

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create a new genus*,* two new subgenera, and 34 new species in the family *Secoviridae* (Picornavirales) | |
| **Code assigned:** | 2024.013P.N.v1.Secoviridae\_1ng\_2nsg\_39nsp |

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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:** |
| *Secoviridae* |

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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** |
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| **Submission date:** | 10/06/2024 |

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

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| **Executive Committee Meeting Decision code:** |  |
| 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 | **X** |
| 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| W – Withdrawn |  |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 remove *Nepovirus mirae* (GenBank accession numbers not available). Alternatively, provide the sequence with annotations in the proposal.  Please remove *Waikavirus actaeae, Waikavirus caricis, Waikavirus cerastii, Waikavirus fraxini, Waikavirus plagiogyriae* because of incomplete coding sequence from the proposal. Only CCG sequence can be considered, even if I understand that the sequence relevant to species creation is there.  *Nepovirus betaparis* is a complete genome, not CCG.  Demarcation criteria should be reported only once at the beginning of the proposal and not repeated for each species.  The already established species *Waikavirus anthrisci* is the only one excluded in the assignment to *Waikavirus* subgenera. Maybe it could have escaped while producing the tree.  Minor comment: the abbreviation for jujube-associated virus 1 is JaSV; is this correct? |

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

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| **Response of proposer:** |
| * Annotated sequences of *Nepovirus mirae* were included in the revised proposal. Therefore, we would like to keep this species. * *Waikavirus actaeae, Waikavirus caricis, Waikavirus cerastii, Waikavirus fraxini* and *Waikavirus plagiogyriae* were removed from the proposal. * *Waikavirus anthrisci* is an established species in the genus *Waikavirus.* Its classification was based on biological but no sequence data. Even today no sequence information is available for *Waikavirus anthrisci.* We propose to maintain *Waikavirus anthrisci* as a species assigned to the genus *Waikavirus* and to remove it in a new proposal next year. * The *Nepovirus betaparis* genome was indicated as complete. * JaSV is the correct abbreviation for jujube-associated virus 1 or jujube-associated secovirus. To avoid any confusion, jujube-associated secovirus with the abbreviation JaSV was used throughout the revised proposal. |

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| **Revision date:** | 11/10/2024 |

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

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| **Name of accompanying Excel module:** |
| 2024.013P.N.v2.Secoviridae\_1ng\_2nsg\_39nsp |

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

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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: genus, subgenus, species  *Description of current taxonomy*: The recognition of new virus species is based on demarcation criteria in the family *Secoviridae* of less than 75% amino acid sequence identity in the coat protein (CP)(s) and/or less than 80% amino acid sequence identity in the conserved Protease (Pro)-Polymerase (Pol) region (from the protease CG motif to the polymerase GDD motif), and/ordistinct plant hosts and biological properties.  *Proposed* *taxonomic change(s):*   * Create a newgenus in the family*: Mersevirus* * Create two newsubgenera in the genus *Waikavirus: Ritunrivirus, Actinidivirus* * Create two new species in the genus *Fabavirus: Fabavirus betavitis, Fabavirus cirsii* * Create four new species in the proposed new genus *Mersevirus: Mersevirus merculiaris, Mersevirus paris, Mersevirus boehmeriae, Mersevirus jujubae* * Createtwo new species in the genus *Nepovirus: Nepovirus betaparis, Nepovirus mirae* * Create three new species in the genus *Sadwavirus: Sadwavirus cattleyae, Sadwavirus gymnemae, Sadwavirus chrysanthemi* * Create three new species in the genus *Torradovirus: Torradovirus physalis, Torradovirus nanorugosum, Torradovirus arctii* * Create20 new species in the genus *Waikavirus: Waikavirus ajugae, Waikavirus anacycli, Waikavirus betacammelliae, Waikavirus eleocharis, Waikavirus hirtae, Waikavirus juglandis, Waikavirus ligustici, Waikavirus mertensiae, Waikavirus populi, Waikavirus pedicularis, Waikavirus primulae, Waikavirus querci, Waikavirus ranunculi, Waikavirus thymi, Waikavirus trifoccidentale, Waikavirus thapsiae, Waikavirus violae, Waikavirus carotae, Waikavirus celtis, Waikavirus pittospori*   *Justification*:   * The creation of the proposed new genus *Mersevirus* is justified based on the distinct genome organization of *Mersevirus merculiaris, Mersevirus paris, Mersevirus boehmeriae, and Mersevirus jujubae* with a Ham1 domain with predicted inosine triphosphate pyrophosphatase activity at the C-terminus of the RNA-dependent RNA polymerase -a feature unique among members of the family *Secoviridae*- and a grouping on a monophyletic clade of the amino acid sequence of the CPs and conserved Pro-Pol region. * The creation of the proposed new subgenus *Ritunrivirus* is justified based on a statistically supported single lineage of 22 distinct species in the genus *Waikavirus* defined by the amino acid sequence of the combined three CPs and the conserved Pro-Pol region. * The creation of the proposed new subgenus *Actinidivirus* is justified based on a statistically supported single lineage of 16 distinct species in the genus *Waikavirus* defined by the amino acid sequence of the combined three CPs and conserved Pro-Pol region. * The creation of the proposed new 34 species is justified based on less than 75% amino acid sequence identity in the CP(s) and/or less than 80% amino acid sequence identity in the conserved Pro-Pol region (from the protease CG motif to the polymerase GDD motif) compared with classified species of the family *Secoviridae*. |

