

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create 62 new species and abolish one species in the family *Phenuiviridae* |
| **Code assigned:**  | 2025.008M.Ac.v3.Phenuiviridae\_62nsp+1asp |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
| Yasuhiro | Tomitaka | Institute for Plant Protection, NARO, Tsukuba, Japan | tomitaka.yasuhiro839@naro.go.jp |  |
| Thomas | Briese | Center for Infection and Immunity, and Department of Epidemiology, Columbia University, New York, USA | thomas.briese@columbia.edu |  |
| Cécile | Desbiez | Pathologie Végétale, INRAE, Montfavet, France | cecile.desbiez@inrae.fr |  |
| Francesco | Di Serio | Institute for Sustainable Plant Protection-CNR, Bari, Italy | francesco.diserio@ipsp.cnr.it |  |
| Dimitre | Mollov | USDA-APHIS, Plant Protection and Quarantine, Riverdale, MD 20737 | dimitre.mollov@ars.usda.gov |  |
| Yutaro | Neriya | Faculty of Agriculture, Utsunomiya University, Utsunomiya, Japan | neriya@a.utsunomiya-u.ac.jp |  |
| Jin-Won  | Song | Department of Microbiology, Korea University, Seoul, Republic of Korea | jwsong@korea.ac.kr |  |
| Massimo | Turina | Institute for Sustainable Plant Protection-CNR, Torino, Italy | massimo.turina@ipsp.cnr.it |  |
| Gustavo | Palacios | Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, USA | gustavo.palacios@mssm.edu |  |
| Takahide | Sasaya | Bio-oriented Technology Research Advancement Institution, NARO, Kawasaki, Japan | sasaya.takahide907@naro.go.jp | **X** |

**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:** |
|  |

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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** |
| Phenuiviridae SG | 10 | 0 | 0 |

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| **Submission date:** |   |

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 ensure the inclusion of bisegmented uukuviruses is complete genome. If any references are available for lack of M segment please include as appropriate.  |

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

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| **Response of proposer:**  |
| When the genus *Uukuvirus* was established (2019.026M), the bisegmented uukuviruses, such as American dog tick virus and Pacific coast tick virus, have been registered as complete genomes. According to that, the bisegmented uukuviruses were also proposed as complete genomes. It is impossible to prove that the M segment is truly lacking, but considering that the ixoviruses have bisegmented genomes lacking the M segment, I believe it is not an issue if there are bisegmented uukuviruses. There is a reference proposing M segment-deficient phleboviruses (uukuviruses), which is cited at the beginning of the genus *Uukuvirus*. |

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| **Revision date:** | 19/8/2025 |

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*, in which DTPV was discovered |
| *Beidivirus ischnurae* | Named after host genus name *Ischnura*, in which FsPV1 was discovered |
| *Beidivirus liriomyzae* | Named after host genus name *Liriomyza*, in which LMBV was discovered |
| *Bocivirus fusaculense*  | Named using a portmanteau of host genus name *Fusarium* and host species name *culmorum*, in which FcPV1 was first discovered |
| *Bocivirus fusafujiense* | Named using a portmanteau of host genus name *Fusarium* and host species name *fujikuroi*, in which FfNSRV1 was first discovered |
| *Bocivirus sanyae* | Named after 三亞 (Sānyà) City, China |
| *Coguvirus rubusense* | Named after host name Rubus, in which BlaLPV was first discovered |
| *Entovirus guangxiense* | Named after 廣西 (Guǎngxī) Province, China |
| *Entovirus mongoliae* | Named after 内蒙古 (Nèi Měnggǔ, English 'Inner Mongolia') Resion, China |
| *Entovirus jiangsuense* | Named after 江苏 (Jiāngsū) Province, China |
| *Entovirus yunnanense* | Named after 云南 (Yúnnán) Province, China |
| *Goukovirus blattellae* | Named after host genus name *Blattella*, in which CfPV1 was discovered |
| *Goukovirus culequiense* | Named using a portmanteau of host genus name *Culex* and host species name *quinquefasciatus*, in which CuGV1 was discovered |
| *Goukovirus hodosjostense* | Named using a portmanteau of host genus name *Hodotermopsis* and host species name *sjostedti*, in which HsPV1 was discovered |
| *Goukovirus culedecense* | Named using a portmanteau of host genus name *Culex* and host species name *decens*, in which SFMV was discovered |
| *Goukovirus shahense* | Named after 沙河 (Shāhé) Area, Beijing, China |
| *Goukovirus retichinense* | Named using a portmanteau of host genus name *Reticulitermes* and host species name *chinensis*, in which RcPV1 was discovered |
| *Hudovirus culexense* | Named after host genus name *Culex*, in which CuHV was discovered |
| *Hudovirus pectinophorae* | Named after host genus name *Pectinophora*, in which PBV3 was discovered |
| *Ixovirus gakugsae* | Named after Gakugsa village, Russia, where OTPV was first discovered |
| *Ixovirus antarcticae* | Named after Antarctica, where PigV was discovered |
| *Ixovirus paradisense* | Named after Paradise Bay, Antarctica, where RonV was discovered |
| *Ixovirus yichunense* | Named after宜春 (Yíchūn) City, China, where STPV was discovered |
| *Ixovirus garrapatae* | Named after Garrapata, USA, where ShoCV was discovered |
| *Laulavirus cordycepsense* | Named after host genus name *Cordyceps*, in which CJNSRV1 was discovered |
| *Laulavirus panicumense* | Named after host genus name *Panicum*, in which SGPLV1 was discovered |
| *Laulavirus valsae* | Named after host genus name *Valsa*, in which VMNSRV1 was first discovered |
| *Lentinuvirus alphaarmillariae* | Named after host genus name *Armillaria*, in which ArBLV1 was first discovered, merged with Greek alpha |
| *Lentinuvirus betaarmillariae* | Named after host genus name *Armillaria*, in which ArBLV1 was first discovered, merged with Greek beta |
| *Lentinuvirus edodesense* | Named after host species name *edodes*, in which LeNSRV3 was first discovered |
| *Mobuvirus anophelesense* | Name after host genus name *Anopheles*, where ABV1 was discovered |
| *Mobuvirus alphabafoussae* | Named after Bafoussam, Cameroon, merged with Greek alpha |
| *Mobuvirus betabafoussae* | Named after Bafoussam, Cameroon, merged with Greek beta |
| *Mobuvirus coquillettidiae* | Name after host genus name *Coquillettidia*, where CoqBV was discovered |
| *Mobuvirus cotesiae* | Name after host genus name *Cotesia* |
| *Mobuvirus alamedae* | Named after Alameda County, USA, where ClBV2 was discovered |
| *Mobuvirus isahayae* | Named after 諫早(Isahaya) City, Japan, where CPBLV was discovered |
| *Mobuvirus culexense* | Name after host genus name Culex, where FaBLV was discovered |
| *Mobuvirus sanyae* | Named after 三亞(Sānyà) City, China, where SCMPV1 was discovered |
| *Mobuvirus zhejiangense* | Named after 浙江 (Zhèjiāng) Province, China, where SGIV3 was discovered |
| *Phasivirus siavongae* | Named after Siavonga, Zambia, where APV1 was discovered |
| *Phasivirus zambiae* | Named after Zambia, where APV2 was discovered |
| *Phasivirus alamedae* | Named after Alameda, USA, where NLV was discovered |
| *Phlebovirus alxae* | Named after 阿拉善 (Ālāshàn, English Alxa) Left Banner, China |
| *Phlebovirus baishanense* | Named after 白山(Báishān) City, China, where MuPV was first discovered |
| *Phlebovirus pangoli* | Named after host name 'pangolin' |
| *Phlebovirus wuxiangense* | Named after 武乡(Wǔxiāng) County, China, where HEDV was first discovered |
| *Uukuvirus bolea* | Named after 博乐 (Bólè) City, China, where BoTV1 was discovered |
| *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 (Chāngpíng), China, where CPTV1 was first discovered |
| *Uukuvirus qiluense* | Named after 齊魯 (Qílǔ, English Cheeloo) University, China |
| *Uukuvirus croatiae* | Named after Croatia, where DRUV was discovered |
| *Uukuvirus dermae* | Name after a part of host genus name *Dermacentor* |
| *Uukuvirus meccae* | Named after Makkah/Mecca, Saudi Arabia where IfTV was first discovered |
| *Uukuvirus mbalambalae* | Named after Mbalambala, Kenya, where MbTV was first discovered |
| *Uukuvirus akirunoense* | Named after あきる野 (Akiruno) City, Okutama-like place, Japan, where OkLTV was discovered |
| *Uukuvirus okutamae* | Named after 奥多摩 (Okutama) Town, Japan, where OkTV was first discovered |
| *Uukuvirus qinghaiense* | Named after 青海 (Qīnghǎi) Lake, China, where QHLUV was discovered |
| *Uukuvirus anatoliae* | Named after Anatolia, Turkey, where TiPV was first discovered |
| *Uukuvirus xinjiangense* | Named after 新疆维吾尔 (Xīnjiāng Wéiwú'ěr) Autonomous Region, China, where XTPV was first discovered |
| *Wenrivirus yellowseae* | Named after 黃海 (Huáng hǎi, English Yellow Sea), China, where OWV1 was idetified |

