

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Establish 62 new species and abolish one species in the family *Phenuiviridae* |
| **Code assigned:** | 2025.008M.Ac.v4.Phenuiviridae\_62nsp+1asp | |

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**Part 1b: Taxonomy Proposal Submission** <To be completed on initial submission>

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses | **X** | Fungal and protist viruses | **X** |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| ICTV *Phenuiviridae* Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
| ICTV *Phenuiviridae* Study Group | 11 | 0 | 0 |

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| **Submission date:** | June 7, 2025 |

Enter date of the initial submission (DD/MM/YYYY).

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **X** |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
| Please double-check the inclusion of bisegmented uukuviruses, i.e., that these virus genomes are indeed complete and not missing an M segment. Please correct all species names regarding proper Latinization. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| When the genus *Uukuvirus* was established (TaxoProp 2019.026M), viruses such as American dog tick virus (ADAV) and Pacific coast tick virus (PACV) have been classified under the assumption that they are bisegmented (L + S segment) due to the absence of any M-segment-like sequences in the examined datasets. Consequently, and again due to the absence of M-segment-like sequences in the datasets we analyzed for this proposal, we assume the uukuviruses proposed to be classified here as bisegmented and their genomes as likely (coding) complete. In addition, ixoviruses, also classified in family *Phenuiviridae* are equally considered to be bisegmented. |

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| **Revision date:** | 10/19/2025 |

Enter date of the revised version (DD/MM/YYYY).

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

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon | **X** | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Beidivirus drosophilae* | Named after host genus name *Drosophila* |
| *Beidivirus ischnurae* | Named after host genus name *Ischnura* |
| *Beidivirus liriomyzae* | Named after host genus name *Liriomyza* |
| *Bocivirus flakkebjergense* | Named after Flakkebjerg, Zealand, Denmark |
| *Bocivirus gibberellae* | Named after host genus name *Gibberella* |
| *Bocivirus sanyaense* | Named after 三亚市 [Sānyà ), 海南省 [Hǎinán Province], China |
| *Coguvirus rubi* | Named after host name *Rubus* |
| *Entovirus guangxiense* | Named after Guǎngxī Zhuàng Autonomous Region [广西壮族自治区], China |
| *Entovirus neimengguense* | Named after 内蒙古自治区 [Nèiměnggǔ Zìzhìqū - Inner Mongolia Autonomous Region], China |
| *Entovirus jiangsuense* | Named after 江苏省 [Jiāngsū Province], China |
| *Entovirus yunnanense* | Named after云南省 [Yúnnán Province], China |
| *Goukovirus blattellae* | Named after host genus name *Blattella* |
| *Goukovirus culicis* | Named after host genus name *Culex* |
| *Goukovirus hodotermopsidis* | Named after host genus name *Hodotermopsis* |
| *Goukovirus taiense* | Named after Taï National Park, Côte d’Ivoire |
| *Goukovirus shahense* | Named after 沙河 [Shāhé) area, Beijing, China |
| *Goukovirus reticulitermitidis* | Named after host genus name *Reticulitermes* |
| *Hudovirus culicis* | Named after host genus name *Culex* |
| *Hudovirus pectinophorae* | Named after host genus name *Pectinophora* |
| *Ixovirus gakugsaense* | Named after Гакугса [Gakugsa], Республика Карелия [Karelia], Russia |
| *Ixovirus antarcticaense* | Named after Antarctica |
| *Ixovirus paradisense* | Named after Paradise Harbour, Antarctica |
| *Ixovirus yichunense* | Named after伊春市 [Yīchūn], 黑龙江省 [Hēilóngjiāng Province], China |
| *Ixovirus garrapataense* | Named after Garrapata State Park, California, USA |
| *Laulavirus cordycipitis* | Named after host genus name *Cordyceps* |
| *Laulavirus panici* | Named after host genus name *Panicum* |
| *Laulavirus valsae* | Named after host genus name *Valsa* |
| *Lentinuvirus alphaarmillariae* | Named after host genus name *Armillaria* |
| *Lentinuvirus betaarmillariae* | Named after host genus name *Armillaria* |
| *Lentinuvirus adlentinulae* | Named after host genus name *Lentinula*; and prefix *ad*-, meaning “additional to distinguish this species from the established *Lentinuvirus lentinulae* |
| *Mobuvirus anophelae* | Name after host genus name *Anopheles* |
| *Mobuvirus alphabafoussamense* | Named after Bafoussam, Cameroon, merged with Greek alpha |
| *Mobuvirus betabafoussamense* | Named after Bafoussam, Cameroon, merged with Greek beta |
| *Mobuvirus coquillettidiae* | Name after host genus name *Coquillettidia* |
| *Mobuvirus cotesiae* | Name after host genus name *Cotesia* |
| *Mobuvirus alamedaense* | Named after Alameda County, California, USA |
| *Mobuvirus isahayaense* | Named after諫早市 [Isahaya], 長崎県 [Nagasaki Prefecture], Japan |
| *Mobuvirus culicis* | Name after host genus name *Culex* |
| *Mobuvirus sanyaense* | Named after三亚市 [Sānyà], 海南省 [Hǎinán Province], China |
| *Mobuvirus shuangaoense* | Named after双岙村 [Shuāngào Village], 浙江省 [Zhèjiāng Province], China |
| *Phasivirus siavongaense* | Named after Siavonga, Southern Province, Zambia |
| *Phasivirus zambiae* | Named after Zambia |
| *Phasivirus alamedaense* | Named after Alameda County, California, USA |
| *Phlebovirus alxaense* | Named after阿拉善左旗 [Alxa Left Banner], , China |
| *Phlebovirus baishanense* | Named after白山市 [Báishān], 吉林省 [Jílín Province], China |
| *Phlebovirus manidae* | Named after host family Manidae |
| *Phlebovirus wuxiangense* | Named after武乡县 [Wǔxiāng County], 山西省 [Shānxī Province], China |
| *Uukuvirus boleense* | Named after博乐市 [Bólè], 新疆维吾尔自治区 [Xīnjiāng Uygur Autonomous Region], China |
| *Uukuvirus trinidadense* | Named after Trinidad, Republic of Trinidad and Tobago |
| *Uukuvirus tobagoense* | Named after Tobago, Republic of Trinidad and Tobago |
| *Uukuvirus changpingense* | Named after昌平区 [Chāngpíng District], Beijing, China |
| *Uukuvirus shandongense* | Named after山东省 [Shāndōng Province], China |
| *Uukuvirus croatiaense* | Named after Croatia |
| *Uukuvirus addermacentoris* | Name after a part of host genus name *Dermacentor*; and prefix *ad*-, meaning “additional to distinguish this species from the established *Uukuvirus dermacentoris* |
| *Uukuvirus iftinense* | Named after Iftin, Kenya |
| *Uukuvirus mbalambalaense* | Named after Mbalambala, Garissa County, Kenya |
| *Uukuvirus akirunoense* | Named after あきる野市 [Akiruno], Tokyo Metropolis, Japan |
| *Uukuvirus okutamaense* | Named after 奥多摩町 [Okutama], Tokyo Metropolis, Japan |
| *Uukuvirus qinghaiense* | Named after青海省 [Qīnghǎi Province], China |
| *Uukuvirus anatoliaense* | Named after Anatolia, Turkey |
| *Uukuvirus xinjiangense* | Named after新疆维吾尔自治区 [Xīnjiāng Uygur Autonomous Region], China |
| *Wenrivirus huanghaiense* | Named after 黃海 [Huánghǎi/the Yellow Sea], China |

