

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create one (1) new species in the genus *Cilevirus*, and 12 novel species in the genus *Blunervirus,* family *Kitaviridae*, order *Martellivirales*. |
| **Code assigned:** | 2025.004P.Kitaviridae\_13nsp | |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| 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:** |
| Family Kitaviridae SG |

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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** |
| Family *Kitaviridae* SG | 6 |  | 1 |
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| **Submission date:** | 03/06/2025 |

**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 |  |
| 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| W – Withdrawn |  |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:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

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

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | 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** |
| *Cilevirus chilense* | The species epithet is adopted from the geographical origin of the samples where the virus was identified. Vinca ringspot virus was detected in the O'Higgins region, south of Santiago, Chile. It is the first cilevirus detected in that country. |
| *Blunervirus cinnamomi* | The species epithet is adopted from the genus name of the camphor tree (*Cinnamomum camphora*), an evergreen tree native to East Asia. A sample of one tree of this species was the source from which the member virus was detected. |
| *Blunervirus torreyae* | The species epithet is adopted from the genus name of the Chinese fragrant nutmeg yew (*Torreya grandis*) plant. Also known as Chinese torreya, an exemplar of this ornamental coniferous tree was the source of the sample from which the member virus was detected. |
| *Blunervirus chrysanthemi* | The species epithet is adopted from the genus name of the ornamental florist's daisy (*Chrysanthemum morifolium*), also known as hardy garden mum. A sample from this perennial herbaceous plant was the source from which the member virus was detected. |
| *Blunervirus cupressus* | The species epithet is adopted from the genus name of the Min River cypress (*Cupressus chengiana*) tree, endemic to China, found only in Gansu and Sichuan Provinces. A sample of this tree was the source from which the member virus was detected. |
| *Blunervirus festucae* | The species epithet is adopted from the genus name of the grass *Festuca sinensis*. An exemplar of this plant, endemic to China, was the source from which the member virus was detected. |
| *Blunervirus quercus* | The species epithet is adopted from the genus name of the California live oak (*Quercus agrifolia*) tree. This is a medium-sized tree native to the California Floristic Province, on the Pacific coast of North America. California live oak may also be shrubby, depending on its age and growing location. A plant of this species was the source of the sample in which the member virus was detected. |
| *Blunervirus portulacae* | The species epithet is adopted from the genus name of common purslane (*Portulaca oleracea*) plants. A sample of this succulent was the source of the sample in which the member virus was detected. |
| *Blunervirus liquidambarum* | The species epithet is adopted from the genus name of American sweetgum (*Liquidambar styraciflua*) plants. A sample of this deciduous tree was the source of the sample in which the member virus was detected. |
| *Blunervirus tritici* | The species epithet is adopted from the genus name of common wheat (*Triticum aestivum*) plants. A sample of this cereal was the source of the sample in which the member virus was detected. |
| *Blunervirus paulowniae* | The species epithet is adopted from the genus name of the princess tree (*Paulownia tomentosa*). A sample of this hardwood tree, native to central and eastern China and the Korean Peninsula, was the source of the sample in which the member virus was detected. |
| *Blunervirus ulmi* | The species epithet is adopted from the genus name of the Siberian elm (*Ulmus pumila*) tree. A sample of this small to medium-sized, often bushy, deciduous tree, native to Asia, was the source of the sample in which the member virus was detected. |
| *Blunervirus mali* | The species epithet is adopted from the genus name of the apple tree (*Malus domestica*). A sample of this tree, native to Central Asia, was the source of the sample in which the member virus was detected. |

