

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create 53 new species and abolish three previously recognized species in the family *Secoviridae* (*Picornavirales*) |
| **Code assigned:** | 2025.017P.Ac.v3.Secoviridae\_53nsp\_3abolishsp | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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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** |
| *Secoviridae* | 7 | 0 |  |
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| **Submission date:** | 04/06/2025 |

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

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| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
| The EC voted Ac for this proposal (see the table above for explanation), to allow very minor revisions mainly concerning style issues. Please note that in Figure 2A, *Mersevirus* is duplicated. If possible, genus names should be italicized in the figures. |

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

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| **Response of proposer:** |
| The points raised by the EC are well taken. Thank you very much for the comments. Style issues have been addressed, figure 2A has been improved and the genus names have been italicized in all the figures in the revised version of the taxonomy proposal. |

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| **Revision date:** | 18/08/2025 |

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

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

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| All taxa | Latinized epithets are mainly derived from the host name or geographic location |
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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genera *Comovirus*, *Cheravirus*, *Fabavirus*, *Nepovirus*, *Sadwavirus*, *Stralarivirus*, *Torradovirus*, *Sequivirus*, *Waikavirus* in the family *Secoviridae*  *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 two new species in the genus *Comovirus:* “*Comovirus caricae*”*,* “*Comovirus cardaminis*” * Create three new species in the genus *Cheravirus:* “*Cheravirus lagerstroemiae*”*,* “*Cheravirus corymbii*”*,* “*Cheravirus pternopetali*” * Create five new species in the genus *Fabavirus:* “*Fabavirus phipiperis*”*,* “*Fabavirus camphorae*”*,* “*Fabavirus reaumuriae*”*,* “*Fabavirus multiflorum*”*,* “*Fabavirus squamellariae*” * Create 25 new species in the genus *Nepovirus:* “*Nepovirus alphacucumis*”*,* “*Nepovirus thymi*”*,* “*Nepovirus paeoniae*”*,* “*Nepovirus chrysanthemi*”*,* “*Nepovirus pinnatifolium*”*,* “*Nepovirus glycyrrhizae*”*,* “*Nepovirus pholismae*”*,* “*Nepovirus berberidopsis*”*,* “*Nepovirus silenis*”*,* “*Nepovirus galax*”*,* “*Nepovirus saururi*”*,* “*Nepovirus musae*”*,* “*Nepovirus cenchri*”*,* “*Nepovirus hypolepsis*”*,* “*Nepovirus pogonati*”*,* “*Nepovirus begoniae*”*,* “*Nepovirus caladeniae*”*,* “*Nepovirus astragali*”*,* “*Nepovirus gentianae*”*,* “*Nepovirus leucadendri*”*,* “*Nepovirus yunnanense*”*,* “*Nepovirus rhododendri*”*,* “*Nepovirus hanseniae*”*,* “*Nepovirus beldersayense*”*,* “*Nepovirus jasmini*” * Create two new species in the genus *Sadwavirus:* “*Sadwavirus kappananas*”*,* “*Sadwavirus morifolii*” * Create two new species in the genus *Stralarivirus*: “*Stralarivirus beldersayense*”, “*Stralarivirus* *scaevolae*” * Create four new species in the genus *Torradovirus:* “*Torradovirus rorippae*”*,* “*Torradovirus ophistopappi*”*,* “*Torradovirus lophophyti*”*,* “*Torradovirus sesami*” * Create one new species in the genus *Sequivirus:* “*Sequivirus primulae*” * Createnine new species in the genus *Waikavirus:* “*Waikavirus convallariae*”*,* “*Waikavirus euphorbiae*”*,* “*Waikavirus swalleniae*”*,* “*Waikavirus gentianae*”*,* “*Waikavirus lycopi*”*,* “*Waikavirus pagodae*”*,* “*Waikavirus heveae*”*,* “*Waikavirus artemisiae*”*,* “*Waikavirus duoplantae*” * Abolish two previously recognized species in the genus *Nepovirus: Nepovirus americaense, Nepovirus australiense* * Abolish one previously recognized species in the genus *Waikavirus: Waikavirus anthrisci*   *Justification*:   * The creation of the proposed new 53 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*. * The abolishment of three previous recognized species (*Nepovirus americaense, Nepovirus australiense, Waikavirus anthrisci)* is justified based on a lack of sequence information. |

