviridae* but not into any established genus [[15](#_ENREF_15)] (proposed genus *Citricivirus*); and * melon chlorotic spot virus (MeCSV) [[6](#_ENREF_6)], currently classified in phenuivirid genus *Tenuivirus*, needs to be moved into a new, currently monospecific, genus (proposed genus *Mechlorovirus*).   **Novel phlebovirus species:**  Hédǐ virus (HEDV) was isolated from *Phlebotomus chinensis* Newstead, 1916 sand flies sampled in Hédǐ (河底镇), Shānxī Province (山西省), China [[13](#_ENREF_13)].  **Novel uukuvirus species:**  Tōyo virus (TOYOV) was discovered by HTS in in ixodid *Haemaphysalis formosensis* Neumann, 1913 ticks sampled in Tōyo (東予市), Ehime Prefecture (愛媛県), Japan [[4](#_ENREF_4)].  [Sunday Canyon virus, isolated from argasid *Argas cooleyi* Kohls & Hoogstraal, 1960 ticks sampled in Sunday Canyon, Texas, USA [[14](#_ENREF_14)], was found to be an isolate of the already classified uukuvirus murre virus (MURV)].  **Novel bandavirus species:**  Zwiesel bat bandavirus (ZbbV) was discovered by HTS in northern bats (*Eptesicus nilssonii* (Keyserling et Blasius, 1839)) sampled in Zwiesel, Bavaria (Bayern), Germany [[5](#_ENREF_5)].  [Culex bunyavirus 1 strain CBunV1/Kern, discovered by HTS in culicid *Culex* sp. mosquitoes sampled in the USA [[8](#_ENREF_8)], was found to be an isolate of the already classified phasivirus Wǔtái mosquito virus (WtMV)].  **Novel horwuvirus species:**  Solenopsis invicta virus 14 (SINV-14) was discovered by HTS in red imported fire ants (formicid *Solenopsis invicta* (Buren, 1972)) collected in Mississippi, USA [[12](#_ENREF_12)].  **Novel goukovirus species:**   * Ceraphron bunya-like virus (CerBLV) was discovered in SRA data of ceraphronid *Ceraphron* sp. [[11](#_ENREF_11)]; * Aphalara polygoni (ApBLV) bunya-like virus discovered in SRA data of psyllid *Aphalara polygoni* Foerster, 1848 jumping plant lice [[11](#_ENREF_11)].   **Novel mobuvirus species:**   * Browner virus (BRWV) was discovered by HTS in *Stephanocircus* sp. fleas sampled in New South Wales, Australia [[2](#_ENREF_2)]; and * Euproctis pseudoconspersa bunyavirus (EPBV) was discovered by HTS in tea tussock moths (erebid *Arna pseudoconspersa* Strand, 1914) sampled in Qīngyuǎn (清远市), Guǎngdōng Province (广东省), China [[10](#_ENREF_10)].   **Novel lauravirus species:**  Wardell virus (WRDV) was discovered by HTS in Australian paralysis ticks (ixodid *Ixodes holocyclus* Neumann, 1899) sampled in Wardell, New South Wales, Australia [[1](#_ENREF_1)].  **Novel viruses assignable to established phenuivirid species:**  [Leuven phlebovirus, discovered by HTS in castor bean ticks (ixodid *Ixodes ricinus* (Linnaeus, 1758)) sampled in Belgium [[9](#_ENREF_9)], was found to be an isolate of the already classified ixovirus Fairhair virus]. | |