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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
| NA | NA |  |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: Species  *Description of current taxonomy*:  *Negarnaviricota, Polyplovircotina, Bunyaviricetes, Hareavirales, Phenuiviridae*  The family *Phenuiviridae* currently includes 23 genera and 159 species.  *Proposed* *taxonomic change(s):*  Establish 62 new species in 14 established genera in the family *Phenuiviridae* and abolish one species in thegenus *Laulavirus* in the family *Phenuiviridae.*  *Justification*:  The 62 newly discovered phenuivirids are proposed to be classified into new species in 14 phenuivirid genera on the base of phylogenetic trees constructed from their deduced RNA-directed RNA polymerase (RdRP) amino acid sequences identities. One species was abolished due to the absence of a coding-complete genome sequence of its virus. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Species in the family *Phenuiviridae*  *Description of current taxonomy*:  The family *Phenuiviridae* (*Negarnaviricota*: *Polyploviricotina*: *Bunyaviricetes*: *Hareavirales*: *Phenuiviridae*) harbors viruses with 2–8 segments of negative-sense or ambisense RNA that are 8.1–25.1 kb in total length. Phenuivirids infect animals including livestock and humans, birds, and arthropods as well as plants or fungi that serve as single hosts or act as biological vectors for transmission to animals or plants. The familycurrently includes 23 genera and 159 species for 180 viruses [1].  *Proposed* *taxonomic change(s)*:  Establish 62 new species in 14 established genera in the family *Phenuiviridae* and abolish one species in the genus *Laulavirus* in the family *Phenuiviridae.*  *Demarcation criteria:*  Species demarcation across all genera of the family *Phenuiviridae* relies on the phylogenetic relationship of the RNA-dependent RNA polymerase (RdRP) domain of the large protein (L) encoded by the phenuivirid large (L) segment, with <95% identity of the amino acid sequence marking the threshold for new species [1].  *Justification*:  Based on the phylogenetic trees constructed from the deduced RdRP amino acid sequences, 62 newly discovered phenuivirids are proposed to be classified into new species in the established genera *Beidivirus*, *Bocivirus*, *Coguvirus*, *Entovirus*, *Goukovirus, Hudovirus, Ixovirus, Laulavirus, Lentinuvirus, Mobuvirus, Phasivirus, Phlebovirus, Uukuvirus, and Wenrivirus*, and 13 phenuivirids were assigned to already established species in the genera *Bandavirus,* *Phlebovirus,* and *Uukuvirus* (Figures 1, 2, and 3). In addition, the species *Laulavirus wardellense* was abolished due to the absence of a coding-complete genome sequence of the assigned member virus, Wardell virus (WRDV).  **Novel species in the genus *Beidivirus*:**   * Drosophila Tranent phlebovirus (DTPV) was discovered by high-throughput sequencing (HTS) in unspecified fruit flies (*Drosophila* Fallén, 1823 sp.), collected in Tranent, Scotland, UK. The highest amino acid identity value of DTPV’s RdRP is 37.55% (Húběi diptera virus 3 [HbDV3; species *Beidivirus muscae*]). DTPV is proposed to be classified into species *Beidivirus drosophilae*; * Fǔshùn phenuivirus 1 (FsPV1) was discovered by HTS in common bluetails (*Ischnura senegalensis* (Rambur, 1842)] collected in China. The highest amino acid identity value of FsPV1’s RdRP is 43.65% (Liriomyza bunyavirus (LMBV, see below). FsPV1 is proposed to be classified into species *Beidivirus ischnurae*; and * Liriomyza bunyavirus (LMBV) was discovered by HTS in pea leaf miners [*Liriomyza huidobrensis* (Blanchard, 1926)] collected in South Korea. The highest amino acid identity value of LMBV’s RdRP is 43.65% (FsPV1, see above). LMBV is proposed to be classified into species *Beidivirus liriomyzae.*   **Novel species in the genus *Bocivirus*:**   * Fusarium culmorum phenuivirus 1 (FcPV1) was discovered by HTS in ascomycete fungi (*Fusarium culmorum* (Wm.G. Sm.) Sacc., 1892)] collected in Flakkebjerg, Zealand, Denmark [2]. The highest amino acid identity value of FcPV1’s RdRP is 90.26% (grapevine associated cogu-like virus 1 [GaCLV1; species *Bocivirus viticulum*]). FcPV1 is proposed to be classified into species *Bocivirus flakkebjergense*; * Fusarium fujikuroi negative-strand RNA virus 1 (FfNSRV) was discovered by HTS in ascomycete fungi (*Gibberella fujikuroi* (Sawada) Wollenw., (1931)) collected in China. The highest amino acid identity value of FfNSRV ’s is 82.06% (unclassified Fusarium pseudograminearum coguvirus 1). FfNSRV is proposed to be classified into species *Bocivirus gibberellae*; and * Sānyà phenuivirus 1 (SaPV1) was discovered by HTS in horse flies (*Cydistomyia duplonotata* (Ricardo, 1914)) collected presumably in三亚市 [Sānyà], China. The highest amino acid identity value of SaPV1’s RdRP is 73.32% (Trichoderma gamsii cogu-like virus 1 [TgClV1; species *Bocivirus trichodermae*]). SaPV1 is proposed to be classified into species *Bocivirus sanyaense*.   **Novel species in the genus *Coguvirus*:**   * blackberry line pattern virus (BlaLPV) was discovered by HTS in unspecified blackberry (*Rubus* L.) collected in USA [3]. The highest amino acid identity value of BlaLPV’s RdRP is 69.11% (citrus concave gum-associated virus [CCGaV; species *Coguvirus citri*]). BlaLPV is proposed to be classified into species *Coguvirus rubi*.   **Novel species in the genus *Entovirus*:**   * Guǎngxī phenui-like virus (GPLV) was discovered by soil metagenomic analysis of samples from a barren land of广西壮族自治区 [Guǎngxī Zhuàng Autonomous Region], China [4]. The highest amino acid identity value of GPLV’s RdRP is 91.26% (unclassified Hǎinán phenui-like virus 1). GPLV is proposed to be classified into species *Entovirus guangxiense*; * Inner Mongolia phenui-like virus 2 (IMPLV2) was discovered by soil metagenomic analysis of samples from a grassland of内蒙古自治区 [Inner Mongolia Autonomous Region], China [3]. The highest amino acid identity value of IMPLV2‘s RdRP is 50.17% (unclassified Sìchuān phenui-like virus 1). GPLV is proposed to be classified into species *Entovirus neimengguense*; * Jiāngsū sediment phenui-like virus (JSPLV) was discovered by sediment metagenomic analysis of samples from江苏省 [Jiāngsū Province], China [4]. The highest amino acid identity value of JSPLV’s RdRP is 47.43% (unclassified Hǎinán phenui-like virus 5). JSPLV is proposed to be classified into species *Entovirus jiangsuense*; and * Yúnnán phenui-like virus (YPLV) was discovered by soil metagenomic analysis of samples from a farmland of云南省 [Yúnnán Province], China [4]. The highest amino acid identity value of YPLV ‘s RdRP is 51.87% (unclassified Sìchuān phenui-like virus 4[). YPLV is proposed to be classified into species *Entovirus yunnanense.*   **Novel species in the genus *Goukovirus*:**   * Blattella germanica phenuivirus 1 (BgPV1) was discovered in sequence read archive (SRA) data of *Blattella germanica* Linnaeus, 1767[6]. The highest amino acid identity value of BgPV1‘s RdRP is 52.54% (unclassified Cryptocercus punctulatus phenuivirus 1). BgPV1 is proposed to be classified into species *Goukovirus blattellae*; * Culex goukovirus 1 (CGV1) was discovered by HTS in southern house mosquitos (*Culex quinquefasciatus* Say, 1823], collected in Mwinilunga, North-Western Province, Zambia [5]. The highest amino acid identity value of CGV1’s RdRP is 91.14% (Gouléako virus [GOLV; species *Goukovirus gouleakoense*]). CGV1 is proposed to be classified into species *Goukovirus culicis*; * Hodotermopsis sjostedti phenuivirus 1 (HsPV1) was discovered in SRA data of titan termites (*Hodotermopsis sjostedti* (Holmgren, 1911))[6]. The highest amino acid identity value of HsPV1‘s RdRP is 49.67% (unclassified Coptotermes formosanus phenuivirus 2). HsPV1 is proposed to be classified into species *Goukovirus hodotermopsidis*; * sefomo virus (SFMV) was isolated from mosquitoes (*Culex decens* (Theobald, 1901)) collected in Taï National Park, Côte d’Ivoire [8]. The highest amino acid identity value of SFMV’s RdRP is 77.55% Gouléako virus [GOLV; species *Goukovirus gouleakoense*]. SFMV is proposed to be classified into species *Goukovirus taiense*; * Shāhé heteroptera virus 3 (SHV3) was discovered by HTS in the typical bugs (*Heteroptera* Latreille, 1810 sp.) collected in 沙河 [Shāhé] area, Beijing, China [7]. The highest amino acid identity value of SFMV’s RdRP is 54.06% (Gouléako virus [GOLV; *Goukovirus gouleakoense*]). SHV3 is proposed to be classified into species *Goukovirus shahense*; and * Reticulitermes chinensis phenuivirus 1 (RcPV1) was discovered in SRA data of termites (*Reticulitermes chinensis* (Snyder, 1923)) [6]. The highest amino acid identity value of RcPV1’s RdRP is 56.47% (unclassified Coptotermes formosanus phenuivirus 2). RcPV1 is proposed to be classified into species *Goukovirus reticulitermitidis.*   **Novel species in the genus *Hudovirus*:**   * Culex hudovirus (ClHV) was discovered by HTS in southern house mosquitoes(*Culex quinquefasciatus* Say, 1823], collected in Mongu, Western Province, Zambia [5]. The highest amino acid identity value of ClHV’s RdRP is 53.87% (Pectinophora gossypiella virus 3; see below). ClHV is proposed to be classified into species *Hudovirus culicis*; and * Pectinophora gossypiella virus 3 (PeGV3) was discovered in SRA data of pink bollworms (*Pectinophora gossypiella* (Saunders, 1844)] [9]. The highest amino acid identity value of PeGV3’s RdRP is 56.47% (ClHV; see above). PeGV3 is proposed to be classified into species *Hudovirus pectinophorae.*   **Novel species in the genus *Ixovirus*:**   * Onega tick phlebovirus (OTPV) was discovered by HTS in taiga ticks (*Ixodes persulcatus* (Schulze, 1930)), collected in 塔河(Tǎhé), 黑龙江省 (Hēilóngjiāng Province), China [10]. The highest amino acid identity value of OTPV’s RdRP is 74.61% (blacklegged tick virus 3 [BLTV3; species *Ixovirus ixodis*]). OTPV is proposed to be classified into species *Ixovirus gakugsaense*; * Piguzov virus (PigV) was discovered by HTS in common seabird ticks (*Ixodes uriae* White, 1852) collected in Paradise Harbour, Antarctica [11]. The highest amino acid identity value of PigV’s RdRP is 90.29% (unclassified Bonden virus). PigV is proposed to be classified into species *Ixovirus antarcticaense*; * Ronne virus (RonV) was discovered by HTS in common seabird ticks (*Ixodes uriae* White, 1852), collected in Paradise Harbour, Antarctica [11]. The highest amino acid identity value of RonV’s RdRP is 70.41% (unclassified Bonden virus). RonV is proposed to be classified into species *Ixovirus paradisense*; * Sara tick phlebovirus (STPV) was first fully sequenced after discovery by HTS in taiga ticks (*Ixodes persulcatus* (Schulze, 1930)) collected in 伊春市 [Yīchūn], 黑龙江省 [Hēilóngjiāng Province], China [10]. The highest amino acid identity value of STPV’s RdRP is 87.36% (Fairhair virus [FHAV; species *Ixovirus norvegiae*]). STPV is proposed to be classified into species *Ixovirus yichunense*; and * Shoal Cavern virus (ShoCV) was discovered metagenomic analysis of western blacklegged ticks (*Ixodes pacificus* Cooley & Kohls, 1943) collected in Garrapata State Park, California, USA. The highest amino acid identity value of ShoCV’s RdRP is 79.84% (Fairhair virus [FHAV; species *Ixovirus norvegiae*]. ShoCV is proposed to be classified into species *Ixovirus garrapataense.