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| **Text of Taxonomy proposal:** |
| 1. *Taxonomic rank(s) affected*: Genus *Comovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Comovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 19 species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Comovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The coding-complete genome sequence of papaya comovirus (PCV) was determined from papaya trees in Mexico by high-throughput sequencing [2]. The coding-complete sequences of RNA1 and RNA2 of PCV isolate PCV-1.PC-W are 6,268 nt (MN203153) and 3,448 nt (MN203152) long, respectively. The genome organization of GSV is similar to that of other members of the genus *Comovirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of PCV have 65.01% and 77.15% amino acid sequence identity with pepper mild mosaic virus (PepMMV, a member of the species *Comovirus capsici*), the closest related virus in the genus *Comovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of PCV and representative members of the family *Secoviridae* confirm its clustering in the genus *Comovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify papaya comovirus (PCV) as a member of a novel species named *“Comovirus caricae”* in the genus *Comovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Comovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Comovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 19 species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Comovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of white-flower bittercress comovirus (WfbCV) was determined from *Cardamine leucantha,* a perennial Brassicaceae*,* by mining publicly available plant transcriptome datasets [3]. The coding-complete sequences of RNA1 and RNA2 of WfbCV isolate Car leu are 5,972 nt l (BK065040) and 3,562 nt (BK065041) long, respectively. The genome organization of WfbCV is similar to that of other members of the genus *Comovirus* in the family *Secoviridae* (Figure 1). The two CPs and the conserved Pro-Pol region of WfbCV have 68.26% and 78.34% amino acid sequence identity with Arabidopsis latent virus 1 (ArLV1, a member of the species *Comovirus arabidopsis*), the closest related virus in the genus *Comovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of WfbCV and representative members of the family *Secoviridae* confirm its clustering in the genus *Comovirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify white-flower bittercress comovirus (WfbCV) as a member of a novel species named “*Comovirus cardaminis”* in the genus *Comovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Cheravirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Cheravirus* belongs to the family *Secoviridae* and consists of eight species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Cheravirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Lagerstroemia indica cheravirus (LaiCV) was determined from *Lagerstroemia indica,* a flowering plant of the family *Lythracea,* by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of LaiCV isolate Pogostemon are 7,272 nt (BK065034) and 3,633 nt (BK065035) long, respectively. The genome organization of LaiCV is similar to that of other members of the genus *Cheravirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of LaiCV have 49.82% and 69.74% amino acid sequence identity with alpine wild Prunus virus (AWPV, a member of the species *Cheravirus alpinum*), the closest related virus in the genus *Cheravirus* of the family *Secoviridae*. ML phylogenetic trees generated using the three CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of LaiCV and representative members of the family *Secoviridae* confirm its clustering in the genus *Cheravirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Lagerstroemia indica cheravirus (LaiCV) as a member of a novel species named “*Cheravirus lagerstroemiae”* in the genus *Cheravirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Cheravirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Cheravirus* belongs to the family *Secoviridae* and consists of eight species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Cheravirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Corymbium villosum cheravirus (CvCV) was determined from *Corymbium villosum,* a flowering plant of the family Asteraceae*,* by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CvCV isolate Cor vil are 7,232 nt l (BK065028) and 3,700 nt (BK065029) long, respectively. The genome organization of CvCV is similar to that of other members of the genus *Cheravirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of CvCV have 26.82% and 62.02% amino acid sequence identity with stocky prune virus (StPV, a member of the species *Cheravirus pruni*), the closest related virus in the genus *Cheravirus* of the family *Secoviridae*. ML phylogenetic trees generated using the three CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of CvCV and representative members of the family *Secoviridae* confirm its clustering in the genus *Cheravirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Corymbium villosum cheravirus (CvCV) as a member of a novel species named “*Cheravirus corymbii”* in the genus *Cheravirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Cheravirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Cheravirus* belongs to the family *Secoviridae* and consists of eight species.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the genus *Cheravirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Pternopetalum trichomanifolium cheravirus (PtCV) was determined from *Pternopetalum trichomanifolium,* a flowering plant of the family Apiaceae*,* by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of PtCV isolate Pte tri are 6,469 nt (BK065036) and 3,803 nt (BK065037) long, respectively. The genome organization of PtCV is similar to that of other members of the genus *Cheravirus* in the family *Secoviridae* (Figure 1). The three CPs and the conserved Pro-Pol region of PtCV have 26.15% and 58.02% amino acid sequence identity with arracacha virus B (AVB, a member of the species *Cheravirus arracaciae*), the closest related virus in the genus *Cheravirus* of the family *Secoviridae*. ML phylogenetic trees generated using the three CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of PtCV and representative members of the family *Secoviridae* confirm its clustering in the genus *Cheravirus*. Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Pternopetalum trichomanifolium cheravirus (PtCV) as a member of a novel species named “*Cheravirus pternopetali”* in the genus *Cheravirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Fabavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 13 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) [1]  *Justification*: The complete genome sequence of black pepper virus F (BPVF) was determined from black pepper (*Piper nigrum*) in China, by mining publicly available plant transcriptome datasets [4]. The complete sequences of RNA1 and RNA2 of BPVF isolate ZYP-1 are 6,342 nt (MZ648325) and 3,334 nt (MZ648326) long, respectively, excluding the poly(A) tail. The genome organization of BPVF 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 BPVF have 34.32% and 53.36% amino acid sequence identity with Squamellaria imberbis fabavirus (SiFabV, a newly proposed member of the species *Fabavirus squamellariae* -see below), the closest related virus in the genus *Fabavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of BPVF 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 black pepper virus F (BPVF) as a member of a novel species named “*Fabavirus phipiperis”* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Fabavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 13 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) [1]  *Justification*: The complete coding genome sequence of camphor tree fabavirus (CtFabV) was determined from *Cinnamomum camphora,* an evergreen tree, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CtFabV isolate Cin cam are 6,918 nt (BK065044) and 4,025 nt (BK065043) long, respectively. The genome organization of CtFabV 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 CtFabV have 31.08% and 56.86% amino acid sequence identity with Reaumuria songarica fabavirus (ReFabV, a newly proposed member of the species *Fabavirus reaumuriae* -see below), the closest related virus in the genus *Fabavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2) and Figure 2A and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of CtFabV 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 camphor tree fabavirus (CtFabV) as a member of a novel species named “*Fabavirus camphorae”* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Fabavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 13 species.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the genus *Fabavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Reaumuria songaria fabavirus (RsFabV) was determined from *Cinnamomum camphora,* an evergreen tree, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CtFabV isolate Rea son are 6,644 nt (BK065050) and 3,322 nt (BK065051) long, respectively. The genome organization of RsFabV 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 RsFabV have 31.08% and 56.86% and amino acid sequence identity with camphor tree fabavirus (CtFabV, a newly proposed member of the species *Fabavirus camphorae* -see above), the closest related virus in the genus *Fabavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of RsFabV 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 Reaumuria songaria fabavirus (RsFabV) as a member of a novel species named “*Fabavirus reaumuriae”* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Fabavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 13 species.  *Proposed* *taxonomic change(s)*: Creation of a fourth novel species in the genus *Fabavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of many-flowered stoneseed fabavirus (MsFabV) was determined from *Lithospermum multiflorum,* a perennial flowering herb of the family Boraginaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of MtFabV isolate Lit mul are 5,887 nt (BK065048), and 3,374 nt (BK065049) long, respectively. The genome organization of MsFabV 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 MsFabV have 52.22% and 57.36% amino acid sequence identity with broad bean wilt virus 1 (BBWV, a member of the species *Fabavirus alphaviviae*) the closest related virus in the genus *Fabavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of MsFabV 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 many-flowered stoneseed fabavirus (MsFabV) as a member of a novel species named “*Fabavirus multiflorum”* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Fabavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Fabavirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 13 species.  *Proposed* *taxonomic change(s)*: Creation of a fifth novel species in the genus *Fabavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Squamellaria imberbis fabavirus (SiFabV) was determined from *Squamellaria imberbis,* a flowering plant of the family Rubiaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of SiFabV isolate Squ imbl are 6,351 nt (BK065052) and 4,133 nt (BK065053) long, respectively. The genome organization of SiFabV 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 SiFabV have 38.55% and 51.75% amino acid sequence identity with black pepper virus F (BPVF, a newly proposed member of the species *Fabavirus phipiperis* -see above), the closest related virus in the genus *Fabavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the two CPs (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of SiFabV 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 Squamellaria imberbis fabavirus (SiFabV) as a member of a novel species named “*Fabavirus squamellariae”* in the genus *Fabavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 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) [1]  *Justification*: The complete genome sequence of cucumber nepovirus A (CUNVA) was determined from cucumber plants by high-throughput sequencing [5]. The complete sequences of RNA1 and RNA2 of CUNV isolate Crete are 7,370 nt (PP376097) and 4,707 nt (PP376098) long, respectively. The genome organization of CUNVA 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 CUNVA have 35.24% and 93.67% amino acid sequence identity with beet ringspot virus (BRSV, a member of the species *Nepovirus betae*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of CUNVA 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 cucumber nepovirus A (CUNVA) as a member of a novel species named “*Nepovirus alphacucumis”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of common thyme nepovirus (CtNV) was determined from *Thymus vulgaris*, common thyme of the family Lamiaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CtNV