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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* In the family *Phenuiviridae,* there are currently 23 genera and 159 species.*Proposed* *taxonomic change(s):* Create 62 new species in 14 genera in the family *Phenuiviridae* and abolish one species in thegenus *Laulavirus* in the family *Phenuiviridae.**Justification*:The 62 newly discovered phenuiviruses were classified into new species in 14 phenuivirid genera on the base of phylogenetic trees constructed from the amino acid sequences of the RdRP and amino acid identity values of the RdRP. One species was abolished due to the absence of its coding-complete genome sequence. |

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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*) comprises viruses with 2–8 segments of negative-sense or ambisense RNA, comprising 8.1–25.1 kb in total. Phenuivirids infect animals including livestock and humans, birds, plants or fungi, as well as arthropods 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)*: Create 62 new species in 14 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 phylogenetic relationship based on the RNA-dependent RNA polymerase (RdRP) gene with <95% identity in the amino acid sequence [1]. *Justification*:On the base of phylogenetic trees constructed from the amino acid sequences of the RdRP and amino acid identity values of the RdRP, 62 newly discovered phenuiviruses were classified into the new species in the genera *Beidivirus*, *Bocivirus*, *Coguvirus*, *Entovirus*, *Goukovirus, Hudovirus, Ixovirus, Laulavirus, Lentinuvirus, Mobuvirus, Phasivirus, Phlebovirus, Uukuvirus, and Wenrivirus*, and 13 phenuivirids were classified into the already classified 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 for Wardell virus.**Novel species in the genus *Beidivirus*:*** Drosophila Tranent phlebovirus (DTPV) was discovered by HTS in unspecified fruit flies (*Drosophila* Fallen, 1823), collected in Tranent Town, UK. The highest amino acid identity value of the RdRP is 37.55% between DTPV and Húběi diptera virus 3 [*Beidivirus muscae*]. DTPV is proposed to be classified into species *Beidivirus drosophilae*;
* Fǔshùn phenuivirus 1 (FsPV1) was discovered by HTS in damselflies [*Ischnura senegalensis* (Rambur, 1842)], collected in China. The highest amino acid identity value of the RdRP is 43.65% between FsPV1 and Liriomyza bunyavirus [*Beidivirus liriomyzae*]. FsPV1 is proposed to be classified into species *Beidivirus ischnurae*; and
* Liriomyza bunyavirus (LMBV) was discovered by HTS in pea leafminers [*Liriomyza huidobrensis* (Blanchard, 1926)], collected in South Korea. The highest amino acid identity value of the RdRP is 43.65% between LMBV and FsPV1. 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, Denmark [2]. The highest amino acid identity value of the RdRP is 90.26% between FcPV1 and grapevine associated cogu-like virus 1 [*Bocivirus viticulum*]. FcPV1 is proposed to be classified into species *Bocivirus fusaculense*;
* Fusarium fujikuroi negative-strand RNA virus 1 (FfNSRV) was discovered by HTS in ascomycete fungi (*Fusarium fujikuroi* Nirenberg, 1956], collected in China. The highest amino acid identity value of the RdRP is 82.06% between FfNSRV and Fusarium pseudograminearum coguvirus 1 [*Bocivirus* sp]. FfNSRV is proposed to be classified into species *Bocivirus fusafujiense*; and
* Sānyà phenuivirus 1 (SaPV1) was discovered by HTS in flies (*Cydistomyia duplonotata* Ricardo, 1914), collected in China. The highest amino acid identity value of the RdRP is 73.32% between SaPV1 and Trichoderma gamsii cogu-like virus 1 [*Bocivirus trichodermae*]. SaPV1 is proposed to be classified into species *Bocivirus sanyae*.

**Novel species in the genus *Coguvirus*:*** Blackberry line pattern virus (BlaLPV) was discovered by HTS in unspecified blackberry (*Rubus* L., 1754), collected in USA [3]. The highest amino acid identity value of the RdRP is 69.11% between BlaLPV and citrus concave gum-associated virus [*Coguvirus citri*]. BlaLPV is proposed to be classified into species *Coguvirus rubusense*.