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| * **Text of Taxonomy proposal:** |
| 1. *Taxonomic rank(s) affected*: Genus   *Description of current taxonomy*: Nine genera are classified into the family *Secoviridae.*  *Proposed* *taxonomic change(s)*: Creation of a novel genus of the family *Secoviridae,* subfamily *Comovirinae*  *Demarcation criteria:* Thedemarcation criteria are reported in Fuchs M, Hily JM, Petrzik K, Sanfaçon H, Thompson JR, van der Vlugt R, Wetzel T. and ICTV Report Consortium 2022. [ICTV Virus Taxonomy Profile: Secoviridae2022](https://www.microbiologyresearch.org/content/journal/jgv/10.1099/jgv.0.001807), Journal of General Virology (2022) 103:001807 [19]  *Justification*: Members ofthe proposed four new species *Mersevirus merculiaris*, *Mersevirus paris*, *Mersevirus boehmeriae* and *Mersevirus jujubae* share similarly but distinct genomic features in comparison with other species in the family *Secoviridae*. Their RNA1 codes for a polyprotein that is proteolytically cleaved into six predicted proteins instead of the more conventional five proteins (Figure 1). The sixth protein located at the N-terminus of the polyprotein encoded by RNA1 codes a Ham1 domain with predicted inosine triphosphate pyrophosphatase (ITPase) activities. The exemplar strains of the proposed four new species also group in a monophyletic clade based on the amino acid sequence of the two CPs (Figure 2) and the conversed Pro-Pol region (Figure 3). Considering the species demarcation criteria for the family *Secoviridae* and their monophyletic grouping, we propose to classify these four new species into a novel genus named *Mersevirus* (from Merculiarissecovirus 1, the exemplar isolate of the species *Mersevirus merculiaris*)in the subfamily *Comovirinae* in the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus, subgenus   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a first novel subgenus in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: Members of the 19 species of the genus *Waikavirus* (*Waikavirus rosae*, *Waikavirus ribesnigri*, *Waikavirus zeae*, *Waikavirus trifolii*, *Waikavirus oryzae*, *Waikavirus brassicae*, *Waikavirus campanulae, Waikavirus lactucae*, *Waikavirus ajugae, Waikavirus anacycli, Waikavirus eleocharis, Waikavirus ligustici, Waikavirus mersensiae, Waikavirus pedicularis, Waikavirus primulae, Waikavirus ranunculi, Waikavirus thymi, Waikavirus thapsiae, Waikavirus violae*) share similar genomic features with other species in the family *Secoviridae* (Figure 1) and group in a well-supported lineage based on the amino acid sequence of the combined three CPs (Figure 2) and conversed Pro-Pol region (Figure 3), justifying the creation of a subgenus. The name *Ritunrivirus* (rice tungro spherical virus, the exemplar isolate of the species *Waikavirus oryzae*) is proposed for the new subgenus of the genus *Waikavirus* in the family *Secoviridae*.   1. *Taxonomic rank(s) affected*: Genus, subgenus   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species  *Proposed* *taxonomic change(s)*: Creation of a second novel subgenus in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: Members of the 14 species of the genus *Waikavirus* (*Waikavirus camelliae*, *Waikavirus diospyri*, *Waikavirus actinidae*, *Waikavirus rhododendri*, *Waikavirus liegense*, *Waikavirus betacamelliae, Waikavirus hirtae, Waikavirus juglandis, Waikavirus populi, Waikavirus querci, Waikavirus trifoccidentale, Waikavirus carotae, Waikavirus celtis, Waikavirus pittospori*) share similar genomic features with other species in the family *Secoviridae* (Figure 1) and group in a well-supported lineage based on the amino acid sequence of the combined three CPs (Figure 2) and conversed Pro-Pol region (Figure 3), justifying the creation of a subgenus. The name *Actinidivirus* (actinidia yellowing virus 1, the exemplar isolate of the species *Waikavirus actinidae*) is proposed for the new subgenus of the genus *Waikavirus* in the family *Secoviridae*.   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 11 species  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Fabavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of grapevine secovirus (GSV) was determined from a *Vitis vinifera* L. accession in a germplasm repository in the Rostov region of Russia by high-throughput sequencing [1]. The full-length RNA1 of GSV isolate S1823 from *V. vinifera* is 6,224 nt long (GenBank acc. no. OR947508), and the RNA2 is 5,941 nt long (GenBank acc. no. OR947509), excluding the poly(A) tail. The genome organization of GSV is similar to that of other members of the genus *Fabavirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of GSV have 30.4% and 69.9% amino acid sequence identity with yucca gloriosa secovirus (YgSV, a member of the species *Fabavirus yuccae*), the closest related virus in the genus *Fabavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of GSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Fabavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify grapevine secovirus (GSV) as a member of a novel species named *Fabavirus betavitis* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 11 species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Fabavirus* of the family *Secoviridae*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Cirsium virus A (CiVA) was determined from *Cirsium setidens* plants exhibiting mosaic symptoms in South Korea by high-throughput sequencing [2]. The full-length RNA1 of CiVA isolate SK is 5,828 nt long (GenBank acc. no. OP794357), and the RNA2 is 3,478 nt long (GenBank acc. no. OP794358), excluding the poly(A) tail. The genome organization of CiVA is similar to that of other members of the genus *Fabavirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of CiVA have 56.7% and 70.4% amino acid sequence identity with broad bean wilt virus 2 (BBWV2, a member of the species *Fabavirus betaviciae*), the closest related virus in the genus *Fabavirus*. ML phylogenetic trees generated using the two CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of CiVA and representative members of the family *Secoviridae* confirm its clustering in the genus *Fabavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Cirsium virus A (CiVA) as a member of a novel species named *Fabavirus cirsii* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: In the frame of this proposal, the new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae* has been proposed.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the proposed new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Merculiaris secovirus 1 (MSV1) was determined from *Merculiaris perennis* L. plants exhibiting light green mosaic, vein yellowing and deformations in Switzerland by high-throughput sequencing [3]. The full-length RNA1 of MSV1 isolate MSV1/Changins is 6,298 nt long (GenBank acc. no. OR544055), and the RNA2 is 3,543 nt long (GenBank acc. no. OR544056), excluding the poly(A) tail. The genome organization of GSV is similar that of other members of the proposed new genus *Mersevirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of GSV have 76.3% and 69.9% amino acid sequence identity with boehmeria nivea secovirus (BnSV, a proposed new member of the species *Mersevirus boehmeriae*, see below), the closest related virus in the genus *Mersevirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of MSV1 and representative members of the family *Secoviridae* confirmed its clustering in the genus *Mersevirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Merculiaris secovirus 1 (MSV1) as a member of a novel species named *Mersevirus merculiaris* in the genus *Mersevirus*)in the subfamily *Comovirinae,* family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: In the frame of this proposal, the new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae* has been proposed.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the proposed new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*:The complete genome sequence of Paris polyphylla secovirus 2 (PpSV2) was determined from *Paris polyphylla* L. by mining the transcriptome datasets available at NCBI [4]. The full-length RNA1 of PpSV2 isolate Fruit is 5,595 nt long (GenBank acc. No. BK061330), and the RNA2 is 3,224 nt long (GenBank acc. No. BK061331), excluding the poly(A) tail. The genome organization of PpSV2 is similar to that of other members of the proposed new genus *Mersevirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of PpSv2 have 30.3% and 48% amino acid sequence identity with Boehmeria nivea secovirus (BnSV, a proposed new member of the species *Mersevirus boehmeriae*, see below), the closest related virus in the genus *Mersevirus*. ML phylogenetic trees generated using the two CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PpSV2 and representative members of the family *Secoviridae* confirm its clustering in the genus *Mersevirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Paris polyphylla secovirus 2 (PpSV2) as a member of a novel species named *Mersevirus paris* in the genus *Mersevirus* in the subfamily *Comovirinae,* family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: In the frame of this proposal, the new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae* has been proposed.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the proposed new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Boehmeria nivea secovirus (BnSV) was determined from *Boehmeria nivea* L. by mining the transcriptome datasets available at NCBI [4]. The full-length RNA1 of BnSV isolate Zhongzhu 1 is 5,939 nt long (GenBank acc. no. BK061322), and the RNA2 is 3,192 nt long (GenBank acc. no. BK061323), excluding the poly(A) tail. The genome organization of BnSV is similar to that of other members of the proposed new genus *Mersevirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of BnSV have 30.4% and 47.4% amino acid sequence identity with merculiaris secovirus 1 (MSV1, a proposed new member of the species *Mersevirus merculiaris*, see above), the closest related virus in the genus *Mersevirus*. ML phylogenetic trees generated using the two CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of BnSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Mersevirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Boehmeria nivea secovirus (BnSV) as a member of a novel species named *Mersevirus boehmeriae* in the genus *Mersevirus* in the subfamily *Comovirinae,* family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: In the frame of this proposal, the new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae* has been proposed.  *Proposed* *taxonomic change(s)*: Creation of a fourth novel species in the proposed new genus *Mersevirus* in the subfamily *Comovirinae* of the family *Secoviridae*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*:The complete genome sequence of jujube-associated secovirus (JaSV) was determined from jujube (*Ziziphus jujuba* L.) plants exhibiting mosaic symptoms in China by high-throughput sequencing [5]. The full-length RNA1 of JaSV isolate jujuba is 5,878 nt long (GenBank acc. no. MT375548), and the RNA2 is 3,337 nt long (GenBank acc. no. MT375547), excluding the poly(A) tail. The genome organization of JaSV is similar to that of other members of the proposed new genus *Mersevirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of JaSV have 32.5% and 52.1% amino acid sequence identity with paris polyphylla secovirus 2 (PpSV2, a proposed new member of the species *Mersevirus polyphyllae*, see above), the closest related virus in the genus *Mersevirus*. ML phylogenetic trees generated using the two CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of JaSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Mersevirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify jujube-associated secovirus (JaSV) as a member of a novel species named *Mersevirus jujubae* in the genus *Mersevirus* in the subfamily *Comovirinae,* family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 53 species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete coding genome sequence of Paris polyphylla secovirus 1 (PpSV1) was determined from *Paris polyphylla* cv. *yunnanensis* [4]. The near full-length RNA1 of PpSV1 isolate Dian chonglou is 6,467 nt long (GenBank acc. no. BK061328), and the full-length RNA2 is 6,559 nt long (GenBank acc. no. BK061329), excluding the poly(A) tail. The genome organization of PpSV1 is similar to that of other members of the genus *Nepovirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of PpSV1 have 58.3% and 71% amino acid sequence identity with blackcurrant reversion virus (BRV, a member of the species *Nepovirus ribis*), the closest related virus in the genus *Nepovirus*. ML phylogenetic trees generated using the CP (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PpSV1 and representative members of the family *Secoviridae* confirm its clustering in the genus *Nepovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify grapevine Paris polyphylla secovirus 1 (PpSV1) as a member of a novel species named *Nepovirus betaparis* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 53 species  *Proposed* *taxonomic change(s)*: Creation of a second novel species in genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Prunus mira virus A (PMVA) was determined from smooth stone peach (*Prunus mira*)by mining the transcriptome databases available in NCBI [6]. The full-length RNA1 of PMVA isolate mira is 7,851nt long (GenBank acc. no. BK064709), and the RNA2 is 3,816 nt long (GenBank acc. no. BK064710), excluding the poly(A) tail. See the annotated sequences provided as an appendix to this proposal. he genome organization of PMVA is similar to that of other members of the genus *Nepovirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of PMVA have 56.2% and 71.1% amino acid sequence identity with raspberry ringspot virus (RpRSV, a member of the species *Nepovirus rubi*), the closest related virus in the genus *Nepovirus*. ML phylogenetic trees generated using the CP (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PMVA and representative members of the family *Secoviridae* confirm its clustering in the genus *Nepovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Prunus mira virus A (PMVA) as a member of a novel species named in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Sadwavirus* belongs to the family *Secoviridae* and consists of 2 subgenera and 10 species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Sadwavirus* of the family *Secoviridae*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*:The complete genome sequence of Cattleya purple ringspot virus (CaPRV) was determined from cattleya hybrids exhibiting foliar purple ringspots and smaller sports and flecksin Australiaby high-throughput sequencing [7]. The full-length RNA1 of CaPRV isolate 5854 is 5,910 nt long (GenBank acc. no. OR439368), and the RNA2 is 4,435 nt long (GenBank acc. no. OR439369), excluding the poly(A) tail. The genome organization of CaPRV is similar to that of other members of the subgenus *Cholivirus* in the genus *Sadwavirus* of the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of CaPRV have 53.8% and 65% amino acid sequence identity with pineapple secovirus A (PSVA a member of the species *Sadwavirus alphananas*), the closest related virus in the subgenus *Cholivirus* of the genus *Sadwavirus*. ML phylogenetic trees generated using the CP (Figure 2) and conserved Pro-Pol (Figure 3) sequences of CaPRV and representative members of the family *Secoviridae* confirm its clustering in the subgenus *Cholivirus* of the genus *Sadwavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Cattleya purple ringspot virus (CaPRV) as a member of a novel species named *Sadwavirus cattleyae* in the subgenus *Cholivirus* of the genus *Sadwavirus* in the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Sadwavirus* belongs to the family *Secoviridae* and consists of 2 subgenera and 10 species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Sadwavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Gymnema sylvestre virus 1 (GysV1) was determined by miningthe transcriptome of *Gymnema sylvestre* [8]. The full-length RNA1 of GysV1 isolate India is 6,350 nt long (GenBank acc. no. BK062888), and the RNA2 is 3,980 nt long (GenBank acc. no. BK062889), excluding the poly(A) tail. The genome organization of GysV1 is similar to that of other members of the subgenus *Cholivirus* in the genus *Sadwavirus* of the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of GysV1 have 35.8% and 58% amino acid sequence identity with dioscorea mosaic-associated virus (DMaV, a member of the species *Sadwavirus dioscoreae*), the closest related virus in the subgenus *Cholivirus* of the genus *Sadwavirus*. ML phylogenetic trees generated using the CP (Figure 2) and conserved Pro-Pol (Figure 3) sequences of GysV1 and representative members of the family *Secoviridae* confirm its clustering in the subgenus *Cholivirus* of the genus *Sadwavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Gymnema sylvestre virus 1 (GysV1) as a member of a novel species named *Sadwavirus gymnemae* in the subgenus *Cholivirus* of the genus *Sadwavirus* in the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: species   *Description of current taxonomy*: The genus *Sadwavirus* belongs to the family *Secoviridae* and consists of 2 subgenera and 10 species.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the genus *Sadwavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of chrysanthemum sadwavirus (ChSV) was determined from a *Chrysanthemum morifolium* cv. ZaoXiaoYangJu by high-throughput sequencing [9]. The full-length RNA1 of GSV isolate ZXYJ is 7,016 nt long (GenBank acc. no. OR413567), and the RNA2 is 6,772 nt long (GenBank acc. no. OR413568), excluding the poly(A) tail. The genome organization of ChSV is similar to that of other members of the subgenus *Stramovirus* in the genus *Sadwavirus* of the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of GSV have 59.3% and 42.7% amino acid sequence identity with lettuce secovirus 1 (LSVs, a member of the species *Sadwavirus lactucae*), the closest related virus in the subgenus *Stramovirus* of the genus *Sadwavirus*. ML phylogenetic trees generated using the CP (Figure 2) and conserved Pro-Pol (Figure 3) sequences of ChSV and representative members of the family *Secoviridae* confirm its clustering in the subgenus *Stramovirus* of the genus S*adwavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify chrysanthemum sadwavirus (ChSV) as a member of a novel species named *Sadwavirus chrysanthemi* in the subgenus *Stramovirus* of genus *Sadwavirus* in the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 9 species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Torradovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Physalis torrado virus (PhyTV) was determined from *Physalis peruviana* in Colombiaby high-throughput sequencing [10]. The full-length RNA1 of PhyTV isolate BPP2 is 7,062 nt long (GenBank acc. no. MZ357183), and the RNA2 is 4,758 nt long (GenBank acc. no. MZ357184), excluding the poly(A) tail. The genome organization of PhyTV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PhyTV have 79% and 71.1% amino acid sequence identity with tomato torradovirus (ToTV, a member of the species *Torradovirus lycopersici*), the closest related virus in the genus *Torradovirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PhyTV and representative members of the family *Secoviridae* confirm its clustering in the genus *Torradovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Physalis torrado virus (PhyTV) as a member of a novel species named *Torradovirus physalis* in the genus *Torradovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Species   *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 9 species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Torradovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of potato rugose stunting virus (PotRSV) was determined from potato (*Solanum tuberosum* L.) tubersby high-throughput sequencing [11]. The full-length RNA1 of PotRSV isolate PQ13 is 7,086 nt long (GenBank acc. no. ON871623), and the RNA2 is 5,228 nt long (GenBank acc. no. ON871624), excluding the poly(A) tail. The genome organization of PotRSV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PotRSV have 43.2% and 54.5% amino acid sequence identity with cassava torrado-like virus (CsTLV, a member of the species *Torradovirus manihotis*), the closest related virus in the genus *Torradovirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PotRSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Torradovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify potato rugose stunting virus (PotRSV) as a member of a novel species named *Torradovirus nanorugosum* in the genus *Torradovirus* of the family *Secoviridae* (Table 1).  *17. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 9 species.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the genus *Torradovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of burdock mosaic virus (BdMV) was determined from burdock (*Arctium lappa* L.) plants exhibiting leaf mosaic symptomsby high-throughput sequencing [12]. The full-length RNA1 of BdMV isolate IM is 6,991 nt long (GenBank acc. no. OQ087134), and the RNA2 is 4,700 nt long (GenBank acc. no. OQ087135), excluding the poly(A) tail. The genome organization of BdMV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of BdMV have 61.1% and 69% amino acid sequence identity with codonopsis torradovirus A (CoTVA, a member of the species *Torradovirus codonopsis*), the closest related virus in the genus *Torradovirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of BdMV and representative members of the family *Secoviridae* confirm its clustering in the genus *Torradovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify burdock mosaic virus (BdMV) as a member of a novel species named *Torradovirus arctii* in the genus *Torradovirus* of the family *Secoviridae* (Table 1).  *18. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence of Ajuga reptans waikavirus (AjrWV) was determined by mining the transcriptome datasets of *Ajuga reptans* and *Salix purpurea* that are available in NCBI [13]. The full-length RNA of AjrWV isolate Salix is 11,960 nt long (GenBank acc. no. BK062980), excluding the poly(A) tail. The genome organization of AjrWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of AjrWV have 55.3% and 66.2% amino acid sequence identity with lettuce waikavirus 1 (LWV1, a member of the species *Waikavirus lactucae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of AjrWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Ajuga reptans waikavirus (AjrWV) as a member of a novel species named *Waikavirus ajugae* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *19. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence, including the complete coding sequence, of Anacyclus depressus waikavirus (AdWV) was determined by mining the transcriptome datasets of *Anacyclus depressus* that are available in NCBI [13]. The full-length RNA of AdWV isolate Ana dep is 12,265 nt long (GenBank acc. no. BK062979), excluding the poly(A) tail. The genome organization of AdWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of AdWV have 54.2% and 59.7% amino acid sequence identity with ajuga reptans waikavirus (AjrWV, a proposed new member of the species *Waikavirus ajugae*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of AdWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Anacyclus depressus waikavirus (AdWV) as a member of a novel species named *Waikavirus anacycli* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *20. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a fourth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence, including the complete coding sequence, of Camellia virus B (CamVB) was determined by mining the transcriptome datasets of *Camellia sinensis* var. *sinensis* that are available in NCBI [13]. The full-length RNA of CamVB isolate Cam sin is 12,768 nt long (GenBank acc. no. BK062984), excluding the poly(A) tail. The genome organization of CamVB is like that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of CamVB have 74.7% and 77.4% amino acid sequence identity with camellia virus A (CamVA, a member of the species *Waikavirus camelliae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of CamVB and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify camellia virus B (CamVB) as a member of a novel species named *Waikavirus betacamelliae* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *21. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a seventh novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Eleocharis dulcis waikavirus (EdWV) was determined by mining the transcriptome datasets of *Eleocharis dulcis* cv. Fentithat are available in NCBI [13]. The near full-length RNA of EdWV isolate Ele dul is 11,919 nt long (GenBank acc. no. BK062986), excluding the poly(A) tail. The genome organization of EdWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of EdWV have 35.5% and 51.4% amino acid sequence identity with pedicularis rex waikavirus (PrWV, a proposed new member of the species *Waikavirus pedicularis*, see below), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of EdWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Eleocharis dulcis waikavirus (EdWV) as a member of a novel species named *Waikavirus eleocharis* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *22. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of an eighth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete coding genome sequence of Ficus hirta waikavirus (FhWV) was determined by mining the transcriptome datasets of *Ficus hirta* that are available in NCBI [13]. The full-length RNA of FhWV isolate Fic hir is 12,362 nt long (GenBank acc. no. BK062987), excluding the poly(A) tail. The genome organization of FhWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of FhWV have 39.8% and 54.3% amino acid sequence identity with hackberry virus A (HVA, a proposed new member of the species *Waikavirus sinensis*, see below), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of FhWV and representative members of the family *Secoviridae* confirmed its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Ficus hirta waikavirus (FhWV) as a member of a novel species named *Waikavirus hirtae* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *23. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a tenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Juglans nigra waikavirus (JnWV) was determined by mining the transcriptome datasets of *Junglans nigra* that are available in NCBI [13]. The partial full-length RNA of JnWV isolate Jug nig is 11,964 nt long (GenBank acc. no. BK062989), excluding the poly(A) tail. The genome organization of JnWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of JnWV have 29.7% and 45.1% amino acid sequence identity with poaceae Liege virus 1 (PolV1, a member of the species *Waikavirus ligense*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of JnWV and representative members of the family *Secoviridae* confirmed its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Juglans nigra waikavirus (JnWV) as a member of a novel species named *Waikavirus juglandis* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *24. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of an eleventh novel species in the genus *Waikavirus* of the family *Secoviridae*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Ligusticum chuanxiong waikavirus (LcWV) was determined by mining the transcriptome datasets of *Ligusticum chuanxiong* that are available in NCBI [13]. The near full-length RNA of LcWV isolate Lig chu is 11,745 nt long (GenBank acc. no. BK062990), excluding the poly(A) tail. The genome organization of LcWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of LcWV have 62.1.4% and 71.2% amino acid sequence identity with bellflower vein necrosis virus (BVCV, a member of the species *Waikavirus campanulae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of LcWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify ligusticum chuanxiong waikavirus (LcWV) as a member of a novel species named *Waikavirus ligustici* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *25. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a twelfth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Mertensia paniculata waikavirus (MpWV) was determined by mining the transcriptome datasets of *Mertensia paniculata* that are available in NCBI [13]. The near full-length RNA of MpWV isolate Mer pan is 11,579 nt long (GenBank acc. no. BK062991), excluding the poly(A) tail. The genome organization of MpWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of MpWV have 55.5% and 68.3% amino acid sequence identity with bellflower vein necrosis virus (BVCV, a member of the species *Waikavirus campanulae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of MpWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Mertensia paniculata waikavirus (MpWV) as a member of a novel species named *Waikavirus mertensiae* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *26. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a thirteenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete coding genome sequence of Populus alba waikavirus (PaWV) was determined by mining the transcriptome datasets of *Populus alba* cv. pyramidalisthat are available in NCBI [13]. The full-length RNA of PaWV isolate Pop alb is 12,166 nt long (GenBank acc. no. BK062992), excluding the poly(A) tail. The genome organization of PaWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PaWV have 44% and 55.4% amino acid sequence identity with camellia virus B (CamVB, a proposed new member of the species *Waikavirus betacamelliae*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PaWV and representative members of the family *Secoviridae* confirmed its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Populus alba waikavirus (PaWV) as a member of a novel species named *Waikavirus populi* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *27. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a fourteenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete coding genome sequence of Pedicularis rex waikavirus (PrWV) was determined by mining the transcriptome datasets of *Pedicularis rex* that are available in NCBI [13]. The full-length RNA of PrWV isolate Ped rex is 11,775 nt long (GenBank acc. no. BK062993), excluding the poly(A) tail. The genome organization of PrWV is like that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PrWV have 58.3% and 80.2% amino acid sequence identity with Primula vulgaris waikavirus (PvSV, a proposed new member of the species *Waikavirus primulae*, see below), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PrWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Pedicularis rex waikavirus (PrWV) as a member of a novel species named *Waikavirus pedicularis* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *28. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of14 species.  *Proposed* *taxonomic change(s)*: Creation of a sixteenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Primula vulgaris waikavirus (PvWV) was determined by mining the transcriptome datasets of *Primula vulgaris* that are available in NCBI [13]. The near full-length RNA of PvWV isolate Pri vul is 11,717 nt long (GenBank acc. no. BK062995), excluding the poly(A) tail. The genome organization of PvWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PvWV have 59.1% and 77.6% amino acid sequence identity with Pedicularis rex waikavirus (PrWV, a proposed new member of the species *Waikavirus pedicularis*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PvWV and representative members of the family *Secoviridae* confirmed its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Primula vulgaris waikavirus (PvWV) as a member of a novel species named *Waikavirus primulae* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *29. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a seventeenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete coding genome sequence of Quercus robur waikavirus (QrWV) was determined by mining the transcriptome datasets of *Quercus robur* that are available in NCBI [13]. The near full-length RNA of QrWV isolate Que rob is 12,444 nt long (GenBank acc. no. BK062996), excluding the poly(A) tail. The genome organization of QrWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of QrWV have 32.3% and 44.6% amino acid sequence identity with Juglans nigra waikavirus (JnSV, a proposed new member of the species *Waikavirus juglandis*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of QrWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Quercus robur waikavirus (QrWV) as a member of a novel species named *Waikavirus querci* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *30. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of an eighteenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Ranunculus cantoniensis waikavirus (RcWV) was determined by mining the transcriptome datasets of *Ranunculus cantoniensis* that are available in NCBI [13]. The near full-length RNA of RcWV isolate Ran can is 11,382 nt long (GenBank acc. no. BK062997), excluding the poly(A) tail. The genome organization of RcWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of RcWV have 53.6% and 69.9% amino acid sequence identity with viola inconspicua waikavirus secovirus (ViWV, a proposed new member of the species *Waikavirus violae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of RcWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Ranunculus cantoniensis waikavirus (RcWV) as a member of a novel species named *Waikavirus ranunculi* in the genus *Waikavirus*, subgenus *Ritunrivirus*, of the family *Secoviridae* (Table 1).  *31. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a nineteenth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Thymus vulgaris waikavirus (ThyWV) was determined by mining the transcriptome datasets of *Thymus vulgaris* cv. Tv4that are available in NCBI [13]. The near full-length RNA of ThyWV isolate Thy vul is 11,662 nt long (GenBank acc. no. BK062999), excluding the poly(A) tail. The genome organization of ThyWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of ThyWV have 46.2% and 60.9% amino acid sequence identity with Mertensia penicula waikavirus (MpWV, a proposed new member of the species *Waikavirus mertensiae*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of ThyWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Thymus vulgaris waikavirus (ThyWV as a member of a novel species named *Waikavirus thymi* in the genus *Waikavirus,* subgenus subgenus *Ritunrivirus,* of the family *Secoviridae* (Table 1).  *32. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a twentieth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Trifolium occidentale waikavirus (ToWV) was determined by mining the transcriptome datasets of *Trifolium occidentale* cv. Margot Forde that are available in NCBI [13]. The full-length RNA of ToWV isolate Tri occ is 12,464 nt long (GenBank acc. no. BK063000), excluding the poly(A) tail. The genome organization of ToWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of ToWV have 26.2% and 51.3% amino acid sequence identity with poaceae Liege virus 1 (PolV1, a member of the species *Waikavirus ligense*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of ToWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Trifolium occidentale waikavirus (ToWV) as a member of a novel species named *Waikavirus trifoccidentale* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *33. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of14 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-first novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The near complete genome sequence (with the complete coding sequence) of Thapsia villosa waikavirus (TvWV) was determined by mining the transcriptome datasets of *Thapsia villosa* cv. laciniata that are available in NCBI [13]. The near full-length RNA of TvWV isolate Tha vil is 12,030 nt long (GenBank acc. no. BK063001), excluding the poly(A) tail. The genome organization of TvWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of TvWV have 55.7% and 73.3% amino acid sequence identity with bellflower vein necrosis virus (BVCV, a member of the species *Waikavirus campanulae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of TvWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Thapsia villosa waikavirus (TvWV)) as a member of a novel species named *Waikavirus thapsiae* in the genus *Waikavirus,* subgenus *Ritunrivirus,* of the family *Secoviridae* (Table 1).  *34. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-second novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete coding genome sequence of Viola inconspicua waikavirus (CiWV) was determined by mining the transcriptome datasets of *Viola inconspicua* that are available in NCBI [13]. The near full-length RNA of CiWV isolate Vio inc is 12,293 nt long (GenBank acc. no. BK063002), excluding the poly(A) tail. The genome organization of CiWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of CiWV have 55.2% and 58.2% amino acid sequence identity with Pedicularis rex waikavirus secovirus (PrWV, a proposed new member of the species *Waikavirus pedicularis*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of CiWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Viola inconspicua waikavirus (CiWV) as a member of a novel species named *Waikavirus violae* in the genus *Waikavirus,* subgenus *Ritunvirus,* of the family *Secoviridae* (Table 1).  *35. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-third novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of carrot psyllid-borne associated virus (CPBaV) was determined from a *Daucus carota* L. plants exhibiting leaf chlorosis and curling symptoms, as well as multiple lateral roots, in Israel by high-throughput sequencing [14]. The full-length RNA of CPBaV isolate Israel is 11,960 nt long (GenBank acc. no. OM801008), excluding the poly(A) tail. The genome organization of CPBaV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of CPBaV have 38.6% and 54.3% amino acid sequence identity with camellia virus A (CamVA, a member of the species *Waikavirus camelliae*), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of CPBaV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify carrot psyllid-borne associated virus (CPBaV) as a member of a novel species named *Waikavirus carotae* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *36. Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-fourth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of hackberry virus A (HAV) was determined from hackberry (*Celtis sinensis* Pers.) in China by high-throughput sequencing [15]. The full-length RNA of HAV isolate NB is 12,691 nt long (GenBank acc. no. OP533794), excluding the poly(A) tail. The genome organization of HAV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of HAV have 43.1% and 57.4% amino acid sequence identity with ficus hirta waikavirus (FhWV, a proposed new member of the species *Waikavirus hirtae*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of HAV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify hackberry virus A (HAV) as a member of a novel species named *Waikavirus celtis* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1).  *37 . Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 14 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-fifth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [19]  *Justification*: The complete genome sequence of Pittosporum tobira virus (PtWV) was determined from *Pittosporum tobira* in China by high-throughput sequencing [16]. The full-length RNA of PtWV isolate Pitt is 12,709 nt long (GenBank acc. no. OR659471), excluding the poly(A) tail. The genome organization of PtWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PtWV have 33.6% and 52.3% amino acid sequence identity with Populus alba waikavirus (PaWV, a proposed new member of the species *Waikavirus populi*, see above), the closest related virus in the genus *Waikavirus*. ML phylogenetic trees generated using the three CPs (Figure 2) and conserved Pro-Pol (Figure 3) sequences of PtWV and representative members of the family *Secoviridae* confirm its clustering in the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Pittosporum tobira virus (PtWV) as a member of a novel species named *Waikavirus pittospori* in the genus *Waikavirus*, subgenus *Actinidivirus*, of the family *Secoviridae* (Table 1). |