*   **Novel species in the genus *Laulavirus*:**   * Cordyceps javanica negative-strand RNA virus 1 (CJNSRV1) was discovered by HTS in entomopathogenic fungi (*Cordyceps javanica* (Frieder. & Bally) Kepler, B. Shrestha & Spatafora, 2017], collected in China [12]. The highest amino acid identity value of CJNSRV1’s RdRP is 81.21% (Laurel Lake virus [LLV; species *Laulavirus laurelense*]. CJNSRV1 is proposed to be classified into species *Laulavirus cordycipitis*; * switchgrass phenui-like virus 1 (SGPLV1) was discovered by metagenomic analysis of switchgrass (*Panicum virgatum* L.) collected in the USA. The highest amino acid identity value of SGPLV1‘s RdRP is 37.09% (grapevine associated cogu-like virus 4 [GaCLV4; species *Laulavirus gammaviticulum*]). SGPLV1 is proposed to be classified into species *Laulavirus panici*; and * Valsa mali negative-strand RNA virus 1 (VMNSRV1) was discovered by HTS in ascomycete fungi of apple Valsa canker (*Valsa mali* Miyabe & G. Yamada, 1915) collected in China [13]. The highest amino acid identity value of VMNSRV1’s RdRP is 64.32% (grapevine associated cogu-like virus 3 [GaCLV3; species *Laulavirus betaviticulum*]. VMNSRV1 is proposed to be classified into species *Laulavirus valsae.*   **Novel species in the genus *Lentinuvirus*:**   * Armillaria bunya-like virus 1 (ArBLV1) was discovered by HTS in unspecified basidiomycete fungi (*Armillaria* (Fr.) Staude sp.] collected in Finland. The highest amino acid identity value of ArBLV1’s RdRP is 90.99% (Armillaria bunya-like virus 2; see below). ArBLV1 is proposed to be classified into species *Lentinuvirus alphaarmillariae*; * Armillaria bunya-like virus 2 (ArBLV2) was discovered by HTS in unspecified basidiomycete fungi (*Armillaria* (Fr.) Staude sp.] collected in Finland. The highest amino acid identity value of ArBLV2’s RdRP is 90.99% (ArBLV1; see above). ArBLV2 is proposed to be classified into species *Lentinuvirus betaarmillariae*; and * Lentinula edodes negative-strand RNA virus 3 (LeNSRV3) was discovered by HTS in shiitake (*Lentinula edodes* (Berk.) Pegler (1976)] collected in China. The highest amino acid identity value of LeNSRV3‘s RdRP is 42.14% (Lentinula edodes negative-strand RNA virus 2 [LeNSRV2; species *Lentinuvirus lentinulae*]. LeNSRV3 is proposed to be classified into species *Lentinuvirus adlentinulae*.   **Novel species in the genus *Mobuvirus*:**   * Anopheles bunyavirus 1 (ABV1) was discovered by HTS in mosquitos (*Anopheles funestus* Giles, 1900), collected in Kazungula, Southern Province, Zambia [5]. The highest amino acid identity value of ABV1’s RdRP is 80.27% (unclassified Rhodopi bunya-like virus). ABV1 is proposed to be classified into species *Mobuvirus anophelae*; * Bafoussam mosquito bunyavirus 1 (BMBV1) was discovered by HTS in mosquitos (*Aedes africanus* (Theobald, 1901)) collected in Bafoussam, West Region, Cameroon [14]. The highest amino acid identity value of BMBV1’s RdRP is 67.86% (Bafoussam mosquito bunyavirus 2; see below). BMBV1 is proposed to be classified into species *Mobuvirus alphabafoussamense*; * Bafoussam mosquito bunyavirus 2 (BMBV2) was discovered by HTS in mosquitos (*Aedes africanus* (Theobald, 1901)) collected in Bafoussam, West Region, Cameroon [14]. The highest amino acid identity value of BMBV2’s RdRP is 67.86% (BafMBV1; see above). BMBV2 is proposed to be classified into species *Mobuvirus betabafoussamense*; * Coquillettidia bunyavirus (CoqBV) was discovered by HTS in mosquitos (*Coquillettidia aurites* Theobald, 1901) collected in Mongu, Western Province, Zambia [5]. The highest amino acid identity value of CoqBV’s RdRP is 58.14% (unclassified Serbia bunya-like virus 1). CoqBV is proposed to be classified into species *Mobuvirus coquillettidiae*; * Cotesiavirus chinense (CotVchi) was discovered in SRA data of diamondback moth parasitoid wasps (*Cotesia vestalis* (Haliday, 1834)) [15]. The highest amino acid identity value of CotVchi’s RdRP is 44.37% (unclassified hymenopteran phenui-related virus OKIAV282). CotVchi is proposed to be classified into species *Mobuvirus cotesiae*; * Culex bunyavirus 2 (ClBV2) was discovered by HTS in western encephalitis mosquitos (*Culex tarsalis* Coquillett, 1896] collected in Alameda County, California, USA [16]. The highest amino acid identity value of ClBV2’s RdRP is 93.14% (Culex pseudovishnui bunya-like virus; see below). ClBV2 is proposed to be classified into species *Mobuvirus alamedaense*; * Culex pseudovishnui bunya-like virus (CPBLV) was discovered by HTS in mosquitos (*Culex pseudovishnui* Colless, 1957) collected in 諫早市 [Isahaya], 長崎県 [Nagasaki Prefecture], Japan [17]. The highest amino acid identity value of CPBLV’s RdRP is 93.14% (ClBV2; see above). CPBLV is