**Novel species in the genus *Entovirus*:*** Guǎngxī phenui-like virus (GPLV) was discovered by soil metagenomic analysis, sampled from a barren land of Guǎngxī (廣西) Province, China [4]. The highest amino acid identity value of the RdRP is 91.26% between GPLV and Hǎinán phenui-like virus 1 [*Entovirus* sp]. GPLV is proposed to be classified into species *Entovirus guangxiense*;
* Inner Mongolia phenui-like virus 2 (IMPLV2) was discovered by soil metagenomic analysis, sampled from a grassland of Nèi Měnggǔ/Inner Mongolia (内蒙古) Autonomous Region, China [3]. The highest amino acid identity value of the RdRP is 50.17% between IMPLV2 and Sìchuān phenui-like virus 1 [*Entovirus* sp]. GPLV is proposed to be classified into species *Entovirus mongoliae*;
* Jiāngsū sediment phenui-like virus (JSPLV) was discovered by sediment metagenomic analysis, sampled from Jiāngsū (江苏) Province, China [4]. The highest amino acid identity value of the RdRP is 47.43% between JSPLV and Hǎinán phenui-like virus 5 [*Entovirus* sp]. JSPLV is proposed to be classified into species *Entovirus jiangsuense*; and
* Yúnnán phenui-like virus (YPLV) was discovered by soil metagenomic analysis, sampled from a farmland of Yúnnán (云南) Province, China [4]. The highest amino acid identity value of the RdRP is 51.87% between YPLV and Sìchuān phenui-like virus 4 [*Entovirus* sp]. YPLV is proposed to be classified into species *Entovirus yunnanense.*

**Novel species in the genus *Goukovirus*:*** Blattella germanica phenuivirus 1 (BgPV1) was discovered in SRA data of *Blattella germanica* Linnaeus, 1767[6]. The highest amino acid identity value of the RdRP is 52.54% between BgPV1 and Cryptocercus punctulatus phenuivirus 1 [*Goukovirus* sp]. 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, Zambia [5]. The highest amino acid identity value of the RdRP is 91.14% between CGV1 and Gouléako virus [*Goukovirus gouleakoense*]. CGV1 is proposed to be classified into species *Goukovirus culequiense*;
* Hodotermopsis sjostedti phenuivirus 1 (HsPV1) was discovered in SRA data of *Hodotermopsis sjostedti* (Holmgren, 1911)[6]. The highest amino acid identity value of the RdRP is 49.67% between HsPV1 and Coptotermes formosanus phenuivirus 2 [*Goukovirus* sp]. HsPV1 is proposed to be classified into species *Goukovirus hodosjostense*;
* Sefomo virus (SFMV) was isolated from *Culex decens* (Theobald, 1901), collected from the Taï National Park, Côte d’Ivoire in 2004 [8]. The highest amino acid identity value of the RdRP is 77.55% between SFMV and Gouléako virus [*Goukovirus gouleakoense*]. SFMV is proposed to be classified into species *Goukovirus culedecense*;
* Shāhé heteroptera virus 3 (SHV3) was discovered by HTS in the freshwater *Heteroptera* collected in Shāhé (沙河) Area, Beijing, China [7]. The highest amino acid identity value of the RdRP is 54.06% between SHV3 and Gouléako virus [*Goukovirus gouleakoense*]. SHV3 is proposed to be classified into species *Goukovirus shahense*; and
* Reticulitermes chinensis phenuivirus 1 (RcPV1) was discovered in SRA data of *Reticulitermes chinensis* (Snyder, 1923) [6]. The highest amino acid identity value of the RdRP is 56.47% between RcPV1 and Coptotermes formosanus phenuivirus 2 [*Goukovirus* sp]. RcPV1 is proposed to be classified into species *Goukovirus retichinense.*

**Novel species in the genus *Hudovirus*:*** Culex hudovirus (ClHV) was discovered by HTS in southern house mosquito[*Culex quinquefasciatus* Say, 1823], collected in Mongu, Zambia [5]. The highest amino acid identity value of the RdRP is 53.87% between ClHV and Pectinophora gossypiella virus 3 [*Hudovirus pectinophorae*]. ClHV is proposed to be classified into species *Hudovirus culexense*; and
* Pectinophora gossypiella virus 3 (PeGV3) was discovered in SRA data of pink bollworm [*Pectinophora gossypiella* (Saunders, 1844)] [9]. The highest amino acid identity value of the RdRP is 56.47% between PeGV3 and ClHV. 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 Tahe, Heilongjiang, China [10]. The highest amino acid identity value of the RdRP is 74.61% between OTPV and blacklegged tick virus 3 [*Ixovirus ixodis*]. OTPV is proposed to be classified into species *Ixovirus gakugsae*;
* Piguzov virus (PigV) was discovered by HTS in common seabird ticks (*Ixodes uriae* White, 1852), collected in Paradise Bay, Antarctica [11]. The highest amino acid identity value of the RdRP is 90.29% between PigV and Bonden virus [*Ixovirus sp*]. PigV is proposed to be classified into species *Ixovirus antarcticae*;
* Ronne virus (RonV) was discovered by HTS in common seabird ticks (*Ixodes uriae* White, 1852), collected in Paradise Bay, Antarctica [11]. The highest amino acid identity value of the RdRP is 70.41% between RonV and Bonden virus [*Ixovirus sp*]. RonV is proposed to be classified into species *Ixovirus paradisense*;
* Sara tick phlebovirus (STPV) was discovered by HTS in taiga ticks (*Ixodes persulcatus* Schulze, 1930), collected in Yíchūn (宜春) City, China [10]. The highest amino acid identity value of the RdRP is 87.36% between STPV and Fairhair virus [*Ixovirus norvegiae*]. STPV is proposed to be classified into species *Ixovirus yichunense*; and
* Shoal Cavern virus (ShoCV) was discovered metagenomic analysis of western blacklegged tick (*Ixodes pacificus* Cooley & Kohls, 1943), collected in Garrapata State Park, USA. The highest amino acid identity value of the RdRP is 79.84% between ShoCV and Fairhair virus [*Ixovirus norvegiae*]. ShoCV is proposed to be classified into species *Ixovirus garrapatae.*

**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 the RdRP is 81.21% between CJNSRV1 and Laurel Lake virus [*Laulavirus laurelense*]. CJNSRV1 is proposed to be classified into species *Laulavirus cordycepsense*;
* Switchgrass phenui-like virus 1 (SGPLV1) was discovered by metagenomic analysis of switchgrass (*Panicum virgatum* L., 1753) in USA. The highest amino acid identity value of the RdRP is 37.09% between SGPLV1 and grapevine associated cogu-like virus 4 [*Laulavirus gammaviticulum*]. SGPLV1 is proposed to be classified into species *Laulavirus panicumense*; 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 the RdRP is 64.32% between VMNSRV1 and grapevine associated cogu-like virus 3 [*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, 1857], collected in Finland. The highest amino acid identity value of the RdRP is 90.99% between ArBLV1 and Armillaria bunya-like virus 2 [*Lentinuvirus betaarmillariae*]. 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, 1857], collected in Finland. The highest amino acid identity value of the RdRP is 90.99% between ArBLV2 and ArBLV1. 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 mushrooms [*Lentinula edodes* (Berk.) Pegler, 1976], collected in China. The highest amino acid identity value of the RdRP is 42.14% between LeNSRV3 and Lentinula edodes negative-strand RNA virus 2 [*Lentinuvirus lentinulae*]. LeNSRV3 is proposed to be classified into species *Lentinuvirus edodesense*.