**Supporting evidence**

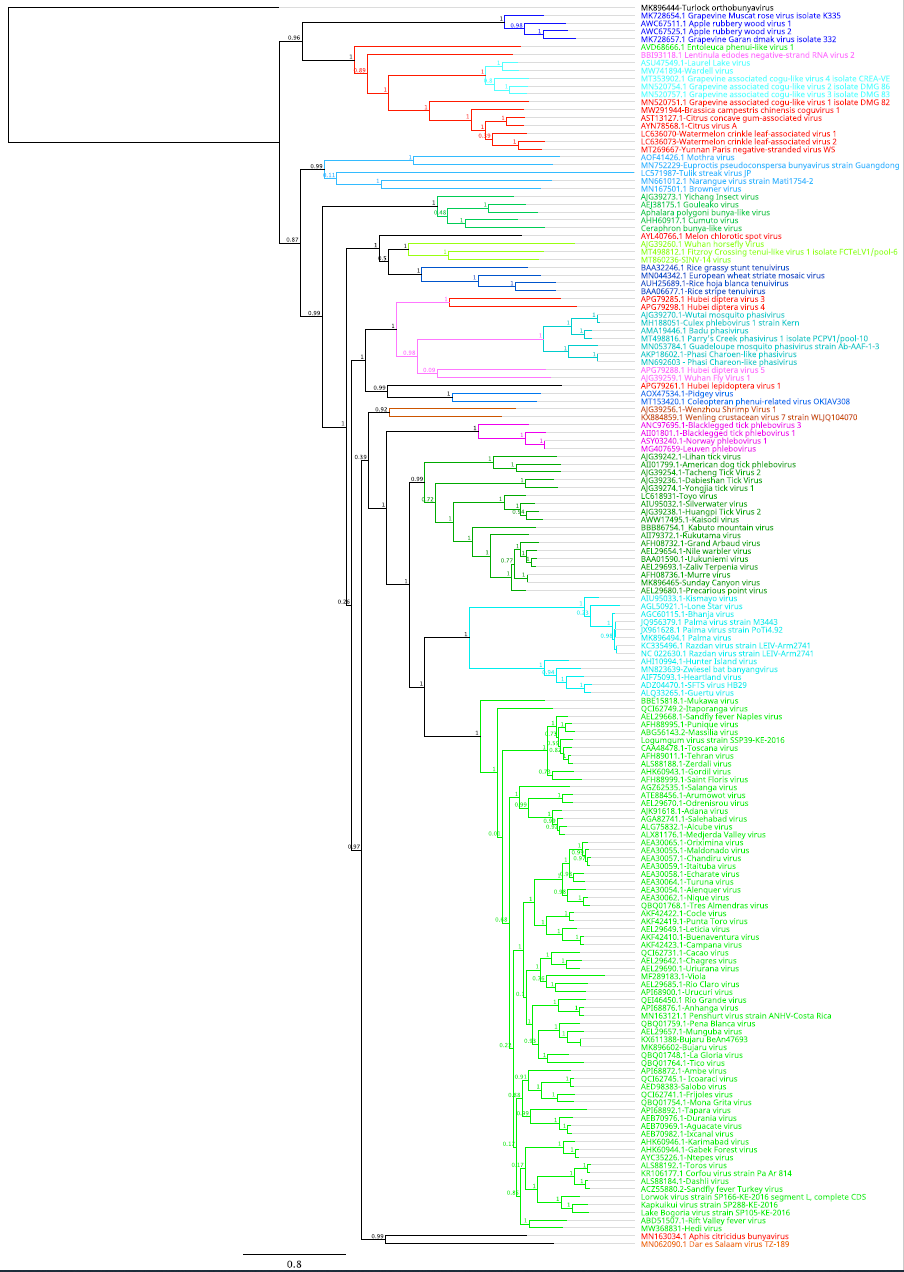
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Figure 1. Maximum-likelihood (ML) phylogeny is based on a MAFFT-alignment of the RNA‑directed RNA polymerase (RdRp) amino-acid sequences of phenuivirids and phenuivirid‑like sequences using E-INS algorithm. The ML phylogenetic tree was inferred using IQ-TREE [[7](#_ENREF_7)]; the numbers on the nodes represent bootstrap values derived from the ultrafast bootstrap algorithm [[3](#_ENREF_3)]. Trees were inferred under the LG+G+I substitution model. Tree branches are proportional to genetic distances between sequences and the scale bars at the top indicate substitutions per amino acid. For all taxa shown here, the complete genome or complete coding sequence is available at the GenBank nucleotide sequence database. Accession numbers are shown next to the respective virus taxon.

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