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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** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus, species.  *Description of current taxonomy*:  Kitaviruses comprise a group of plant-infecting viruses with single-stranded (ss), positive-sense (+), split RNA genomes. The family *Kitaviridae,* order *Martellivirales*, is subdivided into three genera, currently including eight species in the genus *Cilevirus*, and three in each of the genera *Higrevirus* and *Blunervirus*. Most members of the genera *Cilevirus* and *Higrevirus* are transmitted by tenuipalpid mites of the genus *Brevipalpus*,whereas at least two blunerviruses are shown to be transmitted by eriophyid mites.  *Proposed* *taxonomic change(s):*  Create one and 12 new species in the genera *Cilevirus* and *Blunervirus*, respectively, in the family *Kitaviridae,* order *Martellivirales*.  *Justification*:  Novel identified viruses possess relatively high nucleotide sequence identity, a compatible genomic organization, and/or a phylogenetic relationship with members of the known species within the family *Kitaviridae*. Biological and molecular characterization of a virus identified in large periwinkle (*Vinca major*) plants demonstrated that it should be classified into a novel species within the genus *Cilevirus*. Genomic analyses of the other 12 novel viruses, obtained from either original high-throughput sequencing (HTS) data or publicly accessible sequence repositories, indicate they belong to new species in the genus *Blunervirus*. Deduced amino acid sequences of these novel viruses share less than 70% amino acid sequence identity with those of known and novel tentative blunerviruses. Phylogenetic analyses using the replication proteins place these novel viruses in the clade containing viruses of the known species of blunerviruses. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus, Species.  *Description of current taxonomy*:  Viruses classified in the family *Kitaviridae*, order *Martellivirales*, infect plants, and have linear single-stranded (ss) positive (+) split RNA genomes [1]. They are assigned to the genera *Cilevirus*, *Higrevirus*, or *Blunervirus* [2]. Fourteen species of kitaviruses are recognized by ICTV. Most kitavirids cause non-systemic diseases in which only the locally infected tissues typically develop chlorotic and/or necrotic lesions. Systemic movement of some blunerviruses has been noticed, but genomic segments are not always simultaneously detected in non-inoculated tissues even after relatively long infection periods [3–5]. Most cileviruses and higreviruses are transmitted by mites of the genus *Brevipalpus*, whereas two blunerviruses have been proven to be transmitted by eriophyid mites [3, 5, 6]. The genomes of the cileviruses are divided into two molecules, in which RNA1, *ca*. 9 kb, comprises two open reading frames (ORFs), RNA-dependent RNA polymerase (*RdRP*) and coat protein(*p29*), whereas RNA2, *ca*. 5 kb, includes four canonical ORFs (*p15*, *p61*, *p32*, and *p24*). ORF *p32* encodes the movement protein (MP), whereas *p61* and *p24* encode proteins likely involved in the virion structure. P24 is a transmembrane (TM) protein, and P61 is a putative glycoprotein. Other cileviruses, such as hibiscus yellow blotch virus (HYBV, *Cilevirus oahuense*) and Solanum violifolium ringspot virus (SvRSV, *Cilevirus solani*), have genomic organizations that differ from those observed in citrus leprosis virus C (CiLV-C, *Cilevirus leprosis*) and citrus leprosis virus C2 (CiLV-C2, *Cilevirus colombiaense*) [7–9]. Higreviruses have three genomic segments [10–12]. RNA1 segments contain a large (ORF) encoding a polyprotein with the conserved domains of viral methyltransferase (VMT), RNA helicase (HEL), and RNA-dependent RNA polymerase (RdRP). The RNA2 segments consist of two or three major ORFs, whose proteins are involved in cell-to-cell viral movement. The RNA3 segments have three putative ORFs, and only one encodes a putative transmembrane protein with an SP24 domain [10, 11]. Blunervirus genomes are multipartite and divided into four molecules [13–15]. RNA1 and RNA2 are monocistronic segments having 5.7–6.0 kb and 3.5–4.1 kb, respectively. Proteins encoded by these two segments contain helicase domains. Besides, each protein contains either a methyltransferase domain or an RdRP\_2 domain, in the polyproteins expressed from RNA1 and 2, respectively. RNA3 of these viruses has the *ORF3*, which encodes the SP24 ortholog protein. RNA4 of some blunerviruses harbors a single ORF that encodes the putative MP containing the 3A motif. Besides, blunerviruses encode several proteins with very low similarity to proteins in public databases [13]. Genomes of kitaviruses, particularly those of blunerviruses, are considered natural genetic chimeric systems [16].  *Proposed* *taxonomic change(s)*:  This taxonomy proposal aims to classify 13 novel viruses into 13 new species distributed as follows:   1. one new species in the genus *Cilevirus*, family *Kitaviridae* 2. twelve new species in the genus *Blunervirus*, family *Kitaviridae*   *Demarcation criteria:*   1. **Genus *Cilevirus***   The current demarcation criteria for species of the genus *Cilevirus* are based on:  A. The extent of the serological relationship as determined by immunodiffusion and/or ELISA  B. Less than 85% aa sequence identity for the proteome  C. Natural host range  D. Artificial host range reactions  E. Vector species and transmission  While the information on the serological relationship of ViRSV with other viruses in the genus is not available, the virus assigned to the new species *Cilevirus chilense,* described in this proposal, meets the criteria B, C, and E.   1. **Genus *Blunervirus***   The current demarcation criteria for species of the genus *Blunervirus* are based on:  A. The extent of the serological relationship as determined by immunodiffusion and/or ELISA  B. Less than 75% aa sequence identity for the polyprotein containing the conserved domains of viral methyltransferase (VMT), RNA helicase (HEL), and RNA-dependent RNA polymerase (RdRP). Typically encoded by two viral RNA segments, comparisons must be performed considering the concatenated products of these domains.  C. Natural host range  D. Vector species and transmission  The blunerviruses assigned to the new species described in this proposal have been obtained from analyses based on RNA-seq data. Therefore, the biological and ecological characteristics described by criteria A, C, and D are not available. All viruses meet criterion B.  *Justification*:   1. **Vinca ringspot virus** (ViRSV) was first identified in symptomatic large periwinkle (*Vinca major*) plants collected in La Punta, southern Santiago, Chile, in 2019 (Ramos-Gonzalez et al., unpublished). ViRSV-infected leaves show green ringspots and chlorotic spots, which can turn into green islands during senescence. In addition to large periwinkle samples collected in 2019, 2020-2021 and 2023, matico (*Buddleja globosa*) plants found in Chile in 2023 were also infected with ViRSV. Experimentally, ViRSV has been successfully transmitted to *Arabidopsis thaliana* and *Nicotiana tabacum* plants using viruliferous mites of the species *Brevipalpus chilensis*. Virions from ViRSV are short bacilliform, which are commonly enclosed inside endoplasmic reticulum cisternae in the cytoplasm of parenchyma and epidermis cells. The size and shape of ViRSV virions and the morphoanatomical disorders observed in the infected cells are compatible with those described for other cileviruses. The full genome sequence of ViRSV isolate LPa1 (GenBank accession numbers OQ116675 & OQ116676) was obtained by HTS and RACE analysis. RNA1 of ViRSV\_LPa1 (8,810 nt) has two ORFs: *RdRP* and *p32* (likely to encode the coat protein), whereas RNA2 (3,585 nt) has three ORFs: *p62* (putative glycoprotein), *p33* (movement protein), and *p23* (likely a transmembrane protein with the SP24 motif) (Figure 1A). The RNA2 of ViRSV lacks the ORF *p15* and sequences of the intergenic region between the ORFs *p15* and *p61* present in CiLV-C, CilV-C2, and PfGSV. However, this absence has also been detected in other cileviruses, *i*,*e*., SvRSV [7]. Deduced amino acid (aa) sequences of proteins encoded by each ORF show identity values not exceeding 67% with their orthologues in members of the genus (Table 1). Based on a maximum likelihood (ML) tree generated from RdRP protein sequences, ViRSV is placed in an independent branch shared with SvRSV, inside a large clade comprising members of the genus *Cilevirus* (Figure 2). 