**Novel species in the genus *Mobuvirus*:*** Anopheles bunyavirus 1 (ABV1) was discovered by HTS in African malaria mosquitos (*Anopheles funestus* Giles, 1900), collected in Kazungula, Zambia [5]. The highest amino acid identity value of the RdRP is 80.27% between ABV1 and Rhodopi bunya-like virus [*Mobuvirus* sp]. ABV1 is proposed to be classified into species *Mobuvirus anophelesense*;
* Bafoussam mosquito bunyavirus 1 (BMBV1) was discovered by HTS in mosquitos [*Aedes africanus* (Theobald, 1901)], collected in Bafoussam, Cameroon [14]. The highest amino acid identity value of the RdRP is 67.86% between BMBV1 and Bafoussam mosquito bunyavirus 2 [*Mobuvirus betabafoussae*]. BMBV1 is proposed to be classified into species *Mobuvirus alphabafoussae*;
* Bafoussam mosquito bunyavirus 2 (BMBV2) was discovered by HTS in mosquitos [*Aedes africanus* (Theobald, 1901)], collected in Bafoussam, Cameroon [14]. The highest amino acid identity value of the RdRP is 67.86% between BMBV2 and BafMBV1. BMBV2 is proposed to be classified into species *Mobuvirus betabafoussae*;
* Coquillettidia bunyavirus (CoqBV) was discovered by HTS in mosquitos [*Coquillettidia aurites* (Theobald, 1901)], collected in Mongu, Zambia [5]. The highest amino acid identity value of the RdRP is 58.14% between CoqBV and Serbia bunya-like virus 1 [*Mobuvirus* sp]. CoqBV is proposed to be classified into species *Mobuvirus coquillettidiae*;
* Cotesiavirus chinense (CotVchi) was discovered in SRA data of diamondback moth parasitoids [*Cotesia vestalis* (Haliday, 1834)] [15]. The highest amino acid identity value of the RdRP is 44.37% between CotVchi and Hymenopteran phenui-related virus OKIAV282 [*Mobuvirus* sp]. CotVchi is proposed to be classified into species *Mobuvirus cotesiae*;
* Culex bunyavirus 2 (ClBV2) was discovered by HTS in mosquitos [*Culex tarsalis* Coquillett, 1896], collected in Alameda, California, USA [16]. The highest amino acid identity value of the RdRP is 93.14% between ClBV2 and Culex pseudovishnui bunya-like virus. ClBV2 is proposed to be classified into species *Mobuvirus alamedae*;
* Culex pseudovishnui bunya-like virus (CPBLV) was discovered by HTS in mosquitos [*Culex pseudovishnui* Colless. 1957], collected in Isahaya (諫早) City, Japan [17]. The highest amino acid identity value of the RdRP is 93.14% between CPBLV and ClBV2. CPBLV is proposed to be classified into species *Mobuvirus isahayae*;
* Fángshān bunya-like virus (FSBLV) was discovered in SRA data of southern house mosquito [*Culex quinquefasciatus* Say, 1823] [18]. The highest amino acid identity value of the RdRP is 65.97% between FSBLV and CPBLV. FSBLV is proposed to be classified into species *Mobuvirus culexense*;
* Sānyà conocephalus maculatus phenuivirus 1 (SCMPV1) was discovered by HTS in maculated rice katydids [*Conocephalus maculatus* (Le Guillou, 1841)], collected in China. The highest amino acid identity value of the RdRP is 37.53% between SCMPV1 and Weta phenui-like virus [*Mobuvirus* sp]. SCMPV1 is proposed to be classified into species *Mobuvirus sanyae*; and
* Shuangao insect virus 3 (SGIV3) was discovered by HTS in unspecified green lacewings (*Chrysopidae*), collected in Zhèjiāng (浙江) Province, China [19]. The highest amino acid identity value of the RdRP is 30.83% between SGIV3 and Ogsystermes virus [*Mobuvirus* sp]. SGIV3 is proposed to be classified into species *Mobuvirus zhejiangense.*

**Novel species in the genus *Phasivirus*:*** Anopheles phasivirus 1 (APV1) was discovered by HTS in mosquitos (*Anopheles rufipes* Gough, 1910), collected in Siavonga, Zambia [5]. The highest amino acid identity value of the RdRP is 51.60% between APV1 and Phasi Charoen-like phasivirus [*Phasivirus phasiense*]. APV1 is proposed to be classified into species *Phasivirus siavongae*;
* Anopheles phasivirus 2 (APV2) was discovered by HTS in African malaria mosquitos (*Anopheles funestus* Giles, 1900), collected in Livingstone, Zambia [5]. The highest amino acid identity value of the RdRP is 51.19% between APV2 and APV1. APV2 is proposed to be classified into species *Phasivirus zambiae*; and
* Niwlog virus (NLV) was discovered by HTS in mosquitos (*Culex erythrothorax* Dyar, 1907), collected in Alameda, USA [16]. The highest amino acid identity value of the RdRP is 59.32% between NLV and Phasi Charoen-like phasivirus [*Phasivirus phasiense*]. NLV is proposed to be classified into species *Phasivirus alamedae*.