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| **Tables, Figures:** |

**Table 1:** List of newly proposed virus species in the family *Secoviridae* with their exemplar virus, genus, and NCBI accession numbers.

Virus name Virus species Genus GenBank acc. no.

# grapevine secovirus *Fabavirus betavitis* *Fabavirus* RNA1 OR947508

# RNA2 OR947509

Cirsium virus A *Fabavirus cirsii Fabavirus* RNA1 OP794357

RNA2 OP794358

Merculiaris secovirus 1 *Mersevirus merculiaris Mersevirus* RNA1 OR544055

RNA2 OR544056

Paris polyphylla secovirus 2 *Mersevirus paris* *Mersevirus* RNA1 BK061330

RNA2 BK061331

Boehmeria nivea secovirus *Mersevirus boehmeriae* *Mersevirus* RNA1 BK061322

RNA2 BK061323

jujube-associated secovirus *Mersevirus jujubae* *Mersevirus* RNA1 MT375548

RNA2 MT375547

Paris polyphylla secovirus 1 *Nepovirus betaparis Nepovirus* RNA1 BK061328

RNA2 BK061329

# Prunus mira virus A *Nepovirus mirae Nepovirus* RNA1 BK064709

# RNA2 BK064710

Cattleya purple ringspot virus *Sadwavirus cattleyae* *Sadwavirus* RNA1 OR439368

RNA2 OR439369

Gymnema sylvestre virus 1 *Sadwavirus gymnemae* *Sadwavirus* RNA1 BK062888

RNA2 BK062889

chrysanthemum sadwavirus *Sadwavirus chrysanthemi* *Sadwavirus* RNA1 OR413567

RNA2 OR413568

Physalis torrado virus *Torradovirus physalis Torradovirus* RNA1 MZ357183

RNA2 MZ357184

potato rugose stunting virus *Torradovirus nanorugosum Torradovirus* RNA1 ON871623

RNA2 ON871624

burdock mosaic virus *Torradovirus arctii Torradovirus* RNA1 OQ087134

RNA2 OQ087135

Ajuga reptans waikavirus *Waikavirus ajugae Waikavirus* RNA BK062980

Anacyclus depressus waikavirus *Waikavirus anacycli Waikavirus* RNA BK062979

Camellia virus B *Waikavirus betacamelliae Waikavirus* RNA BK062984

Eleocharis dulcis waikavirus *Waikavirus eleocharis Waikavirus* RNA BK062986

Ficus hirta waikavirus *Waikavirus hirtae Waikavirus* RNA BK062987

Juglans nigra waikavirus *Waikavirus juglandis Waikavirus* RNA BK062989

Ligusticum chuanxiong waikavirus *Waikavirus ligustici Waikavirus* RNA BK062990

Mertensia paniculata waikavirus *Waikavirus mertensiae Waikavirus* RNA BK062991

Populus alba waikavirus *Waikavirus populi Waikavirus* RNA BK062992

Pedicularis rex waikavirus *Waikavirus pedicularis Waikavirus* RNA BK062993

Primula vulgaris waikavirus *Waikavirus primulae Waikavirus* RNA BK062995

Quercus robur waikavirus *Waikavirus querci Waikavirus* RNA BK062996

Ranunculus cantoniensis waikavirus *Waikavirus ranunculi Waikavirus* RNA BK062997

Thymus vulgaris waikavirus *Waikavirus thymi Waikavirus* RNA BK062999

Trifolium occidentale waikavirus *Waikavirus trifoccidentale Waikavirus* RNA BK063000

Thapsia villosa waikavirus *Waikavirus thapsiae Waikavirus* RNA BK063001

Viola inconspicua waikavirus *Waikavirus violae Waikavirus* RNA BK063002

carrot psyllid-borne associated virus *Waikavirus carotae* *Waikavirus* RNA OM801008

hackberry virus A *Waikavirus celtis Waikavirus* RNA OP533794

Pittosporum tobira virus *Waikavirus pittospori Waikavirus* RNA OR659471

A diagram of dna sequence

Description automatically generated with medium confidence

**Figure 1.** Genome organization of representative members of the 10 genera (*Comovirus*, *Fabavirus*, *Mersevirus*, *Nepovirus*, *Stralarivirus*, *Cheravirus*, *Sadwavirus*, *Torradovirus*, *Sequivirus*, *Waikavirus*) in the family *Secoviridae*. Each RNA is shown with open reading frames (ORFs) represented with boxes. Circles at the 5' end of viral genomic RNA depict viral genome-linked proteins (VPg). Black circles represent VPg experimentally confirmed and open circles represent putative VPgs. The poly(A) tails at the 3' end of viral genomic RNAs are depicted with (An), when appropriate. Protein domains with conserved motifs for the putative NTP-binding domain protein (Hel, green), VPg (peach), 3C-like proteinase (Pro, dark blue), RNA-dependent RNA polymerase (Pol, light blue), Ham1 domain (light blue diagonal stripes), movement protein (MP, orange) and coat protein(s) (CPs, red) are shown. Proteinase cleavage sites identified experimentally or predicted by sequence comparisons are indicated by solid vertical lines. The three sub-genera of sadwaviruses are indicated. Virus acronyms are: CPMV: cowpea mosaic virus (exemplar isolate of the species *Comovirus vignae*); BBWV2: broad bean wilt virus 2 (exemplar isolate of the species *Fabavirus betaviciae*); MSV1: Merculiaris secovirus 1 (exemplar isolate of the species *Mersevirus merculiaris*); ArMV: Arabis mosaic virus (exemplar isolate of the species *Nepovirus arabis*); TBRV: tomato black ring virus (exemplar isolate of the species *Nepovirus nigranuli*); ToRSV: tomato ringspot virus (exemplar isolate of the species *Nepovirus lycopersici*); SLRSV: strawberry latent ringspot virus (exemplar isolate of the species *Stralarivirus fragariae*); CLRV: cherry rasp leaf virus (exemplar isolate of the species *Cheravirus avii*): SMoV: strawberry mottle virus (exemplar isolate of the species *Sadwavirus fragariae*); CLVA: chocolate lily virus A (exemplar isolate of the species *Sadwavirus fritillariae*); SDV: satsuma dwarf virus (exemplar isolate of the species *Sadwavirus citri*): ToTV: tomato torradovirus (exemplar isolate of the species *Torradovirus lycopersici*); PYVF: parsnip yellow fleck virus (exemplar isolate of the species *Sequivirus pastinacea*); and RTSV: rice tungro spherical virus (exemplar isolate of the species *Waikavirus oryzae*).