2. **Camphor tree blunervirus 1** (CtBlV1)was identified by analyzing the publicly available transcriptome dataset derived from leaf tissues of *Cinnamomum camphora* (L.) J. Presl. plants, NO.95 cultivar, grown in Guangxi, China [17]. The coding-complete genome of CtBlV1 includes four RNA segments (GenBank accession numbers: BK068192–BK068195) (Figure 1B). CtBlV1 RNA1 (5,781 nt) contains a large ORF encoding a polyprotein with the conserved VMT, OTU-like protease and HEL domains. CtBlV1 RNA2 (4,025 nt) has a single ORF encoding the conserved HEL and RdRP domains. CtBlV1 RNA3 (2,784 nt) encodes four putative proteins: a 17 kDa hypothetical protein, a 29 kDa hypothetical protein with three transmembrane helices, a 21 kDa putative transmembrane protein with the conserved SP24 motif and a 19 kDa hypothetical protein. CtBlV1 RNA4 (2,246 nt) with a single ORF encodes a protein with the conserved 3A-like movement protein domain (Table 2). The deduced amino acid sequences of proteins encoded by CtBlV1 ORFs shared a maximum of <55% identities with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed CtBlV1 in a distinct subclade within blunerviruses (Figure 2). 3. **Chinese nutmeg tree blunervirus 1** (CntBlV1) was identified by analyzing the public domain transcriptome dataset derived from fresh twigs of *Torreya grandis* Fortune ex Lindl [17]. Coding-complete CntBlV1 genome includes four RNA segments (GenBank accession numbers: BK068220–BK068223) (Figure 1C). CntBlV1 RNA1 (5,824 nt) encodes a polyprotein with the conserved VMT, OTU-like protease and HEL domains from its single large ORF. CntBlV1 RNA2 (3,837 nt) contains a single ORF that encodes the conserved HEL and RdRP domain-containing polyprotein. CntBlV1 RNA3 (2,536 nt) contains four ORFs that encode a 15 kDa hypothetical protein, a 28 kDa putative transmembrane protein, a 21 kDa putative transmembrane protein with the conserved SP24 motif and a 20 kDa hypothetical protein. CntBlV1 RNA4 (2,061 nt) encodes a protein with the conserved 3A-like movement protein domain from its single ORF (Table 2). The deduced amino acid sequences of proteins encoded by CntBlV1 ORFs shared the greatest identity of <53% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed CntBlV1 in a sister clade topurslane blunervirus 1 (PuBlV1), a new putative species within the genus *Blunervirus* (Figure 2). 4. **Chrysanthemum blunervirus 1** (ChrBlV1) was identified by analyzing the public domain transcriptome dataset derived from the leaves of *Chrysanthemum* × *morifolium* (Ramat.) Hemsl., cultivar Fiji Yellow, grown in Crimea, Yalta, Russia [17]. The coding-complete genome of ChrBlV1 contains four RNA segments (GenBank accession numbers: BK068200–BK068203) (Figure 1D). ChrBlV1 RNA1 (5,911 nt) and ChrBlV1 RNA2 (3,982 nt), each containing a single ORF encoding a polyprotein with the conserved VMT, OTU-like protease and HEL domains and a polyprotein with the conserved HEL and RdRP domains, respectively. ChrBlV1 RNA3 (2,701 nt) encodes a 16 kDa hypothetical protein, a 28 kDa putative transmembrane protein, a 22 kDa putative transmembrane protein with the conserved SP24 motif and a 16 kDa hypothetical protein. ChrBlV1 RNA4 (1,746 nt) contains a single ORF that encodes a protein with the conserved 3A-like movement protein domain (Table 2). The deduced amino acid sequences of proteins encoded by ChrBlV1 ORFs shared the greatest identity of 48% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed ChrBlV1 in a distinct subclade which was most closely related to tea plant necrotic ring blotch virus (TPNRBV, *Blunervirus camelliae*) (Figure 2). 5. **Cypress blunervirus 1** (CyBlV1) was identified by analyzing the publicly available transcriptome dataset derived from the leaves of *Cupressus chengiana* S.Y.Hu, grown in China [17]. The coding-complete genome of CyBlV1 contains four RNA segments (GenBank accession numbers: BK068188–BK068191) (Figure 1E). CyBlV1 RNA1 (6,094 nt) and CyBlV1 RNA2 (4,196 nt), with one ORF in each, code for a polyprotein with the conserved VMT, OTU-like protease and HEL domains and a polyprotein with the conserved HEL and RdRP domains, respectively. CyBlV1 RNA3 (2,618 nt) contains four ORFs encoding a 16 kDa hypothetical protein, a 28 kDa putative transmembrane protein, a 20 kDa putative transmembrane protein with the conserved SP24 motif and a 20 kDa hypothetical protein. CyBlV1 RNA4 (2,258 nt) encodes a 3A-like movement protein domain-containing protein from its single ORF (Table 2). The deduced amino acid sequences of proteins encoded by CyBlV1 ORFs shared the maximum 59% aa identity with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed CyBlV1 in a distinct subclade that clustered with TPNRBV, ChrBlV1, CntBlV1 and PuBlV1 within blunerviruses (Figure 2). 6. **Festuca sinensis blunervirus 1** (FsBlV1) was identified by analyzing the public domain transcriptome dataset derived from the leaves and stems of *Festuca sinensis* Keng ex E.B. Alexeev, grown in Qinghai Province, China [17]. The coding-complete genome of FsBlV1 contains four RNA segments (GenBank accession numbers: BK068204–BK068207) (Figure 1F). FsBlV1 RNA1 (5,881 nt) contains a single large ORF encoding a polyprotein with the conserved VMT, OTU-like protease and HEL domains while FsBlV1 RNA2 (4,299 nt) encodes a polyprotein with the conserved HEL and RdRP domains. FsBlV1 RNA3 (3,102 nt) encodes a 16 kDa hypothetical protein, a 28 kDa putative transmembrane protein with a signal peptide, a 21 kDa putative transmembrane protein with the conserved SP24 motif and a 19 kDa hypothetical protein. FsBlV1 RNA4 (2,210 nt) encodes a protein with the conserved 3A-like movement protein domain (Table 2). The deduced amino acid sequences of proteins encoded by FsBlV1 ORFs shared the highest identity of <68% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed FsBlV1in a subclade with wheat blunervirus 1 (WhBlV1), another new tentative member, within genus *Blunervirus* (Figure 2). 7. **Oak blunervirus 1** (OaBlV1) was identified by analyzing the publicly available RNA dataset obtained by sequencing the dsRNA pool isolated from the leaves of *Quercus agrifolia* Née, grown in Davis, CA, USA, and collected in 2018 [17]. The coding-complete genome of OaBlV1 includes four RNA segments (GenBank accession numbers: BK068208–BK068211) (Figure 1G). OaBlV1 RNA1 (5,772 nt) and OaBlV1 RNA2 (3,989 nt) encode a polyprotein with the conserved VMT, OTU-like protease and HEL domains and a polyprotein with the conserved HEL and RdRP domains, respectively. OaBlV1 RNA3 (2,842 nt) encodes a 17 kDa hypothetical protein, a 31 kDa putative transmembrane protein with a signal peptide, a 20 kDa putative transmembrane protein with the conserved SP24 motif and a 21 kDa hypothetical protein, while OaBlV1 RNA4 (1,972 nt) encodes a protein with the conserved 3A-like movement protein domain (Table 2). The deduced amino acid sequences of proteins encoded by OaBlV1 ORFs shared the maximum 53% aa identity with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed OaBlV1 in a distinct subclade within blunerviruses (Figure 2). 