isolate Thy vul are 7,944 nt (BK065074) and 6,844 nt (BK065075) long, respectively. The genome organization of CtNV 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 CtNV have 45.61% and 77.37% amino acid sequence identity with chrysanthemum nepovirus (ChrNV, a newly proposed member of the species *Nepovirus ”anthemi” -*see below), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of CtNV 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 common thyme nepovirus (CtNV) as a member of a novel species named “*Nepovirus thymi”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a third novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Tibetan peony nepovirus (TipNV) was determined from *Paeonia ludlowii*, a shrub of the family Paeoniaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of TipNV isolate Pae lud are 7,822 nt (BK065118) and 5,522 nt (BK065119) long, respectively. The genome organization of TipNV 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 TipNV have 39.06% and 69.18% amino acid sequence identity with Silene diclinis nepovirus (SdNV, a newly proposed member of the species *Nepovirus silenis -*see below), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of TipNV 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 Tibetan peony nepovirus (TipNV) as a member of a novel species named “*Nepovirus paeoniae”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a fourth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of chrysanthemum nepovirus (ChrNV) was determined from *Chrysanthemum indicum*, a flowering plant of the family Asteraceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of ChrNV isolate Chy ind are 7,959 nt (BK065072) and 5,778 nt (BK065073) long, respectively. The genome organization of ChrNV 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 ChrNV have 45.76% and 77.51% amino acid sequence identity with common thyme nepovirus (CtNV, a newly proposed member of the species “*Nepovirus thymi” -*see above), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of ChrNV 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 chrysanthemum nepovirus (ChrNV) as a member of a novel species named “*Nepovirus chrysanthemi”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a fifth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Senecio pinnatifolius nepovirus (SepNV) was determined from *Senecio pinnatifolius,* a species of herb of the family Asteraceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of SepNV isolate Sen pin are 6,949 nt (BK065112) and 4,991 nt (BK065113) long, respectively. The genome organization of SepNV 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 SepNV have 40.06% and 69.68% amino acid sequence identity with potato virus U (PVU, a member of the species *Nepovirus usolani*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of SepNV 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 Senecio pinnatifolius nepovirus (SepNV) as a member of a novel species named “*Nepovirus pinnatifolium”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 54 species.  *Proposed* *taxonomic change(s)*: Creation of a sixth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of logan nepovirus (LogNV) was determined from *Glycyrrhiza uralensis*, a flowering plant of the family Fabaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of LogNV isolate Stevia is 6,049 nt (BK065101) and 6,661 nt (BK065099) long, respectively. The genome organization of LogNV 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 LogNV have 80.49% and 73.14% and amino acid sequence identity with blueberry latent spherical virus (BSLV, a member of the species *Nepovirus vaccinii*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of LogNV 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 logan nepovirus (LogNV) as a member of a novel species named “*Nepovirus glycyrrhizae”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a seventh novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of purple sand food nepovirus (PsfNV) was determined from *Pholisma arenarium*, a flowering plant of the family Boraginaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of PsfNV isolate Pho are 6,621 nt (BK065108) and 4,285 nt (BK065109) long, respectively. The genome organization of PsfNV 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 PsfNV have 29.19% and 49.28% amino acid sequence identity with Petunia chlorotic mottle virus (PCMoV, a member of the species *Nepovirus petuniae*) and anemone nepovirus A (AnNVA, a member of the species *Nepovirus anemones*), *t*he closest related viruses in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of PsfNV 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 purple sand food nepovirus (PsfNV) as a member of a novel species named “*Nepovirus pholismae”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of an eighth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of coral plant nepovirus (CopNV) was determined from *Berberidopsis coralina*, an ornamental plant of the family Berberidopsidaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CopNV isolate Ber cor are 6,498 nt (BK065076) and 5,152 nt (BK065077) long, respectively. The genome organization of CopNV 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 CopNV have 51.84% and 60.57% amino acid sequence identity with potato virus U (PVU, a member of the species *Nepovirus usolani*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of CopNV 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 coral plant nepovirus (CopNV) as a member of a novel species named “*Nepovirus berberidopsis”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a ninth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Silene declinis nepovirus (SdNV) was determined from *Berberidopsis coralina*, an ornamental plant of the family Berberidopsidaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of SdNV isolate Sil dic are 7,823 nt (BK065114) and 5,748 nt (BK065115) long, respectively. The genome organization of SdNV 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 SdNV have 40.42% and 65.52% amino acid sequence identity with Tibetan peony nepovirus (TipNV, a newly proposed member of the species *Nepovirus paeoniae -*see above), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 2B) sequences of SdNV 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 Silene declinis nepovirus (SdNV) as a member of a novel species named “*Nepovirus silenis”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a tenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of beetleweed nepovirus (BwNV) was determined from *Galax urceolata*, an evergreen shrub of the family Diapensiaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of BwNV isolate Gal urc are 7,108 nt (BK065062) and 3,512 nt (BK065063) long, respectively. The genome organization of BwNV 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 BwNV have 66.60% and 73.61% amino acid sequence identity with Arabis mosaic virus (ArMV, a member of the species *Nepovirus arabis*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of BwNV 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 beetleweed nepovirus (BwNV) as a member of a novel species named “*Nepovirus galax”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of an eleventh novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Asian lizard’s tail nepovirus (AltNV) was determined from *Saururus chinensis,* an herb of the family Saururaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of AltNV isolate Sau chi are 7,108 nt (BK065058) and 3,512 nt (BK065059) long, respectively. The genome organization of AltNV 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 AltNV have 70.42% and 75.04% amino acid sequence identity with mulberry mosaic leafroll-associated virus (ArMV, a member of the species *Nepovirus mori*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of AltNV 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 Asian lizard’s tail nepovirus (AltNV) as a member of a novel species named “*Nepovirus saururi”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twelfth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Musa nepovirus (MuNV) was determined from a Musa hybrid cultivar*,* a flowering plant of the family Musaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of MuNV isolate Musa are 8,205 nt (BK065102) and 7,032 nt (BK065103) long, respectively. The genome organization of MuNV 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 MuNV have 38.40% and 74.47% amino acid sequence identity with cherry leafroll virus (CLRV, a member of the species *Nepovirus avii*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of MuNV 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 Musa nepovirus (MuNV) as a member of a novel species named “*Nepovirus musae”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a thirteenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of pearl millet nepovirus (PmNV) was determined from *Cenchrus americanus,* a millet of the family Panicoideae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of PmNV isolate Cen am are 7,764 nt (BK065106) and 6,574 nt (BK065107) long, respectively. The genome organization of PmNV 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 PmNV have 41.83% and 71.37% amino acid sequence identity with Stenotaphrum nepovirus (SteNV, a member of the species *Nepovirus stenotaphri*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of PmNV 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 pearl millet nepovirus (PmNV) as a member of a novel species named “*Nepovirus cenchri”* in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a fourteenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of downy ground fern nepovirus (DgfNV) was determined from *Hypolepsis punctate,* a species of fern of the family Polypodiaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of DgfNV isolate Hyp pun are 7,714 nt l (BK065078) and 7,408 nt (BK065079) long, respectively. The genome organization of DgfNV 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 DgfNV have 33.61% and 64.24% amino acid sequence identity with blackcurrant reversion virus (BRV, a member of the species *Nepovirus ribis*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of DgfNV 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 downy ground fern nepovirus (DgfNV) as a member of a novel species named “*Nepovirus hypolepsis*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a fifteenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [1]  *Justification*: The complete coding genome sequence of Aloe haircap nepovirus (AhNV) was determined from *Pogonatum aloides,* a species of moss of the family Polytrichaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of AhNV isolate Pog alo are 7,144 nt (BK065056) and 6,454 nt (BK065057) long, respectively. The genome organization of AhNV 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 AhNV have 41.73% and 61.93% amino acid sequence identity with Begonia plebeja nepovirus (BpNV, a newly proposed member of the species “*Nepovirus begoniae*“-see below), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of AhNV 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 Aloe haircap nepovirus (AhNV) as a member of a novel species named “*Nepovirus pogonati*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a sixteenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Begonia plebeja nepovirus (BpNV) was determined from *Pogonatum aloides,* a species of moss of the family Polytrichaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of BpNV isolate Beg ple are 7,896 nt (BK065064) and 6,645 nt (BK065065) long, respectively. The genome organization of BpNV 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 BpNV have 41.14% and 79.87% amino acid sequence identity with blueberry leaf mottle virus (BLMV, a member of the species *Nepovirus myrtilli*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of BpNV 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 Begonia plebeja nepovirus (BpNV) as a member of a novel species named “*Nepovirus begoniae*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a seventeenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Canberra spider orchid nepovirus (CsoNV) was determined from *Caladenia actensis,* a plant of the family Orchidaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CsoNV isolate Cal act are 7,422 nt l (BK065066) and 6,972 nt (BK065067) long, respectively. The genome organization of CsoNV 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 CsoNV have 56.04% and 80.93% amino acid sequence identity with blueberry leaf mottle virus (BLMV, a member of the species *Nepovirus myrtilli*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of CsoNV 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 Canberra spider orchid nepovirus (CsoNV) as a member of a novel species named “*Nepovirus caladeniae*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of an eighteenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Chinese