**A diagram of a virus

Description automatically generated**

**Figure 2**. Phylogenetic tree of the coat protein(s) amino acid sequences of the exemplified members of the 34 newly proposed species (identified by the full virus name and abbreviation) in the family *Secoviridae* and 114 representatives of the different genera in the family *Secoviridae.* The evolutionary history was inferred by using the Maximum Likelihood method and Le\_Gascuel\_2008 model [17]. The tree with the highest log likelihood (-88120.16) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (3 categories (+G, parameter = 7.1354)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 151 amino acid sequences. All positions with less than 95% site coverage were eliminated, i.e., fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option). There was a total of 321 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [18].Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in the family *Secoviridae* are as follows: ToRSV (tomato ringspot virus, D12477), AnNVA (anemone nepovirus A, MH898478), SteNV (Stenotaphrum nepovirus, MZ325762), BRV (blackcurrant reversion virus, AF020051), GBLV (grapevine Bulgarian latent virus, FN691935), BLSV (blueberry latent spherical virus, AB649297), SLSV (soybean latent spherical virus, KX424572), PRMV (peach rosette mosaic virus, (KJ572573), CawYV (caraway yellow virus, MK492274), CLRV (cherry leaf roll virus, FR851462), GNVA (grapevine nepovirus A, MT507291), MMMoV (melon mild mottle virus, AB518486), RpRSV (raspberry ringspot virus, AY303788), PoLNVA (poaceae Liege nepovirus A, MW289236), MMLRaV (mulberry mosaic leaf roll-associated virus, KC904084), AeRSV (Aeonium ringspot virus, JQ670669), PBRSV (potato black ringspot virus, KC832892), TRSV (tobacco ringspot virus, AY363727), GDefV (grapevine deformation virus, AY291208), ArMV (Arabis mosaic virus, AY017339), GFLV (grapevine fanleaf virus, X16907), OLRSV (olive latent ringspot virus, AJ277435), PCMoV (petunia chlorotic mottle virus, KX812816), BRSV (beet ringspot virus, X04062), RCNA (red clover nepovirus A, MG253829), TBRV (tomato black ring virus, AY157994), AILV (artichoke Italian latent virus, LT608396), GARSV (grapevine Anatolian ringspot virus, AY291207), GCMV (grapevine chrome mosaic virus, X15163), CNSV (cycas necrotic stunt virus, AB073148), PVB (potato virus B, KX656671), GSPNeV (green Sichuan pepper nepovirus, MH323434), ParNV1 (paris nepovirus 1, OP374159), HNVA (horse nettle virus A, OP292295), CwmSV (common water moss secovirus, OX380442), TfSV (tomato fern secovirus, OX380490), SfSV (shoestring fern secovirus, OX380478), APMV (Andean potato mottle virus, L16239),CPSMV (cowpea severe mosaic virus, M83309), PvSMV (Phaseolus vulgaris severe mosaic virus, MN837499), BRMV (bean rugose mosaic virus, KP404603), BPMV (bean pod mosaic virus, U70866), TuRSV (turnip ringspot virus, GQ222382), CPMV (cowpea mosaic virus, X00729), ArLV1 (Arabidopsis latent virus 1, MH899121), RCMV (red clover mottle virus, M14913), BBTMV (broad bean true mosaic virus, GU810904), SqMV (squash mosaic virus, AB054689), PepMMV (pepper mild mosaic virus, MK990556), GFabV (grapevine fabavirus, KX241485), PrVF (prunus virus F, KX269871), CuMMV (cucurbit mild mosaic virus, EU881937), LMMV (lamium mild mosaic virus, KC595305), GeMV (gentian mosaic virus, AB084453), BBWV2 (broad bean wilt virus 2, AF225954), PLPaV (peach latent pitting-associated virus, KY867751), BBWV1 (broad bean wilt virus 1, AB084451), GpSv (Gynostemma pentaphyllum secovirus, BK061325), YgSV (yucca gloriosa secovirus, BK061336), CVF (cherry virus F, MH998217), BRNV (black raspberry necrosis virus, DQ344640), SMoV (strawberry mottle virus, AJ311876), LSV1 (lettuce secovirus 1, KX925438), SDV (satsuma dwarf virus, AB009959), DMaV (dioscorea mosaic-associated virus, KU215539), SnLaSV (surrounding non-legume associated secovirus*,* MN412740), PSVA (pineapple secovirus A, MN809924), PSVB (pineapple secovirus B*,* OM777136), CLVA (chocolate lily virus A, JN052074), AcSv (Ananas comosus secovirus, BK061319), ALSV (apple latent spherical virus, AB030941), CuLV (currant latent virus, KT692953), CRLV (cherry leafroll virus, AJ621358), AVB (arracacha virus B, JQ581051), StPV (stocky prune virus, OP328252), AWPV (alpine wild prunus virus, OP328250), TgCV (Trillium govanianum cheravirus, BK013326), OcSv (Orobanche cernua secovirus, BK061327), ToTV (tomato torrado virus, DQ388880), ToMarV (tomato marchitez virus, EF681765), MYMoV (motherwort yellow mottle virus, KM229701), CoTVA (Codonopsis torradovirus A*,* NC035220), CsTLV (cassava torrado-like virus, OK040226), LNLCV (lettuce necrotic leaf curl virus, KC855267), CaTV1 (carrot torradovirus 1, KF533720), SCLSV (squash chlorotic leaf spot virus, KU052531), FbYMB (fleabane yellow mosaic virus, OL979630), LSMV (lettuce star mosaic virus, MT348706), PYFV (parsnip yellow fleck virus, D14066), AcYV1 (Actinidia yellowing virus 1, MN180070), PWaiV (persimmon waikavirus, LC488189), CamVA (camellia virus A*,* MW545173), PolV1 (poaceae Liege virus 1, MW289237), BCWVA (blackcurrant waikavirus A, MN701059), BnRV1 (brassica napus RNA virus 1, MH844554), RCaV1 (red clover-associated virus 1, MH325329), CNDV (carrot necrotic dieback virus, EU980442), MCDV (maize chlorotic dwarf virus, U67839), RTSV (rice tungro spherical virus, M95497), BVCV (bellflower vein chlorosis virus, KT238881), LWV1 (lettuce waikavirus 1, MY348710), RdSV (Rhododendron delavayi secovirus, BK061334), LycMoV (lychnis mottle virus, KR011033), SLRSV (strawberry latent ringspot virus, AY860979), SRCTaV (sweetbriar rose curly-top associated virus, MT757670), CoAv (cohombrillo-associated virus, OP019482), GSV (grapevine secovirus, OR947509), CiVA (Cirsium virus A, OP794358), MSV1 (Merculiaris secovirus 1, OR544056), PpSV2 (paris polyphylla secovirus 2, BK061331), BnSV (boehmeria nivea secovirus, BK061323), JaSV (jujube-associated secovirus, QNN26327), PpSV1 (paris polyphylla secovirus 1, BK061329), PMVA (Prunus mira virus A**,** BK064710)**,** CaPRV (Cattleya purple ringspot virus, OR439369), GysV1 (Gymnema sylvestre virus 1, BK062889), ChSV (chrysanthemum sadwavirus, OR413568), PhyTV (physalis torrado virus*,* MZ357184), PotRSV (potato rugose stunting virus, ON871624), BdMV (burdock mosaic virus, OQ087135), (Ajuga reptans waikavirus*,* BK062980), AdWV (Anacyclus depressus waikavirus, BK062979), CamVB (camellia virus B*,* BK062984), EdWV (Eleocharis dulcis waikavirus, BK062986), FhWV (Ficus hirta waikavirus, BK062987), JnWV (Juglans nigra waikavirus, BK062989), LcWV (Ligusticum chuanxiong waikavirus, BK062990), MpWV (Mertensia paniculata waikavirus, BK062991), PaWV (Populus alba waikavirus, BK062992), PrWV (Pedicularis rex waikavirus, BK062993), PvWV (Primula vulgaris waikavirus, BK062995), QrWV, Quercus robur waikavirus,BK062996), RcWV (Ranunculus cantoniensis waikavirus, BK062997), ThyWV (Thymus vulgaris waikavirus, BK062999), ToWV (Trifolium occidentale waikavirus, BK063000), TvWV (Thapsia villosa waikavirus, BK063001), ViWV (Viola inconspicua waikavirus, BK063002), CPBAV (carrot psyllid-borne associated virus, OM801008), HVA (hackberry virus A, OP533794), and PtWV (Pittosporum tobira virus, OR659471). The combined sequence of the three CPs from poliovirus (EVC, species *Enterovirus C*, NP\_041277, genus *Enterovirus*, family *Picornaviridae*) was used as an outgroup to root the tree.

**A chart of a virus

Description automatically generated with medium confidence**

**Figure 3.** Phylogenetic tree of the amino acid sequences of the conserved protease-polymerase (Pro-Pol) region (from the protease CG motif to the polymerase GDD motif) of the exemplified members of the 34 newly proposed species (identified by the full virus name and abbreviation) in the family *Secoviridae* and 111 representatives of the different genera in the family *Secoviridae.* The evolutionary history was inferred by using the Maximum Likelihood method and Le\_Gascuel\_2008 model [17]. The tree with the highest log likelihood (-57972.25) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (2 categories (+*G*, parameter = 1.7191)). The rate variation model allowed for some sites to be evolutionarily invariable ([+*I*], 2.96% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 147 amino acid sequences. All positions with less than 95% site coverage were eliminated, i.e., fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option). There was a total of 338 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [18]. Sequence accession numbers of type isolates of recognized species and of viruses proposed as type isolates of new species in the family *Secoviridae* are as follows: ToRSV (tomato ringspot virus, L19655), AnNVA (anemone nepovirus A*,* MH898479), SteNV (Stenotaphrum nepovirus*,* MZ325761), BRV (blackcurrant reversion virus, AF368272), GBLV (grapevine Bulgarian latent virus, FN691934), CawYV (caraway yellow virus, MK494273), BLSV (blueberry latent spherical virus, AB649296), SLSV (soybean latent spherical virus, KX424571), PRMV (peach rosette mosaic virus, AF016626), CLRV (cherry leaf roll virus, FR851461), AYRSV (artichoke yellow ringspot virus, AM087671), GNVA (grapevine nepovirus A, MT507290), MMMoV (melon mild mottle virus, AB518485), RpRSV (raspberry ringspot virus, AY303787), PoLNVA (poaceae Liege nepovirus A, MW289235), MMLRaV (mulberry mosaic leaf roll-associated virus, KC904083), AeRSV (Aeonium ringspot virus, JX304792), PBRSV (potato black ringspot virus, KC832890), TRSV (tobacco ringspot virus, U50869), GDefF (grapevine deformation virus, [HE613269](https://www.ncbi.nlm.nih.gov/nuccore/HE613269)), ArMV (Arabis mosaic virus, AY303786), GFLV (grapevine fanleaf virus, [D00915](https://www.ncbi.nlm.nih.gov/nuccore/D00915)), PCMoV (petunia chlorotic mottle virus, KX812815), BRSV (beet ringspot virus, [D00322](https://www.ncbi.nlm.nih.gov/nuccore/D00322)), RCNA (red clover nepovirus A, MG253828), TBRV (tomato black ring virus, AY157993), AILV (artichoke Italian latent virus, LT608395), GARSV (grapevine Anatolian ringspot virus, [HE774604](https://www.ncbi.nlm.nih.gov/nuccore/HE774604)), GCMV (grapevine chrome mosaic virus, [X15346](https://www.ncbi.nlm.nih.gov/nuccore/X15346)), CNSV (cycas necrotic stunt virus, AB073147), PVB (potato virus B, [KX656670](https://www.ncbi.nlm.nih.gov/nuccore/KX656670)), GSPNeV (green Sichuan pepper nepovirus, MH323435), ParNV1 (paris nepovirus 1, OP374158), HNVA (horse nettle virus A, OP292294), CwmSV (common water moss secovirus, OX380383), TfSV (tomato fern secovirus, OX380481), SfSV (shoestring fern secovirus, OX380465), APMV (Andean potato mottle virus, MN148891), TuRSV (turnip ringspot virus, GQ222381), CPSMV (cowpea severe mosaic virus, M83830), PvSMV (phaseolus vulgaris severe mosaic virus, MN837498), BRMV (bean rugose mosaic virus, KP404602), BPMV (bean pod mosaic virus, U70866), CPMV (cowpea mosaic virus, [X00206](https://www.ncbi.nlm.nih.gov/nuccore/X00206)), ArLV1 (Arabidopsis latent virus 1, MH899120), RCMV (red clover mottle virus, X64886), BBTMV (broad bean true mosaic virus, GU810903), SqMV (squash mosaic virus, AB054688), PepMMV (pepper mild mosaic virus, MK990555), GFabV (grapevine fabavirus, KX241484), PcSMV (phaseolus vulgaris severe mosaic virus, MN837498), PrVF (prunus virus F, KX269870), CuMMV (cucurbit mild mosaic virus, EU881936), LMMV (lamium mild mosaic virus, KC595304), GeMV (gentian mosaic virus, AB084452), BBWV2 (broad bean wilt virus 2, AF225953), PLPaV (peach latent pitting-associated virus, KY867750), BBWV1 (broad bean wilt virus 1, AB084450), GpSV (Gynostemma pentaphyllum secovirus, BK061324), YgSV (yucca gloriosa secovirus, BK061335), CVF (cherry virus F, MH998210), StPV (stocky prune virus, OP328251), AWPV (alpine wild prunus virus, OP328249), TgCV (Trillium govanianum cheravirus, BK013325), OcSv (Orobanche cernua secovirus, BK061326), BRNV (black raspberry necrosis virus, DQ344639), SMoV (strawberry mottle virus, AJ311875), LSV1 (lettuce secovirus 1, KX925437), SDV (satsuma dwarf virus, AB009958), DMaV (dioscorea mosaic-associated virus, KU215538), PSVA (pineapple secovirus A, MN809923), PSVB (pineapple secovirus B*,* OM777135), AcSV (Ananas comosus secovirus, BK061318), SnLaSV (surrounding non-legume associated secovirus*,* MN412739), CLVA (chocolate lily virus A, JN052073), ALSV (apple latent spherical virus, AB030940), CuLV (currant latent virus, KT692952), CRLV (cherry rasp leaf virus, AJ621357), AVB (arracacha virus B, JQ437415), ToTV (tomato torrado virus, DQ388879), ToMarV (tomato marchitez virus, EF681764), MYMoV (motherwort yellow mottle virus, KM229700), CoTVA (Codonopsis torradovirus, NC035128), CsTLV (cassava torrado-like virus*,* OK040225), LNLCV (lettuce necrotic leaf curl virus, KC855266), CaTV1 (carrot torradovirus 1, KF533719), SCLSV (squash chlorotic leaf spot virus, KU052530), FbYMV (fleabane yellow mosaic virus, OL979629), LSMV (lettuce star mosaic virus, MT348706), PYFV (parsnip yellow fleck virus, D14066), AcYV1 (Actinidia yellowing virus 1, MN180070), PWaiV (persimmon waikavirus, LC488189), CamVA (camellia virus A*,* MW545173), PolV1 (poaceae Liege virus 1, MW289237), BCWVA (blackcurrant waikavirus A, MN701059), BnRV1 (brassica napus RNA virus 1, MH844554), RCaV1 (red clover-associated virus 1, MH325329), CNDV (carrot necrotic dieback virus, EU980442), MCDV (maize chlorotic dwarf virus, U67839), RTSV (rice tungro spherical virus, M95497), LWV1 (lettuce waikavirus 1, MY348710), RdSV (Rhododendron delavayi secovirus, BK061334), LycMoV (lychnis mottle virus, KR011032), CoAV (cohombrillo-associated virus, OP019481), SLRSV (strawberry latent ringspot virus, AY860978), SRCTaV (sweetbriar rose curly-top associated virus, MT757671), GSV (grapevine secovirus, OR947508), CiVA (Cirsium virus A, OP794357), MSV1 (Merculiaris secovirus 1, OR544055), PpSV2 (paris polyphylla secovirus 2, BK061330), BnSV (boehmeria nivea secovirus, BK061322), JaSV (jujube-associated secovirus, QNN26328), PpSV1 (paris polyphylla secovirus 1, BK061328), PMVA (Prunus mira virus A, BK064709), CaPRV (Cattleya purple ringspot virus, OR439368), GysV1 (Gymnema sylvestre virus 1, BK062888), ChSV (chrysanthemum sadwavirus, OR413567), PhyTV (physalis torrado virus, MZ357183), PotRSV (potato rugose stunting virus, ON871623)**,** BdMV (burdock mosaic virus, OQ087134), AjrWV (Ajuga reptans waikavirus*,* BK062980), AdWV (Anacyclus depressus waikavirus, BK062979), CamVB (camellia virus B*,* BK062984), EdWV (Eleocharis dulcis waikavirus, BK062986), FhWV (Ficus hirta waikavirus, BK062987), JnWV (Juglans nigra waikavirus, BK062989), LcWV (Ligusticum chuanxiong waikavirus, BK062990), MpWV (Mertensia paniculata waikavirus, BK062991), PaWV (Populus alba waikavirus, BK062992), PrWV (Pedicularis rex waikavirus, BK062993), PvWV (Primula vulgaris waikavirus, BK062995), QrWV, Quercus robur waikavirus,BK062996), RcWV (Ranunculus cantoniensis waikavirus, BK062997), ThyWV (Thymus vulgaris waikavirus, BK062999), ToWV (Trifolium occidentale waikavirus, BK063000), TvWV (Thapsia villosa waikavirus, BK063001), ViWV (Viola inconspicua waikavirus, BK063002), CPBAV (carrot psyllid-borne associated virus, OM801008), HVA (hackberry virus A, OP533794), and PtWV (Pittosporum tobira virus, OR659471). The Pro-Pol sequence of poliovirus (EVC, species *Enterovirus C*, NP\_041277, genus *Enterovirus*, family *Picornaviridae*) was used as an outgroup to root the tree.