8. **Purslane blunervirus 1** (PuBlV1) was identified by analyzing the public domain transcriptome dataset derived from the leaf tissues of *Portulaca oleracea* L., grown under salt stress in the USA [17]. The coding-complete genome of PuBlV1 includes four RNA segments (GenBank accession numbers: BK068216–BK068219) (Figure 1H). PuBlV1 RNA1 (6,475 nt) encodes a polyprotein with the conserved VMT, OTU-like protease and HEL domains while PuBlV1 RNA2 (4,186 nt) encodes a polyprotein with the conserved HEL and RdRP domains. PuBlV1 RNA3 (3,334 nt) contains three ORFs encoding a 20 kDa hypothetical protein, a 29 kDa protein with three transmembrane domains and a signal peptide, and a 23 kDa putative transmembrane protein with the conserved SP24 motif. PuBlV1 RNA4 contains a single ORF that codes for a protein with the conserved 3A-like movement protein domain (Table 2). The deduced amino acid sequences of proteins encoded by PuBlV1 ORFs shared the highest identity of 51% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed PuBlV1 in a sister clade to CntBlV1 within blunerviruses (Figure 2). 9. **Sweetgum blunervirus 1** (SwBlV1) was identified by analyzing the public domain transcriptome dataset derived from the leaf tissues of *Liquidambar styraciflua* L., grown in the USA [17]. The coding-complete genome of SwBlV1 includes four RNA segments (GenBank accession numbers: BK068212–BK068215) (Figure 1I). SwBlV1 RNA1 (6,209 nt) encodes a large polyprotein with the conserved VMT, OTU-like protease and HEL domains. SwBlV1 RNA2 (4,307 nt) encodes a polyprotein with the conserved HEL and RdRP domains. SwBlV1 RNA3 (3,596 nt) encodes four proteins: a 21 kDa hypothetical protein, a 34 kDa putative transmembrane protein with a signal peptide, a 22 kDa putative transmembrane protein with the conserved SP24 motif and a 21 kDa hypothetical protein. SwBlV1 RNA4 (2,173 nt) encodes the conserved 3A-like movement protein domain-containing protein (Table 2). The deduced amino acid sequences of proteins encoded by SwBlV1 ORFs shared the highest aa identity of <50% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed SwBlV1 in a distinct subclade within blunerviruses (Figure 2). 10. **Wheat blunervirus 1** (WhBlV1) was identified by analyzing the public domain transcriptome dataset derived from the flag leaf tissue of leaf rust-diseased *Triticum aestivum* L. plants, cultivar AUS 27378 -C34, grown in Zurich, Switzerland [17]. The coding-complete genome of WhBlV1 includes four RNA segments (GenBank accession numbers: BK068196–BK068199) (Figure 1J). WhBlV1 RNA1 (5,814 nt) and WhBlV1 RNA2 (3,950 nt), each containing a single ORF, encodes a polyprotein with the conserved VMT, OTU-like protease and HEL domains and a polyprotein with the conserved HEL and RdRP domains, respectively. WhBlV1 RNA3 (3,110 nt) encodes four proteins: a 15 kDa hypothetical protein, a 28 kDa putative transmembrane protein, a 21 kDa putative transmembrane protein with the conserved SP24 motif and a 21 kDa hypothetical protein. WhBlV1 RNA4 (2,192 nt) encodes a protein with the conserved 3A-like movement protein domain-containing protein (Table 2). The deduced amino acid sequences of proteins encoded by WhBlV1 ORFs shared the maximum aa identity of <68% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed WhBlV1 in a sister clade to FsBlV1 within blunerviruses (Figure 2). 11. **Paulownia tomentosa blunervirus** (PTBV) was identified by analyzing the public domain transcriptome data derived from the leaf tissue of *Paulownia tomentosa* (Thunb.) Steud. plants, grown in Henan, China [16]. The coding-complete genome of PTBV contains four RNA segments (GenBank accession numbers: GEFV01158142, GEFV01018191, GEFV01018861 and GEFV01018726) (Figure 1K). PTBV RNA1 (6,147 nt) encodes a polyprotein with the conserved VMT, OTU-like protease and HEL domains, while PTBV RNA2 (3,678 nt) encodes a polyprotein with the conserved HEL and RdRP domains. PTBV RNA3 (3,399 nt) encodes five proteins: a 29 kDa hypothetical protein with a signal peptide, a 32 kDa putative transmembrane protein, a 21 kDa putative transmembrane protein with the conserved SP24 motif, a 27 kDa hypothetical protein with a signal peptide and a 15 kDa putative transmembrane protein. PTBV RNA4 (3,003 nt) encodes two proteins: a 66 kDa hypothetical protein and a 21 kDa putative transmembrane protein (Table 2). No conserved 3A-like movement protein domain was found in any of the RNA4-encoded proteins. The deduced amino acid sequences of proteins encoded by PTBV ORFs shared the highest aa identity of <69% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed PTBV in a distinct subclade with apple blunervirus 1 (ApBV1), another new putative blunervirus. This subclade is distantly related to other blunervirus genus members (Figure 2). 12. **Elm blunervirus 1** (ElmBlV1) was identified from *Ulmus pumila* L. plants, grown in China. The coding-complete genome of ElmBlV1 contains four RNA segments (GenBank accession numbers: OL865294–OL865297) (Figure 1L). ElmBlV1 RNA1 (5,873 nt) and RNA2 (3,965 nt) encode a polyprotein with the conserved VMT, OTU-like protease and HEL domains, and a polyprotein with the conserved HEL and RdRP domains, respectively. ElmBlV1 RNA3 (2,971 nt) encodes four proteins: a 14 kDa hypothetical protein, a 29 kDa putative transmembrane protein, a 22 kDa putative transmembrane protein with the conserved SP24 motif, and a 14 kDa hypothetical protein. ElmBlV1 RNA4 (2,078 nt) encodes two proteins: a 37 kDa protein with the conserved 3A-like movement protein domain and a 9 kDa putative transmembrane protein (Table 2). The deduced amino acid sequences of proteins encoded by ElmBlV1 ORFs shared the maximum identity of <57% with the corresponding aa sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed ElmBlV1 in a distinct subclade within blunerviruses (Figure 2). 13. **Apple blunervirus 1** (ApBV1) was identified by HTS of symptomatic *Malus domestica* (Suckow) Borkh. plants, cultivar Starkrimson, grown in Liaoning, China [17]. The coding-complete genome of ApBlV1 includes five RNA segments (GenBank accession numbers: OL344039–OL344043) (Figure 1M). ApBV1 RNA1 (6,014 nt) encodes a polyprotein with the conserved VMT, OTU-like protease, and HEL domains, while ApBV1 RNA2 (3,868 nt) encodes a polyprotein with the conserved HEL and RdRP domains. ApBV1 RNA3 (3,433 nt) encodes five proteins: a 25 kDa hypothetical protein, a 33 kDa putative transmembrane protein, a 22 kDa putative transmembrane protein with the conserved SP24 motif, a 26 kDa hypothetical protein, and a 10 kDa putative transmembrane protein. ApBV1 RNA4 (2,823 nt) encodes four proteins: a 62 kDa hypothetical protein, a 21 kDa putative transmembrane protein, an 8 kDa putative transmembrane protein, and a 20 kDa putative transmembrane protein. ApBV1 RNA5 (2,268 nt) encodes a 68 kDa protein with the conserved HEL domain (Table 2). The deduced amino acid sequences of proteins encoded by ApBV1 ORFs shared the maximum identity of <69% with the corresponding sequences of classified and proposed blunerviruses (Table 3). ML tree constructed based on the RdRP aa sequences placed ApBV1 and PTBV in a distinct subclade that was distantly related to other blunerviruses (Figure 2).   We propose classifying ViRSV into the new species “*Cilevirus chilense*”*,* in the genus *Cilevirus*, family *Kitaviridae*. The epithet in the binomial species name refers to the geographical origin of the sample from which the virus was first detected. Besides, we propose classifying CtBlV1, CntBlV1, ChrBlV1, CyBlV1, FsBlV1, OaBlV1, PuBlV1, SwBlV1, WhBlV1, PTBV, ElmBlV1, and ApBV1 into the new species “*Blunervirus cinnamomi*”, “*Blunervirus torreyae*”, “*Blunervirus chrysanthemi*”, “*Blunervirus cupressus*”, “*Blunervirus festucae*”, “*Blunervirus quercus*”, “*Blunervirus portulacae*”, “*Blunervirus liquidambarum*”, “*Blunervirus tritici*”, “*Blunervirus paulowniae*”, “*Blunervirus ulmi*”*,* and“*Blunervirus mali*”, respectively.The epithets in the binomial species names refer to the genus name of the respective plant sample from which the virus was first detected. |