proposed to be classified into species *Mobuvirus isahayaense*; * Fángshān bunya-like virus (FSBLV) was discovered in SRA data of southern house mosquitos (*Culex quinquefasciatus* Say, 1823] [18]. The highest amino acid identity value of FSBLV’s RdRP is 65.97% (CPBLV; see above). FSBLV is proposed to be classified into species *Mobuvirus culicis*; * Sānyà conocephalus maculatus phenuivirus 1 (SCMPV1) was discovered by HTS in maculated rice katydids (*Conocephalus maculatus* (Le Guillou, 1841)) collected presumably in 三亚市 [Sānyà], 海南省 [Hǎinán Province], China. The highest amino acid identity value of SCMPV1’s RdRP is 37.53% (unclassified Weta phenui-like virus). SCMPV1 is proposed to be classified into species *Mobuvirus sanyaense*; and * Shuāngào insect virus 3 (SGIV3) was discovered by HTS in unspecified green lacewings (Chrysopidae Schneider 1851), collected in 双岙村 [Shuāngào Village], 浙江省 [Zhèjiāng Province], China [19]. The highest amino acid identity value of SGIV3’s RdRP is 30.83% (unclassified Ogsystermes virus). SGIV3 is proposed to be classified into species *Mobuvirus shuangaoense.*   **Novel species in the genus *Phasivirus*:**   * Anopheles phasivirus 1 (APV1) was discovered by HTS in mosquitos (*Anopheles rufipes* Gough, 1910) collected in Siavonga, Southern Province, Zambia [5]. The highest amino acid identity value of APV1’s RdRP is 51.60% (Phasi Charoen-like phasivirus [PCLV; species *Phasivirus phasiense*]). APV1 is proposed to be classified into species *Phasivirus siavongaense*; * Anopheles phasivirus 2 (APV2) was discovered by HTS in mosquitos (*Anopheles funestus* Giles, 1900) collected in Livingstone, Southern Province, Zambia [5]. The highest amino acid identity value of APV2’s RdRP is 51.19% (APV1; see above). APV2 is proposed to be classified into species *Phasivirus zambiae*; and * niwlog virus (NLV) was discovered by HTS in tule mosquitos (*Culex erythrothorax* Dyar, 1907) collected in Alameda County, California, USA [16]. The highest amino acid identity value of NLV ‘s RdRP is 59.32% (Phasi Charoen-like phasivirus [PCLV; species *Phasivirus phasiense*]). NLV is proposed to be classified into species *Phasivirus alamedaense*.   **Novel species in the genus *Phlebovirus*:**   * Alxa tick phlebovirus (APTV) was discovered by HTS in unspecified ticks collected in 阿拉善左旗[Alxa Left Banner], China [20]. The highest amino acid identity value of APTV ‘s RdRP is 94.28% (Mukawa virus [MKWV; species *Phlebovirus mukawaense*]). APTV is proposed to be classified into species *Phlebovirus alxaense*; * Mǔdānjiāng phlebovirus (MuPV) was discovered by HTS in taiga ticks (*Ixodes persulcatus* (Schulze, 1930)) collected in白山市 [Báishān], 吉林省 [Jílín Province], China [10]. The highest amino acid identity value of MuPV’s RdRP is 89.74% (Mukawa virus [MKWV; species *Phlebovirus mukawaense*]). MuPV is proposed to be classified into species *Phlebovirus baishanense*; and * pangolin phlebovirus (PanPV) was discovered in Chinese pangolins (*Manis pentadactyla* Linnaeus, 1758) collected in China. The highest amino acid identity value of PanPV’s RdRP is 85.50% (Mukawa virus [MKWV; species *Phlebovirus mukawaense*]). PanPV is proposed to be classified into species *Phlebovirus manidae*; * Wǔxiāng virus (WUXV) was discovered by HTS in sand flies (*Phlebotomus chinensis* Newstead, 1916) collected in武乡县 [Wǔxiāng County], 山西省 [Shānxī Province], China [21]. The highest amino acid identity value of WUXV’s RdRP is 88.28% (Corfou virus [CFUV; species *Phlebovirus corfouense*]. WUXV is proposed to be classified into species *Phlebovirus wuxiangense*.   **Novel species in the genus *Uukuvirus*:**   * Bólè tick virus 1 (BoTV1) was discovered by HTS in ticks (*Hyalomma asiaticum,* Schülze & Schlottke, 1929) collected in博乐市 [Bólè], 新疆维吾尔自治区 [Xīnjiāng Uygur Autonomous Region], China [19]. The highest amino acid identity value of BoTV1’s RdRP is 88.90% (Iftin tick virus; see below). The common uukuvirus genomes encompass the L, M, and S segments, but some tick-associated uukuvirus genomes lack the M segment [22]. BoTV1 is also considered to be a bisegmented uukuvirus, and is proposed to be classified into species *Uukuvirus boleense*; * brown dog tick phlebovirus 1 (BDTPV1) was discovered by HTS in brown dog ticks (*Rhipicephalus sanguineus* (Latreille 1806)) collected in Trinidad and Tobago [23]. The highest amino acid identity value of BDTPV1’s RdRP is 60.41% (Xīnjiāng tick phlebovirus; see below). BDTPV1 is proposed to be classified into species *Uukuvirus trinidadense*; * brown dog tick phlebovirus 2 (BDTPV2) was discovered by HTS in brown dog ticks (*Rhipicephalus sanguineus* (Latreille, 1806)) collected in Trinidad and Tobago [23]. The highest amino acid identity value of BDTPV2’s RdRP is 92.75% (tick phlebovirus; see below). BDTPV2 is proposed to be classified into species *Uukuvirus tobagoense*; * Chāngpíng tick virus 1 (CPTV1) was discovered by HTS in longhorned ticks (*Haemaphysalis longicornis* Neumann, 1901) collected in 昌平区 [Chāngpíng District], Beijing, China [24]. The highest amino acid identity value of CPTV1’s RdRP is 83.83% (Dermacentor uukuvirus; see below). CPTV1 is proposed to be classified into species *Uukuvirus changpingense*; * Cheeloo uukuvirus (CHUV) was discovered by HTS in longhorned ticks (*Haemaphysalis longicornis* Neumann, 1901) collected in 山东省 [Shāndōng Province], China [24]. The highest amino acid identity value of CHUV’s RdRP is 70.14% (Dàbiéshān tick virus [DbsTV; species *Uukuvirus dabieshanense*]). CHUV is proposed to be classified into species *Uukuvirus shandongense*; * Dermacentor reticulatus uukuvirus (DRUV) was discovered by HTS in ornate cow ticks (*Dermacentor reticulatus* Fabricius, 1794) collected in Croatia [25]. The highest amino acid identity value of DRUV’s RdRP is 66.53% (Tǎchéng tick virus 2 [TcTV2; species *Uukuvirus tachengense*]). DRUV is proposed to be classified into species *Uukuvirus croatiaense*; * Dermacentor uukuvirus (DeUV) was discovered by HTS in ticks (*Dermacentor silvarum* Olenev, 1931) in内蒙古自治区 [Inner Mongolia Autonomous Region], China [26]. The highest amino acid identity value of DeUV’s RdRP is 91.48% (unclassified Meitian tick virus). DeUV is proposed to be classified into species *Uukuvirus addermacentoris*; * Iftin tick virus (IfTV) was discovered by HTS in ticks (*Hyalomma dromedarii* C. L. Koch, 1844), collected in Iftin, Kenya [27]. The highest amino acid identity value of IfTV’s RdRP is 88.97% (BOTV1; see above). IfTV is proposed to be classified into species *Uukuvirus makkahense*; * Mbalambala tick virus (MbTV) was discovered by HTS in ticks (*Hyalomma rufipes* Koch, 1844 ) collected from camels in Mbalambala, Garissa County, Kenya [28]. The highest amino acid identity value of MbTV’s RdRP is 91.44% (unclassified Limansky tick phlebovirus). MbTV is proposed to be classified into species *Uukuvirus mbalambalaense*; * Okutama-like tick virus (OkLTV) was discovered by HTS in ticks (*Haemaphysalis aponommoides* Warburton, 1913) collected in China. The highest amino acid identity value of OkLTV’s RdRP is 69.20% (Okutama tick virus; see below). OkLTV is proposed to be classified into species *Uukuvirus akirunoense*; * Okutama tick virus (OkTV) was first discovered in ticks (*Haemaphysalis flava* Neumann, 1897) collected in 奥多摩町 [Okutama], Tokyo Metropolis, Japan [29]. The highest amino acid identity value of OkTV’s RdRP is 76.33% (Yǒngjiā tick virus 1 [YONV; species *Uukuvirus yongjiaense*). OkTV is proposed to be classified into species *Uukuvirus okutamaense*; * Qīnghǎi Lake uukuvirus (QHLUV) was discovered by HTS in ticks (*Dermacentor nuttalli* Olenev, 1928) collected in 青海省 [Qīnghǎi Province], China [30]. The highest amino acid identity value of QHLUV’s RdRP is 93.13% (unclassified Zhāngjiākŏu phenu tick virus 1). QHLUV is proposed to be classified into species *Uukuvirus qinghaiense*; * tick phlebovirus (TiPV) was first discovered in longhorned ticks (*Haemaphysalis longicornis* Neumann, 1901) collected in Anatolia, Turkey, and its coding-complete genome was determined by HTS from ticks collected in 山东省 [Shāndōng Province], China [24]. The highest amino acid identity value of TiPV’s RdRP is 92.89% (BDTPV2; see above). TiPV is proposed to be classified into species *Uukuvirus anatoliaense*; and * Xīnjiāng tick phlebovirus (XTPV) was discovered by HTS in ticks (*Hyalomma scupense* Schulze, 1919) collected in 新疆维吾尔自治区 [Xīnjiāng Uygur Autonomous Region], China, [20]. The highest amino acid identity value of XTPV’s RdRP is 82.75% (unclassified Limansky tick phlebovirus). XTPV is proposed to be classified into species *Uukuvirus xinjiangense.*   **Novel species in the genus *Wenrivirus*:**   * oriental wenrivirus 1 (OWV1) was discovered by HTS in fleshy prawns [*Fenneropenaeus chinensis* (Osbeck, 1765)] collected in 黃海 (Huánghǎi/the Yellow Sea), China [31]. The highest amino acid identity value of OWV1’s RdRP is 79.63% Mourilyan virus [MoV; species *Wenrivirus penaei*]. OWV1 is proposed to be classified into species *Wenrivirus huanghaiense*.   **Phenuivirids that can be assigned to established species:**   * Forécariah virus (FORV) [17] is an isolate of *Bandavirus bhanjanagarense* (RdRP identity with Bhanja virus 99.04%); * Palma virus (PaV) [17] is an isolate of *Bandavirus razdanense* (RdRP identity with Razdan virus 97.98%); * Arrábida virus (ARRV) [32] is an isolate of *Phlebovirus napoliense* (RdRP identity with Granada virus 99.24%); * Belterra virus (BELTV) [33] is an isolate of *Phlebovirus saloboense* (RdRP identity with Salobo virus 99.61%); * Drin virus (DRIV) [34] is an isolate of *Phlebovirus corfouense* (RdRP identity with Corfou virus 98.80%); * Kuriyama virus (KYV) [20] is an isolate of *Phlebovirus mukawaense* (RdRP identity with Mukawa virus 96.07%); * Ponticelli I virus (PONVI) [35] is an isolate of *Phlebovirus salehabadense* (RdRP identity with Bregalaka virus 98.37%); * Catch-me-cave virus (CMCV) [36] is an isolate of *Uukuvirus macquariense* (RdRP identity with Precarious point virus 99.81%); * Chize virus (ChiV) [37] is an isolate of *Uukuvirus schmidti* (RdRP identity with Nile warbler virus 99.81%); * Khasan virus (KHAV) [38] is an isolate of *Uukuvirus huangpiense* (RdRP identity with Huángpí tick virus 2 98.82%); * Komandory virus (KOMV) [39] is an isolate of *Uukuvirus rukutamaense* (RdRP identity with Rukutama virus 99.47%); and * Rhipicephalus associated phlebovirus 1 (RaPV1) [40] is an isolate of *Uukuvirus lihanense* (RdRP identity with Lǐhán tick virus 99.77%); * Sunday Canyon virus (SCV) [41] is an isolate of *Uukuvirus uriae* (RdRP identity with Murre virus 99.95%). |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.008M.Ac.v4.Phenuiviridae\_62nsp+1asp | Excel file |