**Appendix: Annoted RNA1 and RNA2 sequences of Nepovirus mirae**

**>Seq1 [organism=Prunus mira virus A] Prunus mira virus A RNA1, complete sequence**

CTACTTCTCTATACGTGCTCTCGCACTTATCTCTAGTTTGAATCTCTATCTCTCGGTTATTCTGATTTGTTTCATTGCAAAGTTTATTGACTTTCCTTTTAATTGTTTTGAAAGTCTCCACGCAACATGGGTTTTGTTTGCCCTTCCCCCGGCTGTATCAACAGCCGGAATTCTTGGTCGCGTAAGGAATTACGCGAAGAACGTATCTTTGATATGCGTTGTCCCGCTCCTTTCTGTGGTGCCCTCCTCATCTCAAACACTCCTTCTCCCTCTGTTGCTCCCGTGGTGTGCGCCAAGCCTTTGGCCGCCACTATTCCCGTGGCGTGTGCCAAACCATTGGCCGCCACACAACCTCCTCGCAAGCAAGATTGCGAGGTTGTAGTTGAAGTAGGGTCTCCCGCCCTACTTTCTTTGACTTATCCCGCTCTGAGCGGAAGAACTCGCTTTCCCGGCGAGTTTGACGAGTCTCTCCTCGAGAGGCGCCCCTGCAGTGGGGGTTTTTTCCCTGCACCTTCCGGCTGGTCTAAGCCGAGGCAATCTGTGGAGATTGCTCCCAGGAAGGCAATCCCTTCCTGGCTTTCTGAAGCCCGCTCATTGTTGAAGCGGGCACTTTCTGGGTCGAATGCTTTCGGCCCCCGATACTGCCGGCAGACTATGCCGAGGGCCCGCATTTTGTGGGTCTATGGTCTTCTGATGAAGAAGGCCCCCATTTCCACTGCATTTAATATGCAGGTGAAGAAGAGCTTTTTAGCTCTTTCTGCTCGGATCGCCAAAGCTTTGGCGAAGAAACAAGCGCAGCGTGCTGCGCGCAGGCAGGATGCCTGCAAAAAAATCCGGATGGCCCGCTTCCAGGCCACCGGACTTGCTGCCTACGCTAGGCAGCAGGGGAAGCTCCAATCTGGAGCAGGAATTTACCGCATCGTTCTAGATGCGAAGAGGGTTGCTGGCCCTACTGCTAAATCCTCCCGCAAGAGGTCCGTCAAGAGAAAGACGGTTTGTAAAATTCTCCCTGCTCAACGTGAGCAGGTGTTTCCTGAGGGGTTTATTACCCCTGGTTTCTGGGAGTCATCTGGACTCCTTGCTGAGAAGAGGGTTCTACAGCCCTCTCCCTTTATTGTGCATACTGATGTGCACACCTCCGAGGTTCTGTCCTCTGAGGAATTCACTGTAGGTCCTAAGAGGGCCTACTTGGGGTTGGGGGCTCCTGCTCCGCGAATCCCGCAATCCTGTCACGAGGCTTTGTGTCTCTTGCAGGTTTCTGGTCTGTTTACTGACTATGAGATCTGCATGTTTACACAAGTTTGTGATGAGGGCCTCGACCAACCCGAGGTTTTCTTTAACGCGACTGCTCTAGTTACCTACTATGGGCAGGAACAAATGGTTGATGATTTTGCCTGCATTATTGCGGGTGATCTCCCTGAGAGCGTGTGTGCTGCTATTGCACATGATGCTGCGCAGCTTGATTTTTCTGCTGTCACTGCGTGTTGGCTTTCTGGTTTCGTCTCTGGAATCCGGAAATCTTTGAGGGAGTGGTTGGTGGACCCTGTGCTTACACGGTCATCCAAGTGGTGTGATACCATTGTGGATACTGTCAAGGGTCTGTTTGAAAAGTTCCTCGGGCCATACAAGAGAATTGTTGATGGCCTGTCCTATGTTGACTCCTTGTGGGGGAAATGTAAGACCTGGGCCCAGAATGTTTTGGCCGAGGGATCCAAAGTGTTTTCCGTCATGTGGGAAACGCACTGCATTTCTTTTGTGGTGATAATCGCATGCGCGTGTACAATATTGGTTGAGAACGTATTGTGCACGTTGGGGATTGTGCCTATGGTGGGCACTCTTACTGGTTTTGTTCTCTCTGCTGCCCTTGGAATTTTGGGATGTGGCAGTATTCTGGCTAAGTCTGAAGATATGGCACTTGTGTCAGTTTCTATTAAGACTTTTCTTGGGATTCTGTTGTGCCCACCCAACCTCCAGGGTGATGGACCGGGCCTAGATCTGAGTAGGCCCTTGGTTGCTGAAGATGTCCCAGCCATGTCGTGGACTGGTGTTGACCGAGTCTTATCTGCTCTTTCCTCTGTGGGAACGGGGCTTTGTGGATTCCGGGCTGATACCATTATCTATTGGGGACGGTTTGCCCAAGCTTTTGATTCTTTCAAGCGAGGGAAGGATGCTCTTTGTAGCATGGCTTCCTGGATCTTTGAAAAGCTTGGTGAAGTGTACAATCGCGTGACTGGGAAAGAAGCTGCTTTCTTTCACGAATTATCTACTCTGGTGGCGATTGACATACAAGGCTGGTTGAGGGATTCTCGGCGGGTTATTGCCGAGTCTGTTACTTTTGCGCTCACTGATTCCGTTGCCCTCACGACGGTTGAGCGTTTGATAAATGACGGCGAGACCATCCAGACCACTGCTGCTTCCACGCATAAGCAGCATTCCATGCAATTTGGTCAGATTCTTGCTGAAAGAATGCGTGAATTGAAGAAACTCCGGAAGGATATGGCACATGCTGGTGAGTTTGAAGGCCGTAGATGTACTCCTTTTTGGTTGTATGTTTATGGCCCATCTGGTTGCGGAAAGACCACCACCATGCATTCCATAACACAGGCGCTATTGCAGGCGTTTGAGTTCCCTTCCGATAGCTTCTGCTCCAAAAATCCAAAGGATGCCTTTTGGTCTATGTATAGGCGCCAAGCGCTTGTGCAAATTGATGACCTGGGTGCTGTTACTGAGAGTGGCCTTGAACAAGAAATGATGGCAGTGGTTTCATCTGCTTCCTACAATCCCACAATGGCCATTGCTGAGGACAAGACCACGCTGTTTGATAGTCGTTTTTTGGTGACTACTTCAAACTTCTACAGTGCTGGAACGGACGCCAAGATTGCGGATCGCACCGCATATAATCGACGGCGTAAAGTGGTTTTGAAAACGCGTCCTTGGCCCGGAAAAGAGTTCGATCCTGCACATTCAACGGATGCAGTGCAATTTGTGGTGGTCGAACGTGATGATGCAGCCCAGACACCGATCTGGTGCCAGAGTGGTGTGGCTCCTGATGATAAGGAGAAATACTGGATGGATTACCGAACAACCATGGCATATGTCGTGGAACAAGCGCGTATTCACCACACCAATGAGGATATTGAGCAGCGCCAATACATCATGTCTCACTCTCGCTCGCGCCAACTGTATCAAGTGTGTGAAAACTATCTTGATGAGGTTAAGGGTGATGTTGCTGAGTTCATACCTGGTGATCTTGTTGCTGCTAGAAATCTGGTGCCACAGGGGAGATTTTTCTTCTCGTGTGTTGATGGGCGGGCTTACTCCTACGATGCTTCCAGAGTAGCCCACGATGAAGGTCCAGTTGATCCTAGACTCAATTTTGAGCAAAACTGCCTGGACAAACTCTCCTATACAATCCAAAAGCAGATCCAAGGGGGTCCCAAAAGTGCCACTGCTGGTATTTTTCTGCGCTCCATGGTTTCTGGGGAATGTGTGGTTGAAAGTGTTTCCAAGCTCAATTCTACTGCGAGCAAGGAACATAATCTTTTTTTCCATACTCTTCCTTTGGCTGACCGCGTTTATCTGCGGTTGGTTCAGAAGAAGGTTCTCCAGATTTCCATGTGTGGTGACCCGTTAGGCGTGCGTTCCTATAATTGCCTCATGGACGCTTTTAGCGTATCTTACACTTACGTGAAAGAGAATGGAGGCCGCCTATTACTCATTTTGGTCAGTTGTATGCTCCTGGCTTTGGCATGTTATACTTTTTTCAACTGCTTGGCCACTATTTTAGGAGGTACTTCTGTTGCCGCTGGTGCTGCTGCAATGATGAATATTGAGGCTTGTGCGAGTACTTCTGTGTATTCGTCCGAGTACGGTGAGAGAATGCAGCGGCGAAATATGCCCCACAGGAGCAGAAATGTTCCAGCTGTGTGGGGGGAAGAAACTGGGTACGACAATAAATGGCAGTTGTGTGGTTTTCTGAACACGACTCGATCTGATATGCCAGTCGTACACGTGAATTTGGTTCCGGGGAACAAATTTGCGATAACAAAACATCAAGCTAAGGCTATCCCCGAGGGCTCCACTGTGGGCCTGAATTTCCCAGGACACATCTACCGTACTTTTAGGTGGGTGTACTCGGCAATTGAGGAGTTTGAACAGAGTGAAATTTGTTTTTACTTCGATGCTATTGTACCAAGTTTGTCTAAGCAAATGGCTAAAGTCTATGCTCATGCGGATTTGGACGCTTTGGCAGTGAAGTATTTTGAGACTCGAACTCTTCATCTTGGTCTCCAGAAAGACGAAATGACCAAGCGCCACTGGGATGCAAGTGCGACGGTATTATATACCCCAAAAACCATTGTTTCTACCATCAATGGGGTAATATATCGCCAGGAGATACCAACCTCCATCACCTACAAGCGCAATTCTGTGAAGCATGATTGTGGTGCGCTTGTTTTTACTGAGGTGAAGGGCCAACCCATGGTTGTTGGTATGGTCGTTGGATGTCTTGATGGAACTACGTATGTGTGTAAATTTCCAGAAGTGCGCTATGAAGTTCATGCGTGCGTTCCAGAAATACGTGGTTTCAACTTGGAAAGTGGAGTTTCTACCATGGGATACTCCAAACTCGGGTGGATCGATAGGAGGCACCAACCGCATAACTCTGAAAAGAGTGAATTTGTGCCCATTCCCGAGGATAAACAGATGCAGGGGGTTTCGTGTAAGTCTCCTGCGATTTTGAGCGCAAAAGATCCGCGCTTGACTGAAAGGCCCAATTGTGCTGGCTACGATCCCTACAAGGATGGTATGGCCAAATTTGCTGCACCCATGGCCGACATTGACCAAGGACTCCTCGACATTGTGGCTGATGAAATAGCACAGGAGTTTTTGGATGCTGGAGTTAACGGACGTATGGTGTCATCTGATGAAATGATAAATGGACATCAACGTTTGCATCCTATCACACCATTCTATGTCGAGAATGCTGATTCCGCTACTTTGAATGAATTTAGAGCGGAGTGTGATACTGAGGTTTGGTCCGTGGGGGGGCCACCTGCTGAATTTGAGTACCCCTACATTTCCCGCCCTCTTGAGGGTAAATCCAAATGGTTCTGCGACCACCTTTGCCAGGGGCAGGATATTGAAGGCACTTCTGTGTTGGACATTTCCGTTTTTGTCAAGAAGGTTGAACGGTGTTGTGAGGAAATTTTCTTCGATCCTATTGATCTCACAACTTCCGAGGGTTATCCTCTCTTCCTCGATCGCCCTGCGGGTGAGAAAGGGAAAGAACGTTTCTTCTCTGGTGATGCTGGTCAAAAACAGCTCATTCCTGGTAGTGCACTTGCGGTGCTACTGGAGAATGGTCACAAGGAAACGTGTGAAGGCACTCCGACTATCATTATCAAGGAGAGTGCCAAGGATGAACTCCTGAAAGAGAGCAAGGTGCTACCTAGCACCGGAAAACCTGGGACACGATTATTTTCTATTTGTCCTGCTTGGTACAATCTGCTCGTTCGCCAACAATTTGTGTATGTTGCGGAAAAAGTGCGGCGGAAACGGAAAGTACTATGTAGTCAAGTGGGAATTGTCGTTGGTTCCAGGGAATGGGATGATTTGGCCATGCGCTTAAGGTCGAAGAAGAACAGTGATTTATATTGCTGTGATTATTCGAAATTTGATGGACTGATGACTCCTCAGGTTATGCTTGCGATTGCCAACATCTACAACAGAATGTATACGGGCAAGGATGGTATGAACCAGTATAGGATTAATCTCCTTATGGGTCTAACTAACCGTTTGTCTATCTGTGGTTCGCAAGTGTATCGCGTCGGAGCGGGAATTCCTTCGGGGTTTGCTTTAACTGTAGACATCAACTCTATCTTTAACGAGATTTTGGTTCGATGCGCTTACAGATCCCTGGTTCCCGAGATAGAGCGTCCCTTCTTCTCTCGAAATGTTGCCCTGGTTGTTTATGGCGACGACAATGTCTTTGGTGTGCATCCAAATGTTTCATCTGTCTTTAATGGCAATGCACTCAAGACGTTTCTTCGAGAGGAGTTCTCAATCCAAATCACTGATGGGGCTGATAAACTGAGTCCAGTTATCGAGGCGCGTCCGCTTGAACAATGTGAATTTTTGAAGCGCGCCTGGGTTTTGGATAAACAGTACGGACTATTTAGGGCCCCATTGGTGGAAACAAGCATATACTCGTGCCTCAAGTATGTGCGACAACAGAACTTCGACTGGACTATGCCTTTGTTGCAAAACGTCCAGGGGAGTCTTTATGAGGCAAGCCTCCACTCTCGAGAGATGCATGAAAAGATCTATCGCCACTTTGCGCATCATTTTCCAAAGTGGGTACAAGATCGAGAGTTGGACACCTATGAACAGTGCCGAGTGCGATTTATCGCTGCAAAGAATGGGCAGTTTGACTTTCATCCTGCTTCCGCCCAGCTCGGTCATGTTTTCTCCCAACAACCTGAGGTCCAAAGCCTAGCCTCAGGCCAAAATCCAAAAAGAACATATCAGCTCACTGGGAAGTTGTATGTTTGTGCTTCTGGCCACAACGAACCTGAGTGTTTTTATGTGGATGTGCGCTCTAAAGCCCAGATTTTTAAGGGTAACGGAGTTCATGTTCCTCCTCGTTTTGGGAGTGGTTCAGGTCAGATAGCCAGTGTTAAATGGGCTACCAGCTTCCGCTCTTCCAAAGGACTGCCTTGCCGTGATGAAATTTTTGAGGCATACAAGTTGGGCAAATGTATTTACTTCCGTGATTCTGGGGAGTGTATAAATGCTTGGCTTGCTGCCATCAATTTTGGTTGGTCGGTTGGTGCTGATGGGTTAGACGGGTTGTTGCAGCGATATCGGTCTTTGGGACCTTCGCATGTTAATGATTTGTCTTACTACTTTGAAGGAGGAGTGGCTGGGATCAAAGGGCCTCCACTGGTTAAATGTTTTAACATTGATCCAGTTGCTGCGAGTCGTGTCTGTCCAAAAACCACATTTGAGAAGGCAGTCGATTTGCGGCCACAGCATAATGTGAATGCGGCCGGGCAAGTGCAGAATGCGCTTTCACGAGCCAGTGAGGCAGTCCTAGTTTATGCTAAGGACAGTGCCAAATGCTGTGTGGGGCTGAAATGTGGTGAGCAATGTCTTGGGCACAAATCAACGATAAATGTTGTGGCGGGTAGTCCCTACAACGAACGTGCCATGCTCACTGATGTGTTCAGGAGAGGATGTTTCTCACTCACTGAGTGACATTCCCTTCTTTTATCTTTTCTTTTACTTTGCTTTAGGCTACCACTGTTTGGCAGAGTGAGGGCTAGTTTCGCCTAGAAGGAAACAATCCCAAAATCCAAAGTTGTATGGCATTCAATAGGAGGATACTATATGTTCCGTGAAATCGGTAATGAGTCAGACGCTAAACTCTGTGGCTGCTAGGGAGGCAGAATGAAACAGATACCATGAAGCCCATGGTTCCGTGAAATCGGTATAACGTAGTTCGCTCAAACTCTTCCTGGAAGAATGCGCAACAGGACTTCGGCTCCGTCTTTAAACGAGCTAACTAAAGCTGTTTCCAAGTGAGTATTTAATGTACACTTGGAGCCTCTAGGGAGGTGAGATGCCCTTTAGGTTCAGCGGCCAGCGTTCTGGGTTTCCAGGCATGGTGACATGTTACCAACACGACTTGCATAGTGAAAGTCAAGTGTTCGCTTTGAGAGAGTAGTTATCTTCTCATTTATGCTTTTAATTCTGTGTGTTTATTTTCTCGCAGCTCCTGTTTTGCAGGTCGAACCTTCAGCAAGTTCACAAAAATATGCATTTTTCTTTTATTTCCTGTCTTTATGGTTT