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| --- |
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| --- | --- |
| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.004P.N.v2.Kitaviridae\_13nsp | spreadsheet |
|  |  |

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| **Tables, Figures:** |

**Table 1**. Comparison of the deduced amino acid sequences of Vinca ringspot virus proteins with those from other cileviruses and higreviruses. Highest values are indicated in bold.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Virus name  (acronym, species binomial name) | GenBank Genome Accession | Amino acid identity (%) | | | | |
| RNA1 | | RNA2 | | |
| RdRP | P32 (coat protein) | P66 | P33  (movement protein) | P23  (SP24 protein) |
| Citrus leprosis virus C Crd01  (CiLV-C, *Cilevirus leprosis*) | NC\_038847 | 58.5 | 24.6 | 28.3 | 32.3 | 42.3 |
| Citrus leprosis virus C2 Co  (CiLV-C2, *Cilevirus* *colombiaense*) | NC\_043180 | 55.7 | 22.1 | 25.7 | 30.7 | 39.8 |
| Hibiscus yellow blotch virus  (HYBV, *Cilevirus oahuense*) | MN822527 | 48.6 | 17.9 | 19.8 | 25.8 | 31.2 |
| Ligustrum chlorotic spot virus SPa1  (LigCSV, *Cilevirus ligustri*) | OK626447 | 62.3 | 26.4 | 32.2 | 34.2 | 45.5 |
| Ligustrum leprosis vírus Cdb1  (LigLV, *Cilevirus australis*) | OK626451 | 42.5 | 26.4 | 33.1 | 35.1 | 46.2 |
| passion fruit green spot virus Snp1  (PfGSV, *Cilevirus passiflorae*) | MW362076 | 57.9 | 23.2 | 26.8 | 31.8 | 41.9 |
| Solanum violifolium ringspot vírus Prb1  (SvRSV, *Cilevirus solani*) | OK626439 | **66.5** | **27.8** | **35.5** | **38.5** | **48.5** |
| pistachio virus Y  (PisVY, *Cilevirus pistaciae*) | MN822526 | 47.5 | 18.5 | 20.5 | 26.5 | 33.4 |
| Hibiscus green spot virus 2  (HGSV2, *Higrevirus waimanalo*) | NC\_016117 | 52.1 | - | - | - | 35.6 |
| pistachio vírus X  (PisVX, *Higrevirus pistaciae*) | MN822525 | 45.2 | - | - | - | 29.8 |

**Table 2**. Number of genome segments and conserved motifs of the classified and proposed blunerviruses.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Virus name  (acronym, species binomial name) | No. of genome segments (GenBank Accession) | No. of conserved motifs (in segment(s)) | | | | |
| VMT | HEL | RdRP | SP24 | 3A-like MP |
| blueberry necrotic ring blotch virus (BNRBV, *Blunervirus vaccinii*) | 4 (NC\_016084– NC\_016087) | 1 (RNA1) | 2 (RNA1, RNA2) | 1 (RNA2) | 1 (RNA3) | 1 (RNA4) |
| tea plant necrotic ring blotch virus (TPNRBV, *Blunervirus camelliae*) | 4 (NC\_040401– NC\_040404) |
| tomato fruit blotch virus (ToFBV, *Blunervirus solani*) | 4 (NC\_078392– NC\_078395) |
| camphor tree blunervirus 1 (CtBlV1, “*Blunervirus cinnamomi*”) | 4 (BK068192–BK068195) |
| Chinese nutmeg tree blunervirus 1 (CntBlV1, “*Blunervirus torreyae*”) | 4 (BK068220– BK068223) |
| Chrysanthemum blunervirus 1 (ChrBlV1, “*Blunervirus chrysanthemi*”) | 4 (BK068200– BK068203) |
| cypress blunervirus 1 (CyBlV1, “*Blunervirus cupressus*”) | 4 (BK068188– BK068191) |
| Festuca sinensis blunervirus 1 (FsBlV1, “*Blunervirus festucae*”) | 4 (BK068204– BK068207) |
| oak blunervirus 1 (OaBlV1, *Blunervirus quercus*”) | 4 (BK068208– BK068211) |
| purslane blunervirus 1 (PuBlV1, “*Blunervirus portulacae*”) | 4 (BK068216– BK068219) |
| sweetgum blunervirus 1 (SwBlV1, “*Blunervirus liquidambarum*”) | 4 (BK068212– BK068215) |
| wheat blunervirus 1 (WhBlV1, “*Blunervirus tritici*”) | 4 (BK068196– BK068199) |
| Paulownia tomentosa blunervirus (PTBV, “*Blunervirus paulowniae*”) | 4 (GEFV01158142 GEFV01018191, GEFV01018861, GEFV01018726) | Nil |
| elm blunervirus 1 (ElmBlV1, “*Blunervirus ulmi*”) | 4 (OL865294– OL865297) | 1 (RNA4) |
| apple blunervirus 1 (ApBV1, “*Blunervirus mali*”) | 5 (OL344039– OL344043) | 3 (RNA1, RNA2, RNA5) | Nil |

**Table 3**. Comparison of the deduced amino acid sequences of proposed and classified blunerviruses. The highest values of each virus are indicated in bold.