**Novel species in the genus *Phlebovirus*:*** Alxa tick phlebovirus (APTV) was discovered by HTS in unspecified ticks, collected in Ālāshàn/Alxa (阿拉善) Left Banner, China [20]. The highest amino acid identity value of the RdRP is 94.28% between APTV and Mukawa virus [*Phlebovirus mukawaense*]. APTV is proposed to be classified into species *Phlebovirus alxae*;
* Mudanjiang phlebovirus (MuPV) was discovered by HTS in taiga ticks (*Ixodes persulcatus* Schulze, 1930), collected in Báishān (白山) City, China [10]. The highest amino acid identity value of the RdRP is 89.74% between MuPV and Mukawa virus [*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 the RdRP is 85.50% between PanPV and Mukawa virus [*Phlebovirus mukawaense*]. PanPV is proposed to be classified into species *Phlebovirus pangoli*;
* Wǔxiāng virus (WUXV) was discovered by HTS in sand flies (*Phlebotomus chinensis* Newstead, 1916), collected in Wǔxiāng (武乡) County, China [21]. The highest amino acid identity value of the RdRP is 88.28% between WUXV and Corfou virus [*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 tiks (*Hyalomma asiaticum,* Schülze & Schlottke, 1929), collected in Bólè (博乐) City, China [19]. The highest amino acid identity value of the RdRP is 88.90% between BoTV1 and Iftin tick virus [*Uukuvirus meccae*]. The common uukuvirus genomes encompass the L, M, and S segments, but some tick-associated uukuvirus genomes lack the M segment and consist of bisegments [22]. BoTV1 is also considered to be a bisegmented uukuvirus, and is proposed to be classified into species *Uukuvirus bolea*;
* Brown dog tick phlebovirus 1 (BDTPV1) was discovered by HTS in brown dog ticks (*Rhipicephalus sanguineus,* Latreille 1806), collected in Republic of Trinidad and Tobago [23]. The highest amino acid identity value of the RdRP is 60.41% between BDTPV1 and Xīnjiāng tick phlebovirus [*Uukuvirus xinjiangense*]. 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 Republic of Trinidad and Tobago [23]. The highest amino acid identity value of the RdRP is 92.75% between BDTPV2 and tick phlebovirus [*Uukuvirus anatoliae*]. 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 Chāngpíng (昌平) District, China [24]. The highest amino acid identity value of the RdRP is 83.83% between CPTV1 and Dermacentor uukuvirus [*Uukuvirus dermae*]. 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 Shāndōng (山东) Province, China [24]. The highest amino acid identity value of the RdRP is 70.14% between CHUV and Dàbiéshān tick virus [*Uukuvirus dabieshanense*]. CHUV is proposed to be classified into species *Uukuvirus qiluense*;
* Dermacentor reticulatus uukuvirus (DRUV) was discovered by HTS in ticks (*Dermacentor reticulatus* Fabricius, 1794), collected in Croatia [25]. The highest amino acid identity value of the RdRP is 66.53% between DRUV and Tǎchéng tick virus 2 [*Uukuvirus tachengense*]. DRUV is proposed to be classified into species *Uukuvirus croatiae*;
* Dermacentor uukuvirus (DeUV) was discovered by HTS in ticks (*Dermacentor silvarum* Olenev, 1931), in Nèi Měnggǔ/Inner Mongolia (内蒙古) Autonomous Region, China [26]. The highest amino acid identity value of the RdRP is 91.48% between DeUV and Meitian tick virus [*Uukuvirus* sp]. DeUV is proposed to be classified into species *Uukuvirus dermae*;
* Iftin tick virus (IfTV) was discovered by HTS in ticks (*Hyalomma dromedarii* Koch, 1844), collected from camels in Makkah (Mecca) Province, Saudi Arabia [27]. The highest amino acid identity value of the RdRP is 88.97% between IfTV and BOTV1. IfTV is proposed to be classified into species *Uukuvirus meccae*;
* Mbalambala tick virus (MbTV) was discovered by HTS in ticks (*Phlebotomus chinensis* Newstead, 1916), collected from camels in Mbalambala, Garrisa County, Kenya [28]. The highest amino acid identity value of the RdRP is 91.44% between MbTV and Limansky tick phlebovirus [*Uukuvirus* sp]. MbTV is proposed to be classified into species *Uukuvirus mbalambalae*;
* 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 the RdRP is 69.20% between OkLTV and Okutama tick virus [*Uukuvirus okutamae*]. 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 Okutama (奥多摩) Town, Japan [29]. The highest amino acid identity value of the RdRP is 76.33% between OkTV and Yǒngjiā tick virus 1 [*Uukuvirus* sp]. OkTV is proposed to be classified into species *Uukuvirus okutamae*;
* Qīnghǎi Lake uukuvirus (QHLUV) was discovered by HTS in ticks (*Dermacentor nuttalli* Olenev, 1928), collected in Qīnghǎi (青海) Province, China [30]. The highest amino acid identity value of the RdRP is 93.13% between QHLUV and Zhāngjiākŏu phenu tick virus 1 [*Uukuvirus* sp]. 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 it’s coding-complete genome were determined by HTS from the ticks, collected in Shāndōng (山东) Province, China [24]. The highest amino acid identity value of the RdRP is 92.89% between TiPV and BDTPV2. TiPV is proposed to be classified into species *Uukuvirus anatoliae*; and
* Xīnjiāng tick phlebovirus (XTPV) was discovered by HTS in ticks (*Hyalomma detritum* Schulze, 1919), collected in Xīnjiāng Wéiwú'ěr (新疆维吾尔) Autonomous Region, China, [20]. The highest amino acid identity value of the RdRP is 82.75% between XTPV and Limansky tick phlebovirus [*Uukuvirus* sp]. 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 [*Penaeus chinensis* (Osbeck, 1765)], collected in Huáng hǎi /Yellow Sea (黃海), China [31]. The highest amino acid identity value of the RdRP is 79.63% between OWV1 and Mourilyan virus [*Wenrivirus penaei*]. OWV1 is proposed to be classified into species *Wenrivirus yellowseae*.