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| **Tables, Figures:** |

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MW291944\_*Coguvirus chinense*

MW842780*\_ Coguvirus citrulli*

MW842781\_*Coguvirus henanense*

ON602044\_*Coguvirus chrysanthae*

MT269667\_*Coguvirus yunnanense*

ON624095\_blackberry line pattern virus

MG764565\_*Coguvirus eburi*

KX960112\_*Coguvirus citri*

PQ202045\_Fusarium fujikuroi negative-strand RNA virus 1

MZ209936\_Sanya phenuivirus 1

OQ513277\_*Bocivirus trichodermae*

MN617081\_ *Bocivirus botryti*

OQ295987\_*Bocivirus fusarii*

PQ000875\_Fusarium culmorum phenuivirus 1

MN520751\_*Bocivirus viticulu*

PP996022\_Switchgrass phenui-like virus 1

PP544309\_Cordyceps javanica negative-strand RNA virus 1

KX774630\_*Laulavirus laurelense*

MT353902\_*Laulavirus gammaviticulum*

OR209170\_Valsa mali negative-strand RNA virus 1

MN520757\_*Laulavirus betaviticulum*

MN520754\_*Laulavirus alphaviticulum*

ON875995\_Armillaria bunya-like virus 2

ON875993\_Armillaria bunya-like virus 1

MN744715\_Lentinula edodes negative-strand RNA virus 3

LC466008\_*Lentinuvirus lentinulae*

MW896874\_Jiangsu sediment phenui-like virus

MW896866\_Inner Mongolia phenui-like virus 2

MW896879\_Yunnan phenui-like virus

MW896872\_Guangxi phenui-like virus

MF375882\_*Entovirus entoleucae*

LC726787\_Qingdao RNA virus 3

MK728654\_*Rubodvirus argentinaense*

MK728657\_*Rubodvirus armeniaense*

MF062139\_*Rubodvirus prosserense*

MF062125\_*Rubodvirus mali*

KM817681\_Shuangao insect virus 3

BK063683\_Cotesiavirus chinense

MT153385\_Dipteran phenui-related virus OKIAV274

PP868493\_Bafoussam mosquito bunyavirus 2

PP764662\_Bafoussam mosquito bunyavirus 1

OR192222\_Fangshan bunya-like virus

LC514293\_Culex pseudovishnui bunya-like virus

MW434602\_Culex bunyavirus 2

LC772149\_Coquillettidia bunyavirus

LC772143\_Anopheles bunyavirus 1

MN661012\_*Mobuvirus narangueense*

MZ209841\_Sanya conocephalus maculatus phenuivirus 1

MN752229\_*Mobuvirus arnae*

KX272883\_*Mobuvirus mothrae*

BK067085\_Reticulitermes chinensis phenuivirus 1

BK067021\_ Blattella germanica phenuivirus 1

BK067044\_Hodotermopsis sjostedti phenuivirus 1

KX884813\_Shahe heteroptera virus 3

BK062758\_ *Goukovirus aphalarae*

MZ202295\_Sefomo virus

LC772146\_Culex goukovirus 1

HQ541738\_*Goukovirus gouleakoense*

KM817703\_*Goukovirus yichangense*

BK062755\_*Goukovirus ceraphri*

KF543244\_*Goukovirus cumutoense*

MN163034\_ *Citricivirus chongqinense*

MN062090\_*Tanzavirus daressalaamense*

KR094115\_*Mechlorovirus ramuense*

MH817469\_*Mechlorovirus cucumeris*

AB009656\_*Tenuivirus oryzabrevis*

ON156474\_ *Tenuivirus kwazuluense*

D31879\_*Tenuivirus oryzaclavatae*

MZ703097\_*Tenuivirus pontae*

MW678790\_*Tenuivirus festucae*

MG566074\_*Tenuivirus oryzalbae*

MN044342\_*Tenuivirus eurotritici*

MT860240\_*Horwuvirus solenopsidis*

MT498812\_*Horwuvirus fitzroyense*

KM817690\_*Horwuvirus wuhanense*

KX852391\_*Pidchovirus pidgei*

MT153420\_*Pidchovirus stethori*

MN164622\_ Pectinophora gossypiella virus 3

LC772131\_Culex hudovirus

KX884772\_*Hudovirus lepidopteris*

KM817689\_ *Phasivirus wuhanense*

KX884799\_ *Phasivirus hubeiense*

LC772140\_Anopheles phasivirus 2

LC772137\_Anopheles phasivirus 1

MW434727\_Niwlog virus

KR003786\_*Phasivirus phasiense*

MN053784\_*Phasivirus guadeloupeense*

KM817700\_*Phasivirus wutaiense*

MT498816\_*Phasivirus parryense*

KT693187\_*Phasivirus baduense*

KX884809 *Hudivirus muscae*

MZ210024\_Fushun phenuivirus 1

OQ377554\_Liriomyza bunyavirus

OR605718\_Drosophila Tranent phlebovirus

KX884796\_ *Beidivirus muscae*

MK335503\_ oriental wenrivirus 1 (=*Bunyavirales* sp.)

MT241517\_*Wenrivirus penaei*

MT025176\_ Piguzov virus

MT025164\_ Ronne virus

ON408150\_Onega tick phlebovirus

KU230449\_ *Ixovirus ixodis*

PP415842\_Shoal Cavern virus

ON408148\_Sara tick phlebovirus

MF141052\_*Ixovirus norvegiae*

KM048313 *Ixovirus heckscherense*

*Bandavirus, Phlebovirus, Uukuvirus*

*Hudovirus*

*Phasivirus*

*Hudivirus*

*Beidivirus*

*Coguvirus*

*Bocivirus*

*Laulavirus*

*Lentinuvirus*

*Entovirus*

*Rubovirus*

*Mobuvirus*

*Goukovirus*

*Citricivirus*

*Tanzavirus*

*Tenuivirus*

*Horwuvirus*

*Wenrivirus*

*Ixovirus*

*Mechlorovirus*

*Pidochovirus*

**Figure 1.** Maximum likelihood phylogenetic tree of the deduced RNA-directed RNA polymerase (RdRP) amino acid sequences of the members of the *Phenuiviridae* family and viruses proposed to be classified (red colored). MEGAX was used to align the sequences and IQTREE was used to generate a phylogenetic tree. Numbers on branches are bootstrap values (%) obtained from 1,000 replicates. Tree branches are proportional to genetic distances between sequences and the scale bars at the bottom indicated substitutions per amino acid.