**Prunus mira virus A RNA1-encoded polyprotein with the demarcation Pro-Pol sequence highlighted**

MGFVCPSPGCINSRNSWSRKELREERIFDMRCPAPFCGALLISNTPSPSVAPVVCAKPLAATIPVACAKPLAATQPPRKQDCEVVVEVGSPALLSLTYPALSGRTRFPGEFDESLLERRPCSGGFFPAPSGWSKPRQSVEIAPRKAIPSWLSEARSLLKRALSGSNAFGPRYCRQTMPRARILWVYGLLMKKAPISTAFNMQVKKSFLALSARIAKALAKKQAQRAARRQDACKKIRMARFQATGLAAYARQQGKLQSGAGIYRIVLDAKRVAGPTAKSSRKRSVKRKTVCKILPAQREQVFPEGFITPGFWESSGLLAEKRVLQPSPFIVHTDVHTSEVLSSEEFTVGPKRAYLGLGAPAPRIPQSCHEALCLLQVSGLFTDYEICMFTQVCDEGLDQPEVFFNATALVTYYGQEQMVDDFACIIAGDLPESVCAAIAHDAAQLDFSAVTACWLSGFVSGIRKSLREWLVDPVLTRSSKWCDTIVDTVKGLFEKFLGPYKRIVDGLSYVDSLWGKCKTWAQNVLAEGSKVFSVMWETHCISFVVIIACACTILVENVLCTLGIVPMVGTLTGFVLSAALGILGCGSILAKSEDMALVSVSIKTFLGILLCPPNLQGDGPGLDLSRPLVAEDVPAMSWTGVDRVLSALSSVGTGLCGFRADTIIYWGRFAQAFDSFKRGKDALCSMASWIFEKLGEVYNRVTGKEAAFFHELSTLVAIDIQGWLRDSRRVIAESVTFALTDSVALTTVERLINDGETIQTTAASTHKQHSMQFGQILAERMRELKKLRKDMAHAGEFEGRRCTPFWLYVYGPSGCGKTTTMHSITQALLQAFEFPSDSFCSKNPKDAFWSMYRRQALVQIDDLGAVTESGLEQEMMAVVSSASYNPTMAIAEDKTTLFDSRFLVTTSNFYSAGTDAKIADRTAYNRRRKVVLKTRPWPGKEFDPAHSTDAVQFVVVERDDAAQTPIWCQSGVAPDDKEKYWMDYRTTMAYVVEQARIHHTNEDIEQRQYIMSHSRSRQLYQVCENYLDEVKGDVAEFIPGDLVAARNLVPQGRFFFSCVDGRAYSYDASRVAHDEGPVDPRLNFEQNCLDKLSYTIQKQIQGGPKSATAGIFLRSMVSGECVVESVSKLNSTASKEHNLFFHTLPLADRVYLRLVQKKVLQISMCGDPLGVRSYNCLMDAFSVSYTYVKENGGRLLLILVSCMLLALACYTFFNCLATILGGTSVAAGAAAMMNIEACASTSVYSSEYGERMQRRNMPHRSRNVPAVWGEETGYDNKWQLCGFLNTTRSDMPVVHVNLVPGNKFAITKHQAKAIPEGSTVGLNFPGHIYRTFRWVYSAIEEFEQSEICFYFDAIVPSLSKQMAKVYAHADLDALAVKYFETRTLHLGLQKDEMTKRHWDASATVLYTPKTIVSTINGVIYRQEIPTSITYKRNSVKHDCGALVFTEVKGQPMVVGMVVGCLDGTTYVCKFPEVRYEVHACVPEIRGFNLESGVSTMGYSKLGWIDRRHQPHNSEKSEFVPIPEDKQMQGVSCKSPAILSAKDPRLTERPNCAGYDPYKDGMAKFAAPMADIDQGLLDIVADEIAQEFLDAGVNGRMVSSDEMINGHQRLHPITPFYVENADSATLNEFRAECDTEVWSVGGPPAEFEYPYISRPLEGKSKWFCDHLCQGQDIEGTSVLDISVFVKKVERCCEEIFFDPIDLTTSEGYPLFLDRPAGEKGKERFFSGDAGQKQLIPGSALAVLLENGHKETCEGTPTIIIKESAKDELLKESKVLPSTGKPGTRLFSICPAWYNLLVRQQFVYVAEKVRRKRKVLCSQVGIVVGSREWDDLAMRLRSKKNSDLYCCDYSKFDGLMTPQVMLAIANIYNRMYTGKDGMNQYRINLLMGLTNRLSICGSQVYRVGAGIPSGFALTVDINSIFNEILVRCAYRSLVPEIERPFFSRNVALVVYGDDNVFGVHPNVSSVFNGNALKTFLREEFSIQITDGADKLSPVIEARPLEQCEFLKRAWVLDKQYGLFRAPLVETSIYSCLKYVRQQNFDWTMPLLQNVQGSLYEASLHSREMHEKIYRHFAHHFPKWVQDRELDTYEQCRVRFIAAKNGQFDFHPASAQLGHVFSQQPEVQSLASGQNPKRTYQLTGKLYVCASGHNEPECFYVDVRSKAQIFKGNGVHVPPRFGSGSGQIASVKWATSFRSSKGLPCRDEIFEAYKLGKCIYFRDSGECINAWLAAINFGWSVGADGLDGLLQRYRSLGPSHVNDLSYYFEGGVAGIKGPPLVKCFNIDPVAASRVCPKTTFEKAVDLRPQHNVNAAGQVQNALSRASEAVLVYAKDSAKCCVGLKCGEQCLGHKSTINVVAGSPYNERAMLTDVFRRGCFSLTE