**Already classified species:*** Forécariah virus (FORV), discovered by HTS in ticks [*Rhipicephalus geigyi* (Aeschlimann & Morel, 1965)] collected in Guinea, was found to be an additional isolate of *Bandavirus bhanjanagarense* [17]. The amino acid identity value of the RdRP between FORV and Bhanja virus [*Bandavirus bhanjanagarense*] is 99.04%;
* Palma virus (PaV), discovered by HTS in ticks (*Haemaphysalis punctata* Canestrini & Fanzago, 1878) collected in Portugal, was found to be an additional isolate of *Bandavirus razdanense* [17]. The amino acid identity value of the RdRP between PaV and Razdan virus [*Bandavirus razdanense*] is 97.98%;
* Arrábida virus (ARRV), discovered by HTS in sandflies (*Phlebotomus perniciosus* Newstead, 1911), collected in Arrabida, Portugal, was found to be an additional isolate of *Phlebovirus napoliense* [32]. The amino acid identity value of the RdRP between ARRV and Granada virus [*Phlebovirus napoliense*] is 99.24%;
* Belterra virus (BELTV), discovered by HTS in human plasma, collected in Brazil, was found to be an additional isolate of *Phlebovirus saloboense* [33]. The amino acid identity value of the RdRP between BELTV and Salobo virus [*Phlebovirus saloboense*] is 99.61%;
* Drin virus (DRIV), discovered by HTS in sandflies (*Phlebotomus neglectus* Tonnoir, 1921), collected in Albania, was found to be an additional isolate of *Phlebovirus corfouense* [34]. The amino acid identity value of the RdRP between DRIV and Corfou virus [*Phlebovirus corfouense*] is 98.80%;
* Kuriyama virus (KYV), discovered by HTS in taiga tick (*Ixodes persulcatus* Schulze, 1930), collected in Hokkaido, Japan, was found to be an additional isolate of *Phlebovirus mukawaense* [20]. The amino acid identity value of the RdRP between KYV and Mukawa virus [*Phlebovirus mukawaense*] is 96.07%;
* Ponticelli I virus (PONVI), discovered by HTS in unspecified sandflies, collected in Italy, was found to be an additional isolate of *Phlebovirus salehabadense* [35]. The amino acid identity value of the RdRP between PONVI and Bregalaka virus [*Phlebovirus salehabadense*] is 98.37%;
* Catch-me-cave virus (CMCV), discovered by HTS in ticks [*Ixodes uriae* (White, 1852)], collected in Macquarie Island, Australia, was found to be an additional isolate of *Uukuvirus macquariense* [36]. The amino acid identity value of the RdRP between CMCV and Precarious point virus [*Uukuvirus macquariense*] is 99.81%;
* Chize virus (ChiV), discovered by HTS in ticks (*Ixodes frontalis* Panzer, 1798), collected in France, was found to be an additional isolate of *Uukuvirus schmidti* [37]. The amino acid identity value of the RdRP between ChiV and Nile warbler virus [*Uukuvirus schmidti*] is 99.81%;
* Khasan virus (KHAV), discovered by HTS in longhorned ticks (*Haemaphysalis longicornis* Neumann, 1901) from deers, collected in Khasansky District, Russia, was found to be an additional isolate of *Uukuvirus huangpiense* [38]. The amino acid identity value of the RdRP between KHAV and Huángpí tick virus 2 [*Uukuvirus huangpiense*] is 98.82%;
* Komandory virus (KOMV), discovered in ticks [*Ixodes uriae* (White, 1852)] from guillemots, collected in Komandorski Island, Russia, was found to be an additional isolate of *Uukuvirus rukutamaense* [39]. The amino acid identity value of the RdRP between KOMV and Rukutama virus [*Uukuvirus rukutamaense*] is 99.47%;
* Rhipicephalus associated phlebovirus 1 (RaPV1), discovered by HTS in southern cattle ticks [*Rhipicephalus microplus* (Canestrini, 1888)] collected in China, was found to be an additional isolate of *Uukuvirus lihanense* [40]. The amino acid identity value of the RdRP between RaPV1 and Lǐhán tick virus [*Uukuvirus lihanense*] is 99.77%;
* Sunday Canyon virus (SCV), discovered by HTS in ticks (*Argas cooleyi* Kohls & Hoogstraal, 1960) collected in Sunday Canyon area, USA, was found to be an additional isolate of *Uukuvirus uriae* [41]. The amino acid identity value of the RdRP between SCV and Murre virus [*Uukuvirus uriae*] is 99.95%.
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| **References:**  |
| 1. Sasaya T, Palacios G, Briese T, Di Serio F, Groschup M.H, Neriya Y, Song J-W, Tomitaka Y (2023). ICTV Virus Taxonomy Profile: *Phenuiviridae* 2023. J Gen Virol 104(9):001893. PMID: 37702592. DOI: 10.1099/jgv.0.001893.
2. Buivydaitė Ž, Winding A, Jørgensen LN, Zervas A, Rumakanta Sapkota R (2024). New insights into RNA mycoviruses of fungal pathogens causing *Fusarium* head blight. Virus Res 349:199462. PMID: 39260572. PMCID: PMC11417338 DOI: 10.1016/j.virusres.2024.199462.
3. Schnabel E, Xavier CAD, Whitfield AE, Dubrow Z, Pham G, Cieniewicz E (2025). Exploring the virome of blackberry and wild *Rubus* spp. in South Carolina. J Phytobiomes 9: 80-94. DOI: 10.1094/PBIOMES-11-24-0106-R.
4. Chen YM, Sadiq S, Tian JH, Chen X, Lin XD, Shen JJ, Chen H, Hao ZY, Wille M, Zhou ZC, Wu J, Li F, Wang HW, Yang WD, Xu QY, Wang W, Gao WH, Holmes EC, Zhang YZ (2022) RNA viromes from terrestrial sites across China expand environmental viral diversity. Nat Microbiol 7(8):1312-1323.PMID: 35902778. DOI: 10.1038/s41564-022-01180-2.
5. Orba Y, Abu YE, Chambaro HM, Lundu T, Muleya W, Eshita Y, Qiu Y, Harima H, Kajihara M, Mori-Kajihara A, Matsuno K, Sasaki M, Hall WW, Hang'ombe BM, Sawa H (2023) Expanding diversity of bunyaviruses identified in mosquitoes. Sci Rep 13(1):18165. PMID: 37875565. PMCID: PMC10598057. DOI: 10.1038/s41598-023-45443-2.
6. Wu H, Li W, Fan J, Jiang S, Li J, Hu P, Yu Z, Li Y, Pang R, Wu H (2024) The hidden RNA viruses in *Blattodea* (cockroaches and termites). Microb Genom 10(7):001265. PMID: 39037207. PMCID: PMC11316551 DOI: 10.1099/mgen.0.001265.
7. Shi M, Lin XD, Tian JH, Chen LJ, Chen X, Li CX, Qin XC, Li J, Cao JP, Eden JS, Buchmann J, Wang W, Xu J, Holmes EC, Zhang YZ (2016) Redefining the invertebrate RNA virosphere. Nature 22;540(7634):539-543.PMID: 27880757. DOI: 10.1038/nature20167.
8. Hermanns K, Marklewitz M, Zirkel F, Kopp A, Kramer-Schadt S, Junglen S (2023) Mosquito community composition shapes virus prevalence patterns along anthropogenic disturbance gradients. Elife 12: e66550. PMID: 37702388. PMCID: PMC10547478. DOI: 10.7554/eLife.66550.
9. Dou X, Liu S, Soroker V, Harari A, Jurenka R (2021) Novel RNA viruses from the transcriptome of pheromone glands in the pink bollworm moth, *Pectinophora gossypiella*. Insects 12(6):556. PMID: 34203764. PMCID: PMC8232680. DOI: 10.3390/insects12060556.
10. Wang R, Liu S, Sun H, Xu C, Wen Y, Wu X, Zhang W, Nie K, Li F, Fu S, Yin Q, He Y, Xu S, Liang G, Deng L, Wei Q, Wang H (2023). Metatranscriptomics reveals the RNA virome of Ixodes persulcatus in the China-North Korea border, 2017. Viruses 16(1):62. PMID: 38257762. PMCID: PMC10819109. DOI: 10.3390/v16010062.
11. Pettersson JH-O, Ellström P, Ling J, Nilsson I, Bergström S, González-Acuña D, Olsen B, Holmes EC (2020). Circumpolar diversification of the *Ixodes uriae* tick virome. PLoS Pathog 16(8): e1008759. PMID: 32745135. PMCID: PMC7425989. DOI: 10.1371/journal.ppat.1008759.
12. Cao X, Liu B, Wang Z, Pang T, Sun L, Kondo H, Li J, Andika IB, Chi S (2024). Identification of a novel member of the genus *Laulavirus* (family *Phenuiviridae*) from the entomopathogenic ascomycete fungus Cordyceps javanica. Arch Virol 169 (8), 166. PMID: 38995418. DOI: 10.1007/s00705-024-06069-5.
13. Dai R, Yang S, Pang T, Tian M, Wang H, Zhang D, Wu Y, Kondo H, Andika IB, Kang Z, Sun L (2024). Identification of a negative-strand RNA virus with natural plant and fungal hosts. Proc Natl Acad Sci USA 121(12), e2319582121. PMID: 38483998. PMCID: PMC10962957. DOI: 10.1073/pnas.2319582121.
14. Donfack KCM, Coninck LD, Ghogomu SM, Matthijnssens J (2024). *Aedes* mosquito virome in southwestern Cameroon: Lack of core virome, but a very rich and diverse virome in *Ae. africanus* compared to other *Aedes* species. Viruses 16(7):1172. PMID: 39066334. PMCID: PMC11281338. DOI: 10.3390/v16071172.
15. Caldas-Garcia GB, Santos VC, Fonseca PLC, Almeida JPP, Costa MA, Aguiar ERGR (2023). The viromes of six ecosystem service provider parasitoid wasps. Viruses 15(12):2448. PMID: 38140687. PMCID: PMC10747428. DOI: 10.3390/v15122448.
16. Batson J, Dudas G, Haas-Stapleton E, Kistler AL, Li LM, Logan P, Ratnasiri K, Retallack H (2021). Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. Elife 10: e68353. PMID: 33904402.. PMCID: PMC8110308 DOI: 10.7554/eLife.68353.