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KJ939330*\_Phlebovirus adanaense*

KR363190\_*Phlebovirus alcubeense*

KU255114\_*Phlebovirus medjerdaense*

JX472403\_ *Phlebovirus salehabadense*

100

MF593931\_*Phlebovirus arumowotense*

HM566174\_*Phlebovirus odrenisrouense*

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KC669549\_*Phlebovirus salangaens*

98

KF297900\_*Phlebovirus gordilense*

MT270831\_*Phlebovirus kiborgochense*

EU725771\_*Phlebovirus massiliaense*

JF920133\_*Phlebovirus puniqueense*

X68414\_*Phlebovirus toscanaense*

JF939846\_*Phlebovirus tehranense*

KP966616\_*Phlebovirus zerdaliense*

100

JF920136\_*Phlebovirus florisense*

68

99

100

HM119401\_*Phlebovirus alenquerense*

HM119425\_*Phlebovirus niqueense*

MK524348\_*Phlebovirus almendrasense*

100

HM119407\_*Phlebovirus candiruense*

HM119416 \_*Phlebovirus itaitubaense*

HM119413\_*Phlebovirus maldonadoense*

HM119434\_*Phlebovirus oriximinaense*

HM119410\_*Phlebovirus echarateense*

HM119431\_*Phlebovirus turunaense*

100

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KP272001\_*Phlebovirus buenaventuraense*

KP272040\_*Phlebovirus campanaense*

HM566152\_*Phlebovirus leticiaense*

HM566167 \_*Phlebovirus napoliense*

100

100

KP272036\_*Phlebovirus cocleense*

KP272028\_*Phlebovirus toroense*

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MK330756\_*Phlebovirus cacaoense*

HM566147\_*Phlebovirus chagresense*

KX611400\_ *Phlebovirus uriuranaense*

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HM566185\_*Phlebovirus claroense*

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OP313008\_Alxa tick phlebovirus

ON408135Mudanjiang phlebovirus

ON024081\_Pangolin phlebovirus

LC063770\_*Phlebovirus mukawaense*

MK330771\_*Phlebovirus itaporangaensev*

KF297909\_*Phlebovirus karimabadense*

MF695812\_*Phlebovirus ntepesense*

KF297903\_*Phlebovirus gabekense*

GQ847513\_*Phlebovirus siciliaense*

KP771821\_*Phlebovirus dashliense*

MN454526\_Wuxiang virus

KP966619\_*Phlebovirus torosense*

KR106177\_*Phlebovirus corfouense*

MT270834\_*Phlebovirus perkerraense*

MT270825\_*Phlebovirus embossosense*

MT270828\_*Phlebovirus bogoriaense*

MK330765\_*Phlebovirus limboense*

MK524337\_*Phlebovirus monagritaense*

HM627185\_*Phlebovirus saloboense*

MK330768\_*Phlebovirus icoaraciense*

KX611397\_*Phlebovirus taparaense*

KX611382\_*Phlebovirus ambeense*

HM566155\_*Phlebovirus duraniaense*

HM566162\_*Phlebovirus ixcanalense*

HM566138\_*Phlebovirus aguacateense*

MW368831\_*Phlebovirus hediense*

DQ375403\_*Phlebovirus riftense*

MK503253\_*Phlebovirus riograndense*

MN163121\_*Phlebovirus penshurtense*

KX611385\_*Phlebovirus anhangaense*

MK524345\_*Phlebovirus ticoense*

MK524332\_*Phlebovirus gloriaense*

MK524341\_*Phlebovirus penablancaense*

HM566164\_*Phlebovirus mungubaense*

KX611388\_*Phlebovirus bujaruense*

MF289183\_*Phlebovirus pantanalense*

KX611403\_*Phlebovirus urucuriense*

Other Phenuivirus

**Figure 2.** Maximum likelihood phylogenetic tree of the deduced RNA-directed RNA polymerase (RdRP) amino acid sequences of the members of the genus *Phlebovirus* and viruses proposed to be classified (red colored). MEGAX was used to align the sequences and IQTREE was used to generate a phylogenetic tree. Numbers on branches are bootstrap values (%) obtained from 1,000 replicates. Tree branches are proportional to genetic distances between sequences and the scale bars at the bottom indicated substitutions per amino acid.

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LC618931\_*Uukuvirus toyoense*

KM114257\_*Uukuvirus silverwaterense*

MG581739\_*Uukuvirus kaisodiense*

KM817668\_*Uukuvirus huangpiense*

LC153711\_*Uukuvirus kabutoense*

KF892052\_*Uukuvirus rukutamaense*

HM566181\_*Uukuvirus macquariense*

JF838330\_*Uukuvirus uriae*

HM566191\_*Uukuvirus tyulenyense*

D10759\_*Uukuvirus uukuniemiense*

HM566159\_*Uukuvirus schmidti*

JF838327\_*Uukuvirus grandarbaudense*

LC753197\_Okutama tick virus

KM817704\_*Uukuvirus yongjiaense*

PP210661\_Okutama-like tick virus

OR115134\_Cheeloo uukuvirus

KM817666\_*Uukuvirus dabieshanense*

MN025506\_brown dog tick phlebovirus 1

OR115132\_Tick phlebovirus

MN025508\_brown dog tick phlebovirus 2

MH688506\_Xinjiang tick phlebovirus

MW561967\_Mbalambala tick virus

MW561965\_Iftin tick virus

KM817664\_Bole tick virus 1

KM817672\_*Uukuvirus lihanense*

ON684362\_Dermacentor reticulatus uukuvirus

OP863283\_Dermacentor uukuvirus

OR837771\_Qinghai Lake uukuvirus

OR114996\_Changping tick virus 1

KM817684\_*Uukuvirus tachengense*

KU933936\_*Uukuvirus hoplandense*

KM048311\_*Uukuvirus dermacentoris*

Other Phenuivirus

**Figure 3.** Maximum likelihood phylogenetic tree of the deduced RNA-directed RNA polymerase (RdRP) amino acid sequences of the members of the genus *Uukuvirus* and viruses proposed to be classified (red colored). MEGAX was used to align the sequences and IQTREE was used to generate a phylogenetic tree. Numbers on branches are bootstrap values (%) obtained from 1,000 replicates. Tree branches are proportional to genetic distances between sequences and the scale bars at the bottom indicated substitutions per amino acid.