milk vetch nepovirus (CmvNV) was determined from *Astragalus sinicus,* a species of milkvetch of the family Fabaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CmvNV isolate Ast sin are 7,770 nt (BK065070) and 6,382 nt (BK065071) long, respectively. The genome organization of CmvNV 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 CmvNV have 57.51% and 83.28% amino acid sequence identity with grapevine Bulgarian latent virus (GBLV, a member of the species *Nepovirus bulgariense*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of CmvNV 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 Chinese mild vetch nepovirus (CmvNV) as a member of a novel species named “*Nepovirus astragali*” in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a nineteenth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Gentiana ecaudata nepovirus (GeNV) was determined from *Astragalus sinicus,* a species of milkvetch of the family Fabaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1and RNA2 of GeNV isolate Gen eca are 7,262 nt (BK065080) and 3,741 nt (BK065081) long, respectively. The genome organization of GeNV 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 GeNV have 40.58% and 76.36% amino acid sequence identity with arracacha virus A (AVA, a member of the species *Nepovirus arracaciae*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of GeNV 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 Gentiana ecaudata nepovirus (GeNV) as a member of a novel species named “*Nepovirus gentianae*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twentieth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Cederberg conebush nepovirus (CecNV) was determined from *Leucadendron dubium,* a flowering shrub of the family Proteaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of CecNV isolate Leu dub are 7,178 nt (BK065068) and 4,145 nt (BK065069) long, respectively. The genome organization of CecNV 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 CecNV have 32.59% and 48.12% amino acid sequence identity with tomato black ring virus (TBRV, a member of the species *Nepovirus nigranuli*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of CecNV 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 Cederberg conebush nepovirus (CecNV) as a member of a novel species named “*Nepovirus leucadendri*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-first novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Yunnan pine nepovirus (YpNV) was determined from *Pinus yunnanensis,* a species of conifer of the family Pinaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of YpNV isolate Pin yun are 7,178 nt (BK065120) and 4,145 nt (BK065121) long, respectively. The genome organization of YpNV 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 YpNV have 42.16% and 57.27% amino acid sequence identity with grapevine chrome mosaic virus (GCMV, a member of the species *Nepovirus chromusivum*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of YpNV 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 Yunnan pine nepovirus (YpNV) as a member of a novel species named “*Nepovirus yunnanense*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-second novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Rhododendron lacteum nepovirus (RhiNV) was determined from *Rhododendron lacteum,* an evergreen shrub of the family Ericaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of RhiNV isolate Rho lac are 7,042 nt (BK065110) and 3,613 nt (BK065111) long, respectively. The genome organization of RhiNV 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 RhiNV have 40.58% and 76.36% amino acid sequence identity with mulberry mosaic leafroll virus (MMLRaV, a member of the species *Nepovirus mori*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of RhiNV 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 Rhododendron lacteum nepovirus (RhiNV) as a member of a novel species named “*Nepovirus rhododendri*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-third novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Hansenia oviformis nepovirus (HoNV) was determined from *Hansenia oviformis,* a flowering plant of the family Apiaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of HoNV isolate Neotrinia are 7,042 nt (BK065088) and 3,613 nt (BK065089) long, respectively. The genome organization of HoNV 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 HoNV have 62.57% and 86.0% amino acid sequence identity with raspberry ringspot virus (RpRSV, a member of the species *Nepovirus rubi*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of HoNV 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 Hansenia oviformis nepovirus (HoNV) as a member of a novel species named “*Nepovirus hanseniae*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-fourth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Beldersay nepovirus 1 (BelSV1) was determined from *Hansenia oviformis,* a flowering plant of the family *Apiaceae*, by high-throughput sequencing [6]. The coding sequences of RNA1 and RNA2 of BeSsV1 isolate Beldersay U2 are 7,550 nt (OR912380) and 3,860 nt (OR912381) long, respectively. The genome organization of BelSV1V 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 BelSV1 have 62.57% and 52.03% amino acid sequence identity with olive latent ringspot virus (LORSV, a member of the species *Nepovirus oleae*) and arracacha virus A (AVA, a member of the species *Nepovirus arracaciae*), respectively, the closest related viruses in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of BelSV1 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 Beldersay nepovirus 1 (BelSV1) as a member of a novel species named “*Nepovirus beldersayense*”in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Nepovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Nepovirus* belongs to the family *Secoviridae*, subfamily *Comovirinae*, and consists of 55 species.  *Proposed* *taxonomic change(s)*: Creation of a twenty-fifth novel species in the genus *Nepovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Jasminum polyanthum nepovirus 1 (JPV1) was determined fromJasminum polyanthum*,* a flowering plant of the family Oleaceae, by high throughput sequencing [7]. The coding sequences of RNA1 and RNA2 of JPV1 isolate Pinck jasmine are 7,057 nt (OQ943946) and 4,212 nt (OQ943947) long, respectively. The genome organization of JPV1 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 JPV1 have 32.31% and 49.87% amino acid sequence identity with red clover nepovirus A (RCNVA, a member of the species *Nepovirus pratensis*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2B) and conserved Pro-Pol (Figure 3 and Figure 3B) sequences of JPV1 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 Jasminum polyanthum nepovirus 1 (JPV1) as a member of a novel species named “*Nepovirus jasmini*"in the genus *Nepovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Sadwavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Sadwavirus* belongs to the family *Secoviridae* and consists of 13 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) [1]  *Justification*: The coding-complete sequence of pineapple secovirus C (PSVC) was determined from *Ananas comosus,* a tropical plant of the family Bromeliaceae, by high-throughput sequencing [8]. The coding sequences of RNA1 and RNA2 of PSVC isolate PSVC-S2-1 are 6,159 nt (OP860260) and 3,189 nt (OP860285) long, respectively. The genome organization of PSVC is similar to that of other members of the genus *Sadwavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of PSVC have 47.92% and 65.69% amino acid sequence identity with Dioscorea mosaic associated virus (DMaV, a member of the species *Sadwavirus dioscoreae*), the closest related virus in the genus *Nepovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of PSVC and representative members of the family *Secoviridae* confirm its clustering in the genus *Sadwavirus*, subgenu*s Cholivirus,*  Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify pineapple secovirus C (PSVC) as a member of a novel species named “*Sadwavirus kappananas*”in the genus *Sadwavirus,* subgenu*s Cholivirus,* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Sadwavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Sadwavirus* belongs to the family *Secoviridae* and consists of 13 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) [1]  *Justification*: The complete coding genome sequence of chrysanthemum stramovirus (ChrSV) was determined from *Chrysanthemum morifolium,* a perennial Asteraceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of ChrSV isolate Chr mor are 6,970 nt (BK065126) and 6,672 nt (BK065127) long, respectively. The genome organization of ChrSV is similar to that of other members of the genus *Sadwavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of ChrSV have 43.19% and 54.40% amino acid sequence identity with lettuce secovirus 1 (LSV1, a member of the species *Sadwavirus lactucae*), the closest related virus in the genus *Sadwavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of ChrSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Sadwavirus*, subgenus *Stramovirus.* Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify chrysanthemum stramovirus (ChrSV) as a member of a novel species named “*Sadwavirus morifolii*”in the genus *Sadwavirus*, subgenus *Stramovirus*, of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Stralarivirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Stralarivirus* belongs to the family *Secoviridae* and consists of three species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Stralarivirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Beldersay stralarivirus 1 (BesV1) was determined from honeybeeby high-throughput sequencing [6]. The coding sequences of RNA1 and RNA2 of BesV1 isolate Beldersey U2 are 6,938 nt (OR912382) and 3,524 nt (OR912383) long, respectively. The genome organization of BesV1 is similar to that of other members of the genus *Stralarivirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of BesV1 have 70.41% and 71.97% amino acid sequence identity with Cohombrillo-associated virus (CoAV, a member of the species *Stralarivirus elaterii*), the closest related virus in the genus *Stralarivirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of BesV1 and representative members of the family *Secoviridae* confirm its clustering in the genus *Stralarivirus.* Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify Beldersay stralarivirus 1 (BesV1) as a member of a novel species named “*Stralarivirus beldersayense*”in the genus *Stralarivirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Stralarivirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Stralarivirus* belongs to the family *Secoviridae* and consists of three species.  *Proposed* *taxonomic change(s)*: Creation of a second novel species in the genus *Stralarivirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of beach cabbage stralarivirus (BCSV) was determined from *Scaevola taccada,* a flowering plant of the family Goodeniaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of BCSV isolate Sca tac are 6,970 nt (BK065129) and 6,672 nt (BK065130) long, respectively. The genome organization of BCSV is similar to that of other members of the genus *Stralarivirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of BCSV have 36.64% and 42.14% amino acid sequence identity with strawberry latent ringspot virus (SLSRV, a member of the species *Stralarivirus fragariae*), the closest related virus in the genus *Stralarivirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2A) and conserved Pro-Pol (Figure 3 and Figure 3A) sequences of BCSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Stralarivirus.* Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify beach cabbage stralarivirus (BCSV) as a member of a novel species named “*Stralarivirus scaevolae”* in the genus *Stralarivirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Torradovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 12 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) [1]  *Justification*: The complete coding genome sequence of lake cress torradovirus (LcTV) was determined from *Rorippa aquatica*, an aquatic flowering plant in the family Brassicaceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of LcTV isolate Ror aqu are 7,182 nt (BK065131) and 5,142 nt (BK065132) long, respectively. The genome organization of LcTV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of LcTV have 52.25% and 72.94% amino acid sequence identity with carrot torradovirus 1 (CaTV1, a member of the species *Torradovirus carotae*), the closest related virus in the genus *Torradovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of LcTV 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 lake cress torradovirus (LcTV) as a member of a novel species named “*Torradovirus rorippae*”in the genus *Torradovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Torradovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 12 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) [1]  *Justification*: The complete coding genome sequence of Opisthopappus taihangensis torradovirus (OtTV) was determined from *Opisthopappus taihangensis*, a flowering plant in the family Asteraceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of OtTV isolate Opi tai are 7,518 nt (BK065135) and 4,605 nt (BK065136) long, respectively. The genome organization of OtTV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of OtTV have 71.43% and 79.79% amino acid sequence identity with burdock mosaic virus (CaTV1, a member of the species *Torradovirus carotae*), the closest related virus in the genus *Torradovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of OtTV 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 Opisthopappus taihangensis torradovirus (OtTV) as a member of a novel species named “*Torradovirus ophistopappi*”in the genus *Torradovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Torradovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 12 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) [1]  *Justification*: The complete coding genome sequence of Lophophytum mirabile torradovirus (LmTV) was determined from *Lophophytum mirabile*, a flowering plant in the family Balanophoraceae, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of LmTV isolate Lop mir are 6,676 nt (BK065133) and 4,862 nt (BK065134) long, respectively. The genome organization of LmTV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of LmTV have 50.0% and 63.19% amino acid sequence identity with potato rugose stunting virus (PotRSV, a member of the species *Torradovirus nanorugosum*, the closest related virus in the genus *Torradovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of LmV 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 Lophophytum mirabile torradovirus (LmTV) as a member of a novel species named “*Torradovirus lophophyti*”in the genus *Torradovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Torradovirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Torradovirus* belongs to the family *Secoviridae* and consists of 12 species.  *Proposed* *taxonomic change(s)*: Creation of a fourth novel species in the genus *Torradovirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Sesamum torradovirus (SeTV) was determined from *Sesamum indicum* x *Sesamum mulayanum,* an oilseed hybrid in the family *Pedaliaceae*, by mining publicly available plant transcriptome datasets [3]. The coding sequences of RNA1 and RNA2 of SeTV isolate Rehmannia are 8,070 nt (BK065139) and 4,668 nt (BK065140) long, respectively. The genome organization of SeTV is similar to that of other members of the genus *Torradovirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of SeTV have 64.76% and 77.0% amino acid sequence identity with squash chlorotic leaf spot virus (SCLSV, a member of the species *Torradovirus cucurbitae*), the closest related virus in the genus *Torradovirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of SeTV 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 Sesamum torradovirus (SeTV) as a member of a novel species named “*Torradovirus sesami*"in the genus *Torradovirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Sequivirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Sequivirus* belongs to the family *Secoviridae* and consists of four species.  *Proposed* *taxonomic change(s)*: Creation of a novel species in the genus *Sequivirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of cowslip sequivirus (CosSV) was determined from *Primula veris,* a flowering plant in the family Primulaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the CosSV isolate Pri ver RNA is 10,179 nt long (BK065128). The genome organization of CosSV is similar to that of other members of the genus *Sequivirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of CosSV have 59.85% and 67.96% amino acid sequence identity with parsnip yellow fleck virus (PYFV, a member of the species *Sequivirus pastinacae*), the closest related virus in the genus *Sequivirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of CosSV and representative members of the family *Secoviridae* confirm its clustering in the genus *Sequivirus.* Considering the species demarcation criteria for the family *Secoviridae*, we propose to classify cowslip sequivirus (CosSV) as a member of a novel species named “*Sequivirus primulae”* in the genus *Sequivirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 species.  *Proposed* *taxonomic change(s)*: Creation of a first novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of Asian lily-of-the-valley waikavirus (AlWV) was determined from *Concallaria keiskei,* a flowering plant of the family Asparagaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the AlWV isolate Can kai RNA is 11,504 nt long (BK065141). The genome organization of AlWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of AlWV have 70.0% and 70.90% amino acid sequence identity with Pedicularis rex waikavirus (PvWV, a member of the species *Waikavirus* pedicularis), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of AlWV 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 Asian lily-of-the-valley waikavirus (AlWV) as a member of a novel species named “*Waikavirus convallariae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 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) [1]  *Justification*: The complete coding genome sequence of Asian Euphorbia ebracteolata waikavirus (EeWV) was determined from *Euphorbia ebracteolata,* a flowering plant of the family Euphorbiaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the EeWV isolate Eup ebr RNA is 12,829 nt long (BK065142). The genome organization of EeWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of EeWV have 51.75% and 65.65% amino acid sequence identity with Viola inconspicua waikavirus (CiWV, a member of the species *Waikavirus violae*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of EeWV 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 Asian Euphorbia ebracteolata waikavirus (EeWV) as a member of a novel species named “*Waikavirus euphorbiae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 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) [1]  *Justification*: The complete coding genome sequence of Eureka dunegrass waikavirus (EudWV) was determined from *Swallenia alexandrae,* a dune grass of the family Poaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the EudWV isolate Swa ale RNA is 11,866 nt long (BK065143). The genome organization of EudWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of EudWV have 51.05% and 66.28% amino acid sequence identity with maize chlorotic dwarf virus (MCDV, a member of the species *Waikavirus zeae*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of EudWV 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 Asian Eureka dunegrass waikavirus (EudWV) as a member of a novel species named “*Waikavirus swalleniae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 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) [1]  *Justification*: The complete coding genome sequence of Gentiana straminea waikavirus (GesWV) was determined from *Gentiana straminea,* a flowering plant of the family Gentianaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the GesWV isolate Gen Str RNA is 12,270 nt long (BK065144). The genome organization of GesWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of GesWV have 58.52% and 74.5% amino acid sequence identity with Ajuga Reptans waikavirus (AjrWV, a member of the species *Waikavirus* pedicularis), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of GwWV 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 Gentiana straminea waikavirus (GesWV) as a member of a novel species named “*Waikavirus gentianae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 species.  *Proposed* *taxonomic change(s)*: Creation of a fifth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of gypsywort waikavirus (GwWV) was determined from *Lycopus europaeus,* a perennial plant of the family Lamiaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the EudWV isolate Lyc eur RNA is 11,856 nt long (BK065145). The genome organization of GwWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of GwWV have 62.59% and 71.14% amino acid sequence identity with Pedicularis rex waikavirus (PvWV, a member of the species *Waikavirus pedicularis*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of GwWV 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 gypsywort waikavirus (GwWV) as a member of a novel species named “*Waikavirus lycopi*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 species.  *Proposed* *taxonomic change(s)*: Creation of a sixth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al. (2022) [1]  *Justification*: The complete coding genome sequence of pagoda dogwood waikavirus (PdWV) was determined from *Cornus alternifolia,* a flowering plant of the family Cornaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the PdWV isolate Cor alt RNA is 12,089 nt long (BK065147). The genome organization of PdWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of PdWV have 48.64% and 63.57% amino acid sequence identity with blackcurrant waikavirus A (BCWVA, a member of the species *Waikavirus ribesnigri*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of PdWV 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 Pagoda dogwood waikavirus (PdWV) as a member of a novel species named “*Waikavirus pagodae*"in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 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) [1]  *Justification*: The complete coding genome sequence of rubber waikavirus (RuWV) was determined from *Hevea brasilensis,* a rubber tree of the family Euphorbiaceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the RuWV isolate Hev bra RNA is 12,483 nt long (BK065149). The genome organization of RuWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of RuWV have 36.58% and 64.41% amino acid sequence identity with Populus alba waikavirus (PaWV, a member of the species *Waikavirus populi*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of RuWV 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 rubber waikavirus (RuWV) as a member of a novel species named “*Waikavirus heveae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 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) [1]  *Justification*: The complete coding genome sequence of sweet wormwood waikavirus (SwWV) was determined from *Artemisia annua,* an herbaceous Asteraceae, by mining publicly available plant transcriptome datasets [3]. The complete coding sequence of the SwWV isolate Art ann RNA is 11,948 nt long (BK065150). The genome organization of SwWV is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of SwWV have 36.58% and 68.72% amino acid sequence identity with Ajuga Reptans waikavirus (AjrWV, a member of the species *Waikavirus ajugae*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of SwWV 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 sweet wormwood waikavirus (SwWV) as a member of a novel species named “*Waikavirus artemisiae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).   1. *Taxonomic rank(s) affected*: Genus *Waikavirus* in the family *Secoviridae*   *Description of current taxonomy*: The genus *Waikavirus* belongs to the family *Secoviridae* and consists of 34 species.  *Proposed* *taxonomic change(s)*: Creation of a ninth novel species in the genus *Waikavirus* of the family *Secoviridae.*  *Demarcation criteria:* Thedemarcation criteria are as in Fuchs et al (2022) [1]  *Justification*: The complete coding genome sequence of plant associated waikavirus 2 (PaWV2) was determined from *Artemisia annua,* a herbaceous Asteraceae, by high-throughput sequencing [9]. The complete coding sequence of the PaWV2 isolate Art ann RNA is 11,948 nt long (OL472179). The genome organization of PaWV2 is similar to that of other members of the genus *Waikavirus* in the family *Secoviridae* (Figure 1). The CP and the conserved Pro-Pol region of PaWV2 have 57.76% and 73.96% amino acid sequence identity with Pedicularis rex waikavirus (PrWV, a member of the species *Waikavirus pedicularis*), the closest related virus in the genus *Waikavirus* of the family *Secoviridae*. ML phylogenetic trees generated using the CP (Figure 2 and Figure 2C) and conserved Pro-Pol (Figure 3 and Figure 3C) sequences of PaWV2 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 sweet wormwood waikavirus (SwWV) as a member of a novel species named “*Waikavirus duoplantae*”in the genus *Waikavirus* of the family *Secoviridae* (Table 1).  Lastly, we propose to abolish two previously recognized species in the genus *Nepovirus* (*Nepovirus americaense, Nepovirus australiense*)andone previously recognized species in the genus *Waikavirus* (*Waikavirus anthrisci*) based on a lack of sequence information. |