**A. MET-HEL**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
| 1 | ApBV1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | BNRBV | 25.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | ChrBlV1 | 26.3 | 24.6 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | CntBlV1 | 26.9 | 27.9 | 37.9 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 5 | CtBlV1 | 26.7 | 27.4 | 33.9 | 34.5 | 100 |  |  |  |  |  |  |  |  |  |  |
| 6 | CyBlV1 | 27.5 | 26.0 | 37.9 | **39.2** | 33.8 | 100 |  |  |  |  |  |  |  |  |  |
| 7 | ElmBlV1 | 25.0 | 27.0 | 27.0 | **28.8** | 26.9 | 27.4 | 100 |  |  |  |  |  |  |  |  |
| 8 | FsBlV1 | 27.4 | **28.2** | 33.6 | 35.5 | 35.4 | 36.6 | 27.9 | 100 |  |  |  |  |  |  |  |
| 9 | OaBlV1 | 28.6 | 24.8 | 29.9 | 29.6 | 30.2 | **31.0** | 26.0 | 29.7 | 100 |  |  |  |  |  |  |
| 10 | PTBV | **50.6** | 25.1 | 26.5 | 26.4 | 26.9 | 26.7 | 25.0 | 28.1 | 26.2 | 100 |  |  |  |  |  |
| 11 | PuBlV1 | 28.2 | 26.2 | **39.5** | 39.0 | 32.8 | 37.1 | 27.3 | 33.6 | 27.7 | 26.8 | 100 |  |  |  |  |
| 12 | SwBlV1 | 27.0 | 25.6 | 29.4 | 30.2 | 31.1 | 30.5 | 27.8 | 29.6 | 27.9 | 27.3 | 29.2 | 100 |  |  |  |
| 13 | ToFBV | 28.8 | 26.2 | 32.5 | 34.9 | 33.1 | 32.8 | 27.4 | 32.2 | 29.6 | 27.6 | **31.3** | **31.8** | 100 |  |  |
| 14 | TPNRBV | 27.7 | 25.9 | 33.9 | **35.2** | 32.9 | 33.8 | 26.9 | 34.7 | 29.1 | 26.6 | 33.0 | 29.1 | **32.2** | 100 |  |
| 15 | WhBlV1 | 27.6 | 26.7 | 32.8 | 35.6 | **34.9** | 35.6 | 28.5 | **38.8** | 29.3 | 28.2 | 33.6 | 30.1 | 33.0 | 32.4 | 100 |

**B. HEL-RdRP**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
| 1 | ApBV1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | BNRBV | 32.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | ChrBlV1 | 31.9 | 31.3 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | CntBlV1 | 34.2 | 32.9 | 47.7 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 5 | CtBlV1 | 35.6 | 34.1 | 42.7 | **48.6** | 100 |  |  |  |  |  |  |  |  |  |  |
| 6 | CyBlV1 | 33.6 | 34.1 | 47.1 | **52.6** | 45.5 | 100 |  |  |  |  |  |  |  |  |  |
| 7 | ElmBlV1 | 34.9 | **38.2** | 34.1 | 35.9 | 35.4 | 34.3 | 100 |  |  |  |  |  |  |  |  |
| 8 | FsBlV1 | 33.9 | 32.3 | 47.0 | **52.6** | 47.4 | 50.5 | 33.5 | 100 |  |  |  |  |  |  |  |
| 9 | OaBlV1 | 32.8 | 32.7 | 41.8 | 44.2 | 41.3 | 43.2 | 34.9 | **46.7** | 100 |  |  |  |  |  |  |
| 10 | PTBV | **59.5** | 31.6 | 33.9 | 34.6 | 37.4 | 35.5 | 36.7 | 35.6 | 34.5 | 100 |  |  |  |  |  |
| 11 | PuBlV1 | 35.0 | 33.8 | **48.0** | 51.0 | 43.6 | 50.6 | 34.5 | 48.7 | 42.0 | 35.1 | 100 |  |  |  |  |
| 12 | SwBlV1 | 35.2 | 32.5 | 37.2 | 40.2 | 37.8 | 39.3 | 36.5 | 40.8 | 36.1 | 36.3 | 39.5 | 100 |  |  |  |
| 13 | ToFBV | 36.8 | 33.8 | 42.8 | 43.9 | 41.5 | 45.1 | 38.7 | 42.9 | 42.0 | 36.5 | 44.4 | **44.3** | 100 |  |  |
| 14 | TPNRBV | 32.7 | 33.7 | 42.5 | **48.5** | 43.2 | 47.3 | 34.1 | 46.5 | 42.8 | 34.3 | 45.9 | 36.5 | 42.6 | 100 |  |
| 15 | WhBlV1 | 34.6 | 34.4 | 43.2 | **50.0** | 49.1 | 48.8 | 34.8 | 55.7 | 45.6 | 35.5 | **48.4** | 38.6 | 44.1 | 45.4 | 100 |

**C. SP24**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | | 1 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
| 1 | ApBV1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | BNRBV | **34.7** | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | ChrBlV1 | 27.5 | 27.5 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | CntBlV1 | 23.8 | 25.0 | 40.9 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 6 | CtBlV1 | 25.1 | 23.6 | 31.0 | 37.8 | 100 |  |  |  |  |  |  |  |  |  |  |
| 7 | CyBlV1 | 22.1 | 29.1 | **47.7** | 41.7 | 41.5 | 100 |  |  |  |  |  |  |  |  |  |
| 8 | ElmBlV1 | 26.0 | **33.0** | 25.8 | 25.7 | 27.8 | 27.1 | 100 |  |  |  |  |  |  |  |  |
| 9 | FsBlV1 | 30.4 | 26.1 | 38.9 | 37.5 | 40.0 | 44.0 | 31.3 | 100 |  |  |  |  |  |  |  |
| 10 | OaBlV1 | 25.0 | 28.5 | **41.1** | 39.8 | 39.1 | 39.7 | 25.6 | 39.7 | 100 |  |  |  |  |  |  |
| 11 | PTBV | **68.6** | 32.6 | 29.3 | 28.4 | 26.0 | 27.9 | 32.0 | 32.6 | 26.3 | 100 |  |  |  |  |  |
| 12 | PuBlV1 | 26.2 | 22.9 | 46.4 | 41.9 | 36.7 | **48.6** | 28.6 | 39.4 | 38.5 | 28.6 | 100 |  |  |  |  |
| 13 | SwBlV1 | 33.3 | 25.8 | 27.0 | 26.3 | 32.6 | 29.4 | 28.2 | 29.7 | 26.7 | 31.4 | 27.6 | 100 |  |  |  |
| 14 | ToFBV | 27.4 | 26.1 | **35.2** | 30.4 | 31.5 | 29.4 | 29.8 | 31.4 | 28.0 | 28.8 | 31.4 | 31.5 | 100 |  |  |
| 15 | TPNRBV | 25.6 | 28.5 | 40.7 | 37.8 | 33.7 | **44.1** | 26.3 | 35.1 | 34.3 | 24.3 | 44.1 | 27.7 | 31.1 | 100 |  |
| 16 | WhBlV1 | 26.8 | 26.2 | 37.4 | 39.1 | **41.7** | 43.4 | 26.7 | **67.8** | 39.3 | 28.0 | 39.2 | **34.1** | 29.1 | 36.4 | 100 |