17. Faizah AN, Kobayashi D, Isawa H, Amoa-Bosompem M, Murota K, Higa Y, Futami K, Shimada S, Kim KS, Itokawa K, Watanabe M, Tsuda Y, Minakawa N, Miura K, Hirayama K, Sawabe K (2020). Deciphering the virome of *Culex vishnui* subgroup mosquitoes, the major vectors of Japanese *Encephalitis*, in Japan. Viruses 12(3):264. PMID: 32121094. PMCID: PMC7150981. DOI: 10.3390/v12030264.
18. Tang X, Shang J, Chen G, Chan KHK, Shi M, Sun Y (2024). SegVir: Reconstruction of complete segmented RNA viral genomes from metatranscriptomes. Mol Biol Evol 41(8): msae171. PMID: 39137184. PMCID: PMC11346362. DOI: 10.1093/molbev/msae171.
19. Li CX, Shi M, Tian JH, Lin XD, Kang YJ, Chen LJ, Qin XC, Xu J, Holmes EC, Zhang YZ (2015). Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. Elife 4: e05378. PMID: 25633976. PMCID: PMC4384744. DOI: 10.7554/eLife.05378.
20. Kong Y, Zhang G, Jiang L, Wang P, Zhang S, Zheng X, Li Y (2022). Metatranscriptomics reveals the diversity of the tick virome in northwest China. Microbiol Spectr 10(5): e0111522. PMID: 36214702. PMCID: PMC9602664. DOI: 10.1128/spectrum.01115-22.
21. Wang J, Fu S, Xu Z, Cheng J, Shi M, Fan N, Song J, TianX, Cheng J, Ni S, He Y, Lei W, Li F, Peng H, Wang B, Wang H, Lu X, Ma Y, Liang G (2020). Emerging sand fly-borne phlebovirus in China. Emerg Infect Dis 26(10):2435-2438. PMID: 32946723. PMCID: PMC7510709. DOI: 10.3201/eid2610.191374.
22. Kobayashi D, Murota K, Itokawa K, Ejiri H, Amoa-Bosompem M, Faizah AN, Watanabe M, Maekawa Y, Hayashi T, Noda S, Yamauchi T, Komagata O, Sawabe K, Isawa H (2020). RNA virome analysis of questing ticks from Hokuriku District, Japan, and the evolutionary dynamics of tick-borne phleboviruses. Ticks Tick Borne Dis: 11(2):101364. PMID: 31928929. DOI: 10.1016/j.ttbdis.2019.101364.
23. Sameroff S, Tokarz R, Charles RA, Jain K, Oleynik A, Che X, Georges K, Carrington CV, Lipkin WI, Oura C (2019). Viral diversity of tick species parasitizing cattle and dogs in Trinidad and Tobago. Sci Rep 9(1): 10421.PMID: 31320705. PMCID: PMC6639388. DOI: 10.1038/s41598-019-46914-1.
24. Ye RZ, Li YY, Xu DL, Wang BH, Wang XY, Zhang MZ, Wang N, Gao WY, Li C, Han XY, Du LF, Xia LY, Song K, Xu Q, Liu J, Cheng N, Li ZH, Du YD, Yu HJ, Shi XY, Jiang JF, Yi Sun Y, Cui XM Ding SJ, Zhao L, Cao WC (2024). Virome diversity shaped by genetic evolution and ecological landscape of *Haemaphysalis longicornis*. Microbiome 12(1):35. PMID: 38378577. PMCID: PMC10880243. DOI: 10.1186/s40168-024-01753-9.
25. Sameroff S, Tokarz R, Vucelja M, Jain K, Oleynik A, Boljfetić M, Bjedov L, Yates RA, Margaletić J, Oura CAL, Lipkin WI, Krajinović LC, Markotić A (2022). Virome of I*xodes ricinus*, *Dermacentor reticulatus*, and *Haemaphysalis concinna* ticks from Croatia. Viruses 14(5):929. PMID: 35632671. PMCID: PMC9146755. DOI: 10.3390/v14050929.
26. Qin T, Shi M, Zhang M, Liu Z, Feng H, Sun Y (2023). Diversity of RNA viruses of three dominant tick species in North China. Front Vet Sci 13:9:1057977. PMID: 36713863. PMCID: PMC9880493. DOI: 10.3389/fvets.2022.1057977.
27. Zakham F, Albalawi AE, Alanazi AD, Nguyen PT, Alouffi AS, Alaoui A, Sironen T, Smura T, Vapalahti O (2021). Viral RNA metagenomics of Hyalomma ticks collected from dromedary camels in Makkah Province, Saudi Arabia. Viruses 13:1396. PMID: 34372602. PMCID: PMC8310382. DOI: 10.3390/v13071396.
28. Zhang Y, Hu B, Agwanda B, Fang Y, Wang J, Kuria S, Yang J, Masika M, Tang S, Lichoti J, Fan Z, Shi Z, Ommeh S, Wang H, Deng F, Shen S (2021). Viromes and surveys of RNA viruses in camel-derived ticks revealing transmission patterns of novel tick-borne viral pathogens in Kenya. Emerg Microbes Infect 10(1):1975-1987.PMID: 34570681. PMCID: PMC8525980. DOI: 10.1080/22221751.2021.1986428.
29. Mekata H, Kobayashi I, Okabayashi T (2023). Detection and phylogenetic analysis of Dabieshan tick virus and Okutama tick virus in ticks collected from Cape Toi, Japan. Ticks Tick Borne Dis 14(6):102237. PMID: 37595529. DOI: 10.1016/j.ttbdis.2023.102237.
30. Fang Y, Wang J, Sun J, Su Z, Chen S, Xiao J, Ni J, Hu Z, He Y, Shen S, Deng F (2024). RNA viromes of *Dermacentor nuttalli* ticks reveal a novel uukuvirus in Qīnghăi Province, China. Virol Sin 39(4):537-545. PMID: 38679334 PMCID: PMC11401450. DOI: 10.1016/j.virs.2024.04.006.
31. Dong X, Hu T, Ren Y, Meng F, Li C, Zhang Q, Chen J, Song J, Wang R, Shi M, Li J, Zhao P, Li C, Tang KFJ, Cowley JA, Shi W, Huang J (2021) A novel bunyavirus discovered in oriental shrimp (*Penaeus chinensis*). Front Microbiol 12:751112. PMID: 34899637. PMCID: PMC8652140. DOI: 10.3389/fmicb.2021.751112.
32. Remoli ME, Jiménez M, Fortuna C, Benedetti E, Marchi A, Genovese D, Gramiccia M, Molina R, Ciufolini MG (2016). Phleboviruses detection in *Phlebotomus perniciosus* from a human leishmaniasis focus in South-West Madrid region, Spain. Parasit Vectors 9:205. PMID: 27075742. PMCID: PMC4831143. DOI: 10.1186/s13071-016-1488-3.
33. Xu F, Liu D, Nunes MRT, Rosa APADA, Tesh RB, Xiao SY (2007). Antigenic and genetic relationships among Rift Valley fever virus and other selected members of the genus *Phlebovirus* (*Bunyaviridae*). Am J Trop Med Hyg 76(6):1194-200. PMID: 17556635.
34. Bino S, Velo E, Kadriaj P, Kota M, Moureau G, de Lamballerie X, Bagramian A, Charrel RN, Ayhan N (2019). Detection of a novel phlebovirus (Drin virus) from sand flies in Albania. Viruses11(5):469. PMID: 31126034. PMCID: PMC6563191. DOI: 10.3390/v11050469.
35. Calzolari M, Chiapponi C, Bellini R, Bonilauri P, Lelli D, Moreno A, Barbieri I, Pongolini S, Lavazza A, Michele Dottori M (2018). Isolation of three novel reassortant phleboviruses, Ponticelli I, II, III, and of Toscana virus from field-collected sand flies in Italy. Parasit Vectors 11(1):84. PMID: 29409533. PMCID: PMC5802049. DOI: 10.1186/s13071-018-2668-0.
36. O'Brien CA, Huang B, Warrilow D, Hazlewood JE, Bielefeldt-Ohmann H, Hall-Mendelin S, Pegg CL, Harrison JJ, Paramitha D, Newton ND, Schulz BL, Suhrbier A, Hobson-Peters J, Hall RA (2022). Extended characterisation of five archival tick-borne viruses provides insights for virus discovery in Australian ticks. Parasit Vectors 15(1):59. PMID: 35180893. PMCID: PMC8857802. DOI: 10.1186/s13071-022-05176-z.
37. Palacios G, Savji N, da Rosa AT, Guzman H, Yu X, Desai A, Rosen GM, Hutchison S, Lipkin WI, Robert Tesh R (2013). Characterization of the Uukuniemi virus group (*Phlebovirus*: *Bunyaviridae*): evidence for seven distinct species. J Virol 87(6):3187-95. PMID: 23283959. PMCID: PMC3592153. DOI: 10.1128/JVI.02719-12.
38. Al'khovskiĭ SV, L'vov DK, Iu Shchelkanov M, Shchetinin AM, Deriabin PG, Samokhvalov EI, Gitel'man AK, Botikov AG (2013). The taxonomy of the Khasan virus (KHAV), a new representative of phlebovirus genera (*Bunyaviridae*), isolated from the ticks *Haemaphysalis longicornis* (Neumann, 1901) in the Maritime Territory (Russia). Vopr Virusol 58(5):15-8. PMID: 24640166.
39. Al'khovskiĭ SV, L'vov DK, Iu Shchelkanov M, Shchetinin AM, Deriabin PG, Botikov AR, Gitel'man AK, Samokhvalov EI (2013). Genetic characterization of new Komandory virus (KOMV; *Bunyaviridae*, *Phlebovirus*) isolated from the ticks Ixodes uriae, collected in guillemot (*Uria aalge*) nesting sites on Komandorski islands, the Bering Sea. Vopr Virusol 58(6):18-22. PMID: 24772641.
40. Shi J, Shen S, Wu H, Zhang Y, Deng F (2021). Metagenomic profiling of viruses associated with Rhipicephalus microplus ticks in Yunnan Province, China. Virol Sin 36(4):623-635. PMID: 33400089. PMCID: PMC8379324. DOI: 10.1007/s12250-020-00319-x.
41. Kapuscinski ML, Bergren NA, Russell BJ, Lee JS, Borland EM, Hartman D A, King DC, Hughes HR, Burkhalter KL, Kading RC, Stenglein MD (2021). Genomic characterization of 99 viruses from the bunyavirus families *Nairoviridae*, *Peribunyaviridae*, and *Phenuiviridae*, including 35 previously unsequenced viruses. PLoS Pathog 17 (3): e1009315. PMID: 33647063. PMCID: PMC7951987. DOI: 10.1371/journal.ppat.1009315.
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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 RNA-dependent RNA polymerase (RdRP) amino acids between the members of the *Phenuiviridae* family, and proposed viruses (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*