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| **References:** |
| 1. Fuchs M, Hily J-M, Petrzik K, Sanfaçon H, Thompson JR, van der Vlugt R., Wetzel T (2022) ICTV virus taxonomy profile: *Secoviridae*. Journal of General Virology. 103:001807.  2. Alacalá-Briseño RI, Casarrubias-Castillo K, Lópex-Ley D, Garrett KA, Silva-Rosales L (2020) Network analysis of the papaya orchard virome from two agroecological regions of Chiapas, Mexico. mSystems 5:e00423-19.  3. Sidharthan VK, Reddy V, Kiran G, Rajeswari V, Baranwal VK, Kumar MK, Kumar KS (2024) Probing of plant transcriptomes reveals the hidden genetic diversity of the family *Secoviridae*. Archies of Virology 169:150.  4. Ma Y, Che H, Gao S, Lin Y, Li S (2022) The virome of *Piper nigrum*: identification, genomic characterization, prevalence, and transmission of three new viruses of black pepper in China. Plant Disease 106:2082-2089.  5. James A, Kryovrysanaki N Andronis C, Pappi PG, Kalantidis K, Katsarou K (2024) Identification and characterization of *Zucchini yellow fleck virus* and a novel Nepovirus from next-generation sequencing of mixed virus infections in cucumbers (Cucumis sativus) from Crete. Annals of Applied Biology 204:1-14.  6. Kwon M, Zakhidovna RN, Abdiazizovich KB, Jung C, Kil E-J (2024) First metagenomic analysis of virome in Uzbekistan honey bee (*Apis mellifera*): Investigating basic information on honey bee viruses. Journal of Invertebrate Pathology 206:108171.  7. Zhao X, Anane RF, Guo J, Zi S, Chu B, Yang Z, Yan K, Ji K, Li S, Chen Z, Zhao M (2025) Complete genome sequence analysis of a novel nepovirus isolated from *Jasminum polyanthum* in Yunnan, China. Archives of Virology 170:10.  8. Larrea-Sarmiento AE, Olmedo-Velarde A, Wang X, Borth W, Domingo R, Matsumoto TK, Suzuki JY, Wall MM, Melzer MJ, Hu J (2022) Genetic diversity of viral populations associated with *Ananas* germplasm and improvement of virus diagnostic protocols. Pathogens 11:1470.  9. Selda Rivarez MP, Pecman A, Bacnik K, Maksimovic O, Vucurovic A, Seljak G, Mehle N, Gutiérrez-Aguirre I, Ravnikar M, Kutnjak D (2023) In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem. Microbiomes 11:60.  10. Le SQ and Gascuel O 2008. An improved general amino acid replacement matrix. Molecular Biology and Evolution 25:1307-1320.  11. Kumar S, Stecher G, Li M, Knyaz C and Tamura K. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution 35:1547-1549. |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.017P.A.v1.Secoviridae\_53nsp\_3abolishsp | spreadsheet |
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| **Tables, Figures:** |

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

Virus name Virus species Genus GenBank acc. no. Reference

papaya comovirus *Comovirus caricae Comovirus* RNA1 MN203153 Alcala Briseño et al. 2020

RNA2 MN203154

white-flower bittercress comovirus *Comovirus cardaminis Comovirus* RNA1 BK065040 Sidharthan et al. 2024

RNA2 BK065041

Lagerstroemia indica cheravirus*Cheravirus lagerstroemiae Cheravirus* RNA1 BK065034 Sidharthan et al. 2024

RNA2 BK065035

Corymbium villosum cheravirus *Cheravirus corymbii Cheravirus* RNA1 BK065028 Sidharthan et al. 2024

RNA2 BK065029

Pternopetalum trichomanifolium cheravirus *Cheravirus pternopetali Cheravirus* RNA1 BK065036 Sidharthan et al. 2024

RNA2 BK065037

black pepper virus F *Fabavirus phipiperis Fabavirus* RNA1 MZ648325 Ma et al. 2022

RNA2 MZ648326

camphor tree fabavirus *Fabavirus camphorae Fabavirus* RNA1 BK065044 Sidharthan et al. 2024

RNA2 BK065045

Reaumuria songarica fabavirus *Fabavirus reaumuriae Fabavirus* RNA1 BK065050 Sidharthan et al. 2024

RNA2 BK065051

many-flowered stoneseed fabavirus *Fabavirus multiflorum Fabavirus* RNA1 BK065048 Sidharthan et al. 2024

RNA2 BK065049

Squamellaria imberbis fabavirus *Fabavirus squamellariae Fabavirus* RNA1 BK065052 Sidharthan et al. 2024

RNA2 BK065053

cucumber nepovirus A *Nepovirus alphacucumis Nepovirus* RNA1 PP376097 James et al. 2024

RNA2 PP376098

common thyme nepovirus *Nepovirus thymi Nepovirus* RNA1 BK065074 Sidharthan et al. 2024

RNA2 BK065075

Tibetan peony nepovirus *Nepovirus paeoniae Nepovirus* RNA1 BK065118 Sidharthan et al. 2024

RNA2 BK065119

chrysanthemum nepovirus *Nepovirus chrysanthemi Nepovirus* RNA1 BK065072 Sidharthan et al. 2024

RNA2 BK065073

Senecio pinnatifolius nepovirus *Nepovirus pinnatifolium Nepovirus* RNA1 BK065112 Sidharthan et al. 2024

RNA2 BK065113

logan nepovirus *Nepovirus glycyrrhizae Nepovirus* RNA1 BK065100 Sidharthan et al. 2024

RNA2 BK065099

purple sand food nepovirus *Nepovirus pholismae Nepovirus* RNA1 BK065108 Sidharthan et al. 2024

RNA2 BK065109

coral plant nepovirus*Nepovirus berberidopsis Nepovirus* RNA1 BK065076 Sidharthan et al. 2024

RNA2 BK065077

Silene diclinis nepovirus *Nepovirus silenis Nepovirus* RNA1 BK065114 Sidharthan et al. 2024

RNA2 BK065115

beetleweed nepovirus*Nepovirus galax Nepovirus* RNA1 BK065062 Sidharthan et al. 2024

RNA2 BK065063

Asian lizard’s tail nepovirus *Nepovirus saururi Nepovirus* RNA1 BK065058 Sidharthan et al. 2024

RNA2 BK065059

Musa nepovirus*Nepovirus musae Nepovirus* RNA1 BK065102 Sidharthan et al. 2024

RNA2 BK065103

pearl millet nepovirus *Nepovirus cenchri Nepovirus* RNA1 BK065106 Sidharthan et al. 2024

RNA2 BK065107

downy ground fern nepovirus *Nepovirus hypolepsis Nepovirus* RNA1 BK065078 Sidharthan et al. 2024

RNA2 BK065079

Aloe haircap nepovirus *Nepovirus pogonati Nepovirus* RNA1 BK065056 Sidharthan et al. 2024

RNA2 BK065057

Begonia plebeja nepovirus*Nepovirus begoniae Nepovirus* RNA1 BK065064 Sidharthan et al. 2024

RNA2 BK065065

Canberra spider orchid nepovirus*Nepovirus caladeniae Nepovirus* RNA1 BK065066 Sidharthan et al. 2024

RNA2 BK065067

Chinese milk vetch nepovirus *Nepovirus astragali Nepovirus* RNA1 BK065070 Sidharthan et al. 2024

RNA2 BK065071

Gentiana ecaudata nepovirus *Nepovirus gentianae Nepovirus* RNA1 BK065080 Sidharthan et al. 2024

RNA2 BK065081

Cederberg conebush nepovirus *Nepovirus leucadendri Nepovirus* RNA1 BK065068 Sidharthan et al. 2024

RNA2 BK065069

Yunnan pine nepovirus*Nepovirus yunnanense Nepovirus* RNA1 BK065120 Sidharthan et al. 2024

RNA2 BK065121

Rhododendron lacteum nepovirus*Nepovirus rhododendri Nepovirus* RNA1 BK065110 Sidharthan et al. 2024

RNA2 BK065111

Hansenia oviformis nepovirus*Nepovirus hanseniae Nepovirus* RNA1 BK065088 Sidharthan et al. 2024

RNA2 BK065089

Beldersay nepovirus 1 *Nepovirus beldersayense Nepovirus* RNA1 OR912380 Kwon et al. 2024

RNA2 OR912381

Jasminum polyanthum nepovirus 1 *Nepovirus jasmini Nepovirus* RNA1 OQ943946 Zhao et al. 2025

RNA2 OQ943947

pineapple secovirus C *Sadwavirus kappananas Sadwavirus* RNA1 OP860260 Larrea-Sarmiento et al. 2022

RNA2 OP860285

chrysanthemum stramovirus *Sadwavirus morifolii Sadwavirus* RNA1 BK065126 Sidharthan et al. 2024

RNA2 BK065127

Beldersay stralarivirus 1 *Stralarivirus beldersayense Stralarivirus* RNA1 OR912382 Kwon et al. 2024

RNA2 OR912383

beach cabbage stralarivirus*Stralarivirus scaevolae Stralarivirus* RNA1 BK065129 Sidhartan et al. 2024

RNA2 BK065130

lake cress torradovirus*Torradovirus* *rorippae* *Torradovirus* RNA1 BK065131Sidhartan et al. 2024

RNA2 BK065132

Opisthopappus taihangensis torradovirus*Torradovirus ophistopappi* *Torradovirus* RNA1 BK065135Sidhartan et al. 2024

RNA2 BK065136

Lophophytum mirabile torradovirus*Torradovirus lophophyti* *Torradovirus* RNA1 BK065133Sidhartan et al. 2024

RNA2 BK065134

Sesamum torradovirus*Torradovirus* *sesami* *Torradovirus* RNA1 BK065139Sidhartan et al. 2024

RNA2 BK065140

cowslip sequivirus*Sequivirus primulae Sequivirus* BK065128 Sidharthan et al. 2024

Asian lily-of-the-valley waikavirus *Waikavirus convallariae Waikavirus* BK065141 Sidhartan et al. 2024

Euphorbia ebracteolata waikavirus *Waikavirus euphorbiae Waikavirus* BK065142 Sidhartan et al. 2024

Eureka dunegrass waikavirus *Waikavirus swalleniae Waikavirus* BK065143 Sidhartan et al. 2024

Gentiana straminea waikavirus *Waikavirus gentianae Waikavirus* BK065144 Sidhartan et al. 2024

gypsywort waikavirus *Waikavirus lycopi Waikavirus* BK065145 Sidhartan et al. 2024

pagoda dogwood waikavirus *Waikavirus pagodae Waikavirus* BK065147 Sidhartan et al. 2024

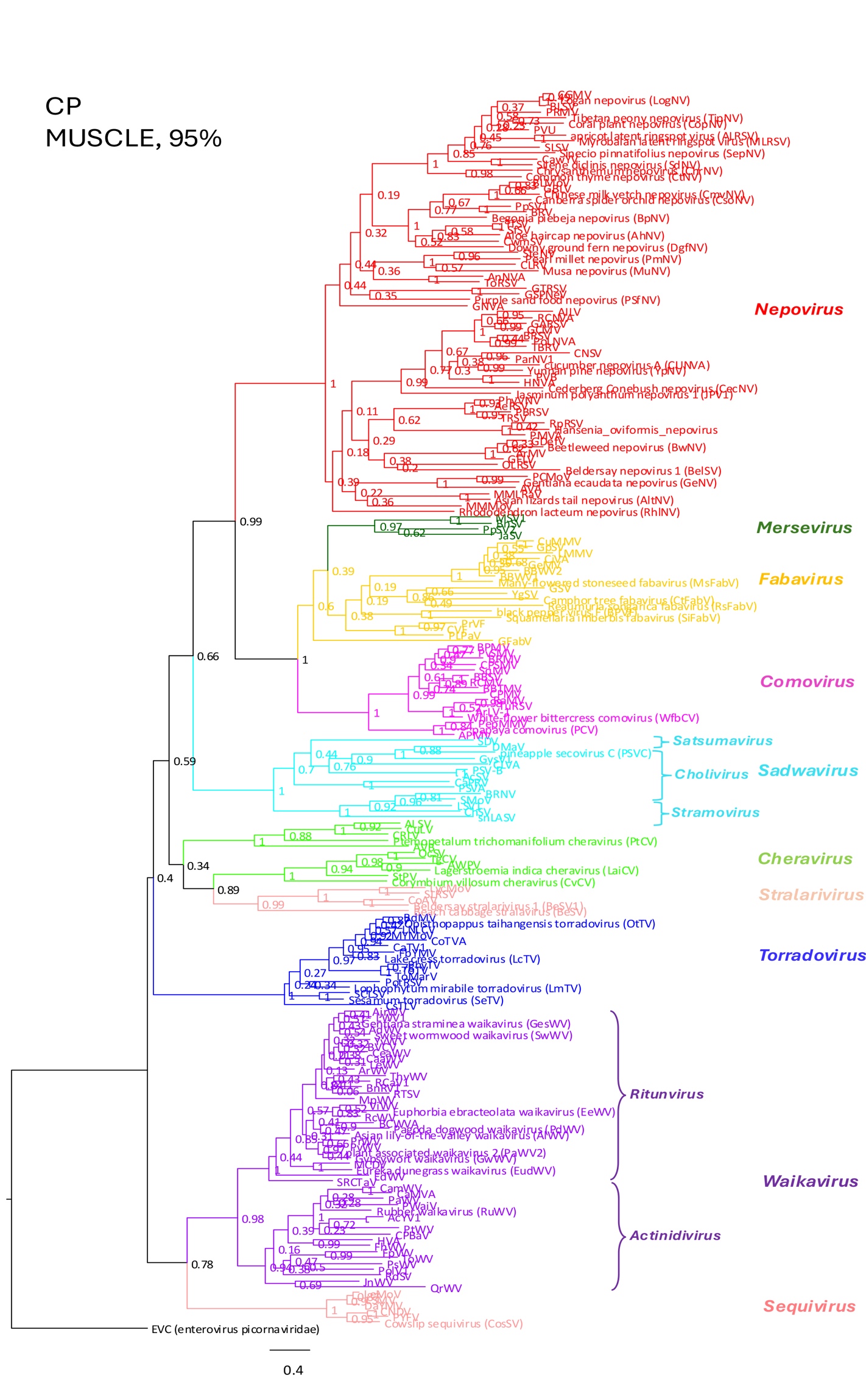
rubber waikavirus *Waikavirus heveae Waikavirus* BK065149 Sidhartan et al. 2024

sweet wormwood waikavirus *Waikavirus artemisiae Waikavirus* BK065150 Sidhartan et al. 2024