**D. MP**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 |
| 1 | BNRBV | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | ChrBlV1 | 31.8 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 3 | CntBlV1 | 32.8 | 32.0 | 100 |  |  |  |  |  |  |  |  |  |  |
| 4 | CtBlV1 | 40.3 | 33.2 | 44.4 | 100 |  |  |  |  |  |  |  |  |  |
| 5 | CyBlV1 | 39.9 | **35.4** | **46.6** | 47.8 | 100 |  |  |  |  |  |  |  |  |
| 6 | ElmBlV1 | **56.2** | 32.3 | 32.7 | 41.4 | 37.4 | 100 |  |  |  |  |  |  |  |
| 7 | FsBlV1 | 40.8 | 30.5 | 43.2 | **54.8** | **48.4** | **42.5** | 100 |  |  |  |  |  |  |
| 8 | OaBlV1 | 40.2 | 31.8 | 41.3 | **53.0** | 52.7 | 36.7 | 49.4 | 100 |  |  |  |  |  |
| 9 | PuBlV1 | 28.7 | 30.9 | 34.5 | 36.5 | **42.2** | 31.3 | 39.5 | 37.8 | 100 |  |  |  |  |
| 10 | SwBlV1 | 38.1 | 30.1 | 41.2 | 47.0 | 48.7 | 40.5 | 47.7 | 44.6 | 35.5 | 100 |  |  |  |
| 11 | ToFBV | 36.1 | 31.2 | 29.7 | **36.9** | 34.6 | 33.5 | 35.2 | 36.8 | 31.2 | 37.4 | 100 |  |  |
| 12 | TPNRBV | 38.0 | 37.7 | 47.1 | 48.2 | 58.8 | 35.0 | 53.4 | 48.4 | 39.0 | **49.4** | 31.8 | 100 |  |
| 13 | WhBlV1 | 43.8 | 33.9 | 38.3 | 50.5 | 48.3 | 40.3 | **54.1** | 44.8 | 34.9 | 43.0 | 35.5 | 48.6 | 100 |

VMT OTU-like HEL

3’

RNA1

5,781 nts

5’

RNA4

2,246 nts

5’

3’

*p35*

RNA3

2,784 nts

*p17*

*p29*

*p21*

5’

3’

*p19*

HEL RdRP

3’

RNA2

4,025 nts

5’

**B**

VMT OTU-like HEL

3’

RNA1

5,824 nts

5’

RNA4

2,061 nts

5’

3’

*p44*

RNA3

2,536 nts

*p15*

*p28*

*p21*

5’

3’

*p20*

HEL RdRP

3’

RNA2

3,837 nts

5’

**C**

VMT OTU-like HEL

3’

RNA1

5,911 nts

5’

RNA4

1,746 nts

5’

3’

*p44*

RNA3

2,701 nts

*p16*

*p28*

*p22*

5’

3’

*p16*

HEL RdRP

3’

RNA2

3,982 nts

5’

**D**

VMT OTU-like HEL

3’

RNA1

6,094 nts

5’

RNA4

2,258 nts

5’

3’

*p35*

RNA3

2,618 nts

*p16*

*p28*

*p20*

5’

3’

*p20*

RNA2

4,196 nts

**E**

HEL RdRP

3’

5’

VMT OTU-like HEL

3’

RNA1

5,881 nts

5’

RNA4

2,210 nts

5’

3’

*p37*

RNA3

3,102 nts

*p16*

*p28*

*p21*

5’

3’

*p19*

RNA2

4,299 nts

**F**

HEL RdRP

3’

5’

3’

RNA2

3,585 nts

*p33*

*p66*

*p23*

5’

3’

**A**

VMT OTU-like HEL RdRP

RNA1

8,810 nts

5’

*p32*

VMT OTU-like HEL

3’

RNA1

5,772 nts

5’

RNA4

1,972 nts

5’

3’

*p38*

RNA3

2,842 nts

*p17*

*p31*

*p20*

5’

3’

*p21*

HEL RdRP

3’

RNA2

3,989 nts

5’

**G**

VMT OTU-like HEL

3’

RNA1

6,475 nts

5’

RNA4

2,678 nts

5’

3’

*p39*

RNA3

3,334 nts

*p20*

*p29*

*p23*

5’

3’

HEL RdRP

3’

RNA2

4,186 nts

5’

**H**

VMT OTU-like HEL

3’

RNA1

6,209 nts

5’

RNA4

2,173 nts

5’

3’

*p37*

RNA3

3,596 nts

*p21*

*p34*

*p22*

5’

3’

*p21*

HEL RdRP

3’

RNA2

4,370 nts

5’

**I**

VMT OTU-like HEL

3’

RNA1

5,814 nts

5’

RNA4

2,192 nts

5’

3’

*p38*

RNA3

3,110 nts

*p16*

*p28*

*p21*

5’

3’

*p21*

*p15*

RNA2

3,950 nts

**J**

HEL RdRP

3’

5’

VMT OTU-like HEL

3’

RNA1

6,147 nts

5’

RNA4

3,003 nts

5’

3’

*p66*

RNA3

3,399 nts

*p32*

*p21*

5’

3’

*p27*

*p21*

*p29*

RNA2

3,676 nts

**K**

HEL RdRP

3’

5’

VMT OTU-like HEL

3’

RNA1

6,014 nts

5’

RNA5

2,268 nts

5’

3’

HEL

RNA4

2,823 nts

5’

3’

*p62*

RNA3

3,433 nts

*p25*

*p33*

*p22*

5’

3’

*p26*

*p21*

*p21*

HEL RdRP

3’

RNA2

3,868 nts

5’

**M**

VMT OTU-like HEL

3’

RNA1

5,873 nts

5’

RNA4

2,078 nts

5’

3’

*p37*

RNA3

2,971 nts

*p14*

*p29*

*p22*

5’

3’

*p14*

*10*

*10*

*8*

HEL RdRP

3’

RNA2

3,965 nts

5’

**L**

VMT OTU-like HEL

3’

RNA1

6,107 nts

5’

RNA4

2,712 nts

5’

3’

*p56*

RNA3

3,348 nts

*p27*

*p33*

*p21*

5’

3’

*p27*

*p20*

HEL RdRP

3’

RNA2

3,941 nts

5’

VMT OTU-like HEL RdRP

3’

RNA1

7,493 nts

5’

**N**

VMT OTU-like HEL

3’

RNA1

5,873 nts

5’

**L**

HEL RdRP

3’

RNA2

3,965 nts

5’

RNA3

2,971 nts

*p14*

*p29*

*p22*

5’

3’

*p14*

*10*

RNA4

2,078 nts

5’

3’

*p37*

**M**

VMT OTU-like HEL

3’

RNA1

6,014 nts

5’

HEL RdRP

3’

RNA2

3,868 nts

5’

*10*

RNA3

3,433 nts

*p25*

*p33*

*p22*

5’

3’

*p26*

*p21*

*p21*

*8*

RNA5

2,268 nts

5’

3’