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MF593931\_*Phlebovirus arumowotense*

HM566174\_*Phlebovirus odrenisrouense*

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KC669549\_*Phlebovirus salangaens*

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KF297900\_*Phlebovirus gordilense*

MT270831\_*Phlebovirus kiborgochense*

EU725771\_*Phlebovirus massiliaense*

JF920133\_*Phlebovirus puniqueense*

X68414\_*Phlebovirus toscanaense*

JF939846\_*Phlebovirus tehranense*

KP966616\_*Phlebovirus zerdaliense*

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JF920136\_*Phlebovirus florisense*

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HM119401\_*Phlebovirus alenquerense*

HM119425\_*Phlebovirus niqueense*

MK524348\_*Phlebovirus almendrasense*

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HM119407\_*Phlebovirus candiruense*

HM119416 \_*Phlebovirus itaitubaense*

HM119413\_*Phlebovirus maldonadoense*

HM119434\_*Phlebovirus oriximinaense*

HM119410\_*Phlebovirus echarateense*

HM119431\_*Phlebovirus turunaense*

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KP272001\_*Phlebovirus buenaventuraense*

KP272040\_*Phlebovirus campanaense*

HM566152\_*Phlebovirus leticiaense*

HM566167 \_*Phlebovirus napoliense*

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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 RNA-dependent RNA polymerase (RdRP) amino acids between the members of the genus *Phlebovirus*, and proposed viruses (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 RNA-dependent RNA polymerase (RdRP) amino acids between the members of the genus *Uukuvirus*, and proposed viruses (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.