**>Seq2 [organism=Prunus mira virus A] Prunus mira virus A RNA2, complete sequence**

TCTCTACCTCTCTATACGTGCTCTCGCACGAATCTCTGGTTACGAATCTCTATCTCTTTTGATCTCCATCTTTGACACAGTCCTGCCTGAGCTTTGTTGTTTTGATTTGTTTCACTGTAAAGTTTACAAATTTTCTTTTAATTGTTTAAAAATTTGTGTGTTTTGAGGGTCCTATGGATCCATTCGCTGGATTCTCCATGTGTGCGCGCATGGTTCACACCAGGCTGGCTTGCCAGCTTGGTTCTGAGCCAGGCCGTCGCCTTTCTTCCCCCCTCTTCCCGGAGCTTTCTAAGCTGCTCATTGAGCAGCAGATGGAAGTTCTTGTTACTTTTGACCTGCCTCTCAATGGTATGGTCACTCCTGGAGTTGTTGAGCAGCTCCAGGATGCTGAAGACGAGCTTGTTGCCGCTCGTCGACGACTCATGGTCGAAAGACTGGAGTCGATGCAATCGGCAACTCGCTGCCCCACGCTTGGGGAATGCATCTATTACGATGCACCTGGTGTAGACCAGGAAACTGCTGAGCTTCAAGACGCGCTTGAGGCCCCAACCCCTGACTGGTGGTTGGAGAAAATTAGGCCCTTGTGGCCCAAGGATGATTACTTTCGTGATTGTCTAGCCGGTCCATACCCTGAGGATTATGGCGATATACCTCTGGGATGTTTTGATGAATTGTTCGCTGCTTTCGATGCTATGGTTGAGGAGCATTGGGAGAGTGTCTACTCAACCCATTTTGAATCGTTGTTTGGTGATTCCTTTTATGAGGAAGAACCATATGATATGTTTGAAATGTGTGTTAACTCCGCAGGTAGTCTGATCCCTGCGTGTATGATGGCTGATTCCCATATTCAGCCTACTGGCCACCGAGCAGATGATGCGAGTGCACGGCAGGACTTTGCAGATTCTTCTGACTCTTTACAGAGTATGGGAGATTTCTGGAAGTCCTTCTACGCCAAAGAGTCCGGAAAGAAGATTAAGGATTCGCACATCTCTCGCATTGCTGACAATCCCAACAAAGTTGGGTTCACAAAGAGTGCTATCTTTCATAAGGTGCCTCTCTCTGAGCAAATGGCCAACTCTTGGTCCCGAATGCGCGGGAAAGAGGATAAAGAATCAGCAGTGAAGGTTACTATGGAATTGAATGTCCAGAAGTATACTGTTCGCATGCCTGATGCGGTCCGGACGAGTGAAGGTCCTCTTTTTATAGAGTGGATCAATCTTCCCCGGATGACTGAAGAAGGAGCCCGCAAAATTGCTGAAGCGGGCTGGAACAACGCCAACATCTGTGGCGTTGATCTTGGGATCAAGTCACACGTGGCTGTGGGAACTCAAGTTCGTGCAATTATTTCCGTCATAGATGGAGCCTGTACGGACCTGCCTACCGCGACTATGTGTGCTTTTGAGATCAACTTGGCGAGTCAGAACAATCGGTCATTAAATCTGCCTCTTATTAACTTGCCATTTTCATCTCTTCTGAATGACATGCATTATTTTCAAAATCGTATCAAAATTGCATGCCAATTCAGAGATCCTGAGGGTTTTTCCCCGTCCACTCCTATGTTCAGCTTCTCTTCCTTGGAGTTTTCCGAAATGACTCAAACTGCTTTCGAGCGTGAGAGTCTATTGAGGGATTCCTGGTCTGAAATTGAAAAGAGGGCTTGCCATGGTGGTGGTAGATGTGTCGCTTCCCAAGGTGTTGTGCAGACCTGGGAAAAGGAGGTCAATCCTCCTCTGAAAGAGTATCCTGCACTTGTCCTGCCTCCACCTCCTGCTCCAATGCGCAATTTTATTGATGCTCAGAGTGGTCAGGTGGTTAAAAACGCTATCTCAAAATCGAGGAGCATGCGTTACCAATCCCCACATGAATTGTGGGCTCGTCCTTCTGTAGATGGGGGATCAACATCTGCCAAACCTCCCGGAGACAATCTCCGATGCTCTAATGTTCCAGGGTGTGCCTATGAGGTTGATCCTTTACATTTGTTGTACTATGAGGTACTAACAATTCCTAAGGACGCCTTAGAAGGTACACTGATTAAGAGGTTTGACATTCGAAAGCAGGGAGCAGCGTTGGATTCACCAGTCTGGCGCAATTGGGTCAAAGACGGAGCCATGAAACCTAAAATCCAAATCAAAATTACAATGGCAGGCTCTGTCTTTTCTGGCATTTCCGTTGGATGTGCCTTTGACGCGTATAGACGTGTTGATCCCAAGCTTACTACAGGGCTGAGTGCTACATTGCTCATGGGCTTGCCAGGTAAAATCTGGCATATGCGTGAAAGTGAGGAAGTTACATGGGAGCTGGATCTTTCTCAAGTGTGTGGACATACGTTCTACGCTCTTGACGATAGTCTGGCAGCTATGGATTTTCTCTTCTATATTGCCCGTGGCAATGAGCTTACCTCTGCTGCTGATTGGCAGGTTTACGTGGCTTTTTACGTTGACTGGTCTCAAGAATCTTTTGAGACTACTTTAGCGCCTACGTTAACCTGGCCACCCCAACCAACTCTGGCCTCCACATTTTCTGAATTGCGCGGGCCTTACTCCTTTGATCTAGCTGGGACTAATAAGTCTGTTGATATAGGGTTTCTCCCTGGTACCAGCGTTTCTATTGGGGGTAAGGTTGTGCGCACATTTAATAGAGTGGTTGCGGCCCACTACCGGTCCTGGACCGGTAAGATCAGGATGAGCATTGAACTGGCATCATCCATTTTCATCACAGGTTCTTTCTGTGTTGGAGTGGATTGGAATGCGAAACCCGACTTCGATGACATGTTAAAGAAAAAACATTGGATCGTCAAGCCTGGGGAAATTTTTGATCTTGATCTGTATGGGCCCTATGGGGAAAATCCAACTGCTGCGGGTCAGTTCACGGGAAAGCCTCATTTAGCGGTCTTTCTTCTTGGAGGAATTGTTGCGCCTAAAGACTCGGTTGGCTCACTCGGTTTCTTTGTCAGAATCCATGAGTTGACTGGTATTTATAAGAACCCAGTCTTGCGTACCGATCGGACTGATCGTGGCATAGCATGGTTTCGGGTTACCAATATCCAAGATGATAACCTGGTTTTTAATGTACCAGGACAGATCGTTGATTTGACAGGGGTGAGTGGCAGTCATGATATTACAAATTATGCCAACCCTACTAGTCTGCTTTTCTCTGTGACTGGAATGCATGGAGGAGTCATCCGTCTCTATGTAACGTGGAGCCCTGTTGGCAAGTTGGGCGATTGTGATGCCAGCATTAAATACATGCAATTTTTGTGGCACACGCCTACCGAAAATTACTATGGTGATCAAGGTACTCGTGGTCTCATTGATATGAATGGATTTTCTGTTGATGTCCGGTGTGGTACTTTTTTTGGTGCTACTAAACCCAACGATGCTCTGGATGTGGAGAGAGTGGCCTTCTACCTGACCAATGGAAAGAAGATCCATGAGATACGTGTTTCATATGAGATACTATCCATGGAATTTTATGGTAGGACCACTTATATCCGTTAAAGACTTCGGCTCCGTCTTTAAATGAGCTAACTAAAGCTGTTTCCAAGTGAGTATTTAATGTACACTTGGAGCCTCTAGGGAGGTGAGATACCCTTTAGGTTCAGCGGCCAGCGTTCTGGACTTCCAGGCATGGTGACATGTTACCAACACGACTTGCATAGTGAAAGTCAAGTGTTCGCTTTGAGAGAGTAGTTATCTTCTCATTTATGCTTTAAATTCTGTGTGTTTATTTTCTCGCAGCTCCTGTTTTGCAGGTCGAACCTTCAGCAAGTTCACAAAAATATGCATTTTTCTTTTATTTCCTGTCTTTATGGTTT

**Prunus mira virus A RNA2-encoded polyprotein with the demarcation CP sequence highlghted**

MDPFAGFSMCARMVHTRLACQLGSEPGRRLSSPLFPELSKLLIEQQMEVLVTFDLPLNGMVTPGVVEQLQDAEDELVAARRRLMVERLESMQSATRCPTLGECIYYDAPGVDQETAELQDALEAPTPDWWLEKIRPLWPKDDYFRDCLAGPYPEDYGDIPLGCFDELFAAFDAMVEEHWESVYSTHFESLFGDSFYEEEPYDMFEMCVNSAGSLIPACMMADSHIQPTGHRADDASARQDFADSSDSLQSMGDFWKSFYAKESGKKIKDSHISRIADNPNKVGFTKSAIFHKVPLSEQMANSWSRMRGKEDKESAVKVTMELNVQKYTVRMPDAVRTSEGPLFIEWINLPRMTEEGARKIAEAGWNNANICGVDLGIKSHVAVGTQVRAIISVIDGACTDLPTATMCAFEINLASQNNRSLNLPLINLPFSSLLNDMHYFQNRIKIACQFRDPEGFSPSTPMFSFSSLEFSEMTQTAFERESLLRDSWSEIEKRACHGGGRCVASQGVVQTWEKEVNPPLKEYPALVLPPPPAPMRNFIDAQSGQVVKNAISKSRSMRYQSPHELWARPSVDGGSTSAKPPGDNLRCSNVPGCAYEVDPLHLLYYEVLTIPKDALEGTLIKRFDIRKQGAALDSPVWRNWVKDGAMKPKIQIKITMAGSVFSGISVGCAFDAYRRVDPKLTTGLSATLLMGLPGKIWHMRESEEVTWELDLSQVCGHTFYALDDSLAAMDFLFYIARGNELTSAADWQVYVAFYVDWSQESFETTLAPTLTWPPQPTLASTFSELRGPYSFDLAGTNKSVDIGFLPGTSVSIGGKVVRTFNRVVAAHYRSWTGKIRMSIELASSIFITGSFCVGVDWNAKPDFDDMLKKKHWIVKPGEIFDLDLYGPYGENPTAAGQFTGKPHLAVFLLGGIVAPKDSVGSLGFFVRIHELTGIYKNPVLRTDRTDRGIAWFRVTNIQDDNLVFNVPGQIVDLTGVSGSHDITNYANPTSLLFSVTGMHGGVIRLYVTWSPVGKLGDCDASIKYMQFLWHTPTENYYGDQGTRGLIDMNGFSVDVRCGTFFGATKPNDALDVERVAFYLTNGKKIHEIRVSYEILSMEFYGRTTYIR