HEL

RNA4

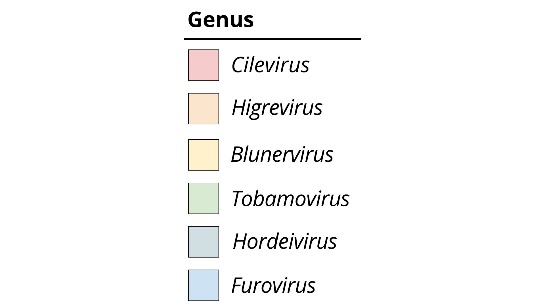
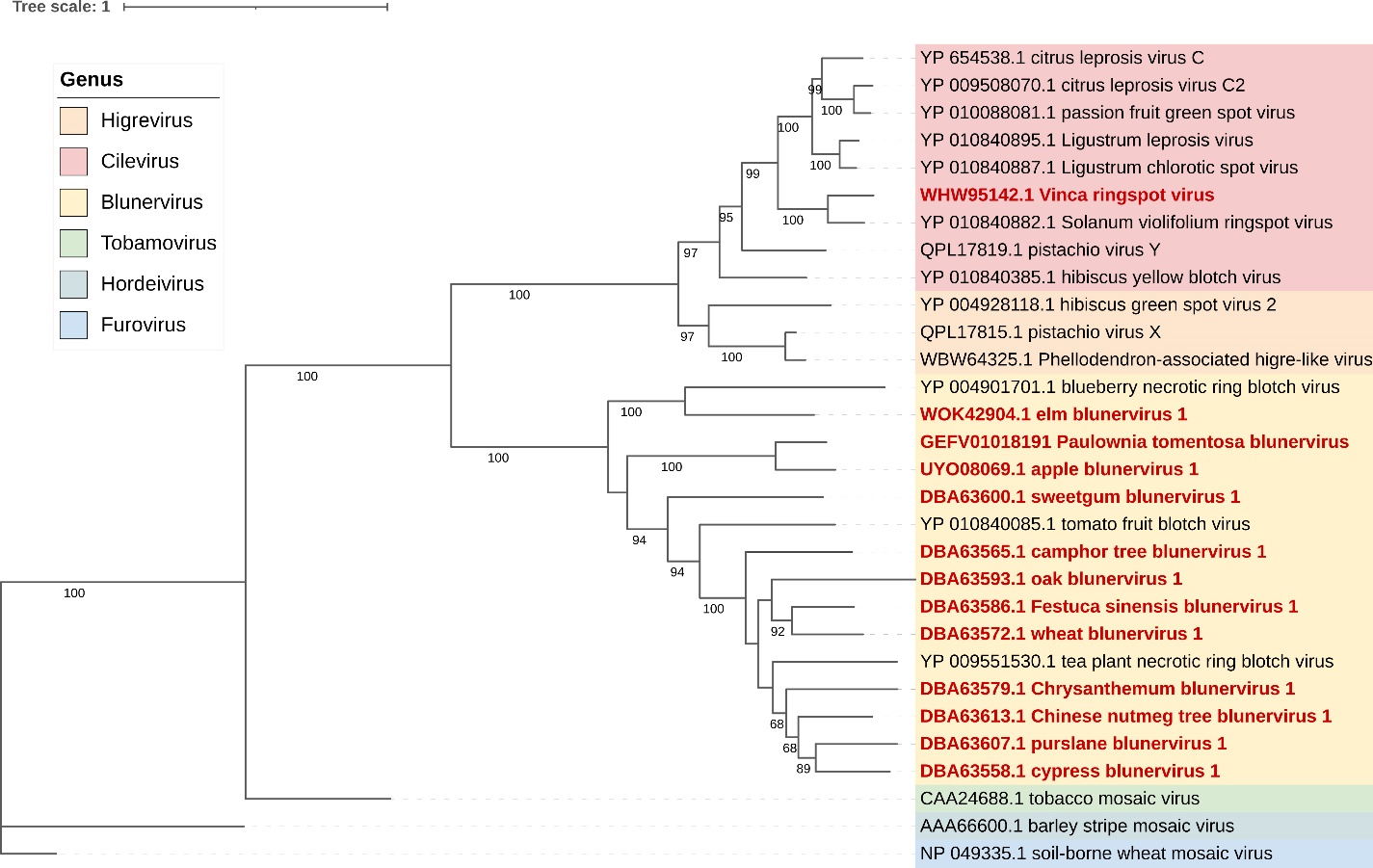
2,823 nts

5’

3’

*p62*

**Figure 1**. Schematic representations of the genomic organization of virus members of the proposed new species of the genera *Cilevirus* and *Blunervirus*. Open reading frames are represented with solid boxes. **A**: Vinca ringspot virus (ViRSV, *Cilevirus chilense*), genus *Cilevirus*; **B**: proposed members of genus *Blunervirus*: camphor tree blunervirus 1 (CtBlV1, “*Blunervirus cinnamomi*”); **C**: Chinese nutmeg tree blunervirus 1 (CntBlV1, “*Blunervirus torreyae*”); **D:** chrysanthemum blunervirus 1 (ChrBlV1, “*Blunervirus chrysanthemi*”); **E:** cypress blunervirus 1 (CyBlV1, “*Blunervirus cupressus*); **F:** Festuca sinensis blunervirus 1 (FsBlV1, “*Blunervirus festucae*”); **G:** oak blunervirus 1 (OaBlV1, “*Blunervirus quercus*”); **H:** purslane blunervirus 1 (PuBlV1, “*Blunervirus portulacae*”); **I:** sweetgum blunervirus 1 (SwBlV1, “*Blunervirus liquidambarum*”); **J:** wheat blunervirus 1 (WhBlV1, “*Blunervirus tritici*”); **K:** Paulownia tomentosa blunervirus (PTBV,“*Blunervirus paulowniae*”); **L:** elm blunervirus 1 (ElmBlV1, “*Blunervirus ulmi*”) and **M:** Apple blunervirus 1 (ApBV1, “*Blunervirus mali*”)*.* VMT: Methyltransferase, HEL: Helicase, RdRP: RNA-dependent RNA polymerase (replicase), SP24-motif containing protein is shown in purple colour and 3A-like movement protein domain-containing protein is shown in green colour.



**Figure 2.** Phylogenetic reconstruction for viruses of the family *Kitaviridae.* Members of the tentative new species are highlighted in red. The maximum-likelihood phylogenetic tree was inferred using IQ-tree software based on the deduced amino acid sequences of RdRP proteins. The alignment was constructed in MAFFT using the E-INS-I iterative refinement method. Phylogenetically informative regions of the multiple sequence alignment included 640 residues selected using BMGE software and its evolutionary history was inferred based on the model LG+F+I+R5. The bootstrap support values (1,000 replications) of branches greater than 50% are indicated next to the corresponding nodes. The tree was rooted using viruses of the genera *Hordeivirus*, *Tobamovirus,* and *Furovirus* as an external group. The scale bar specifies the average number of amino acid substitutions per site, and the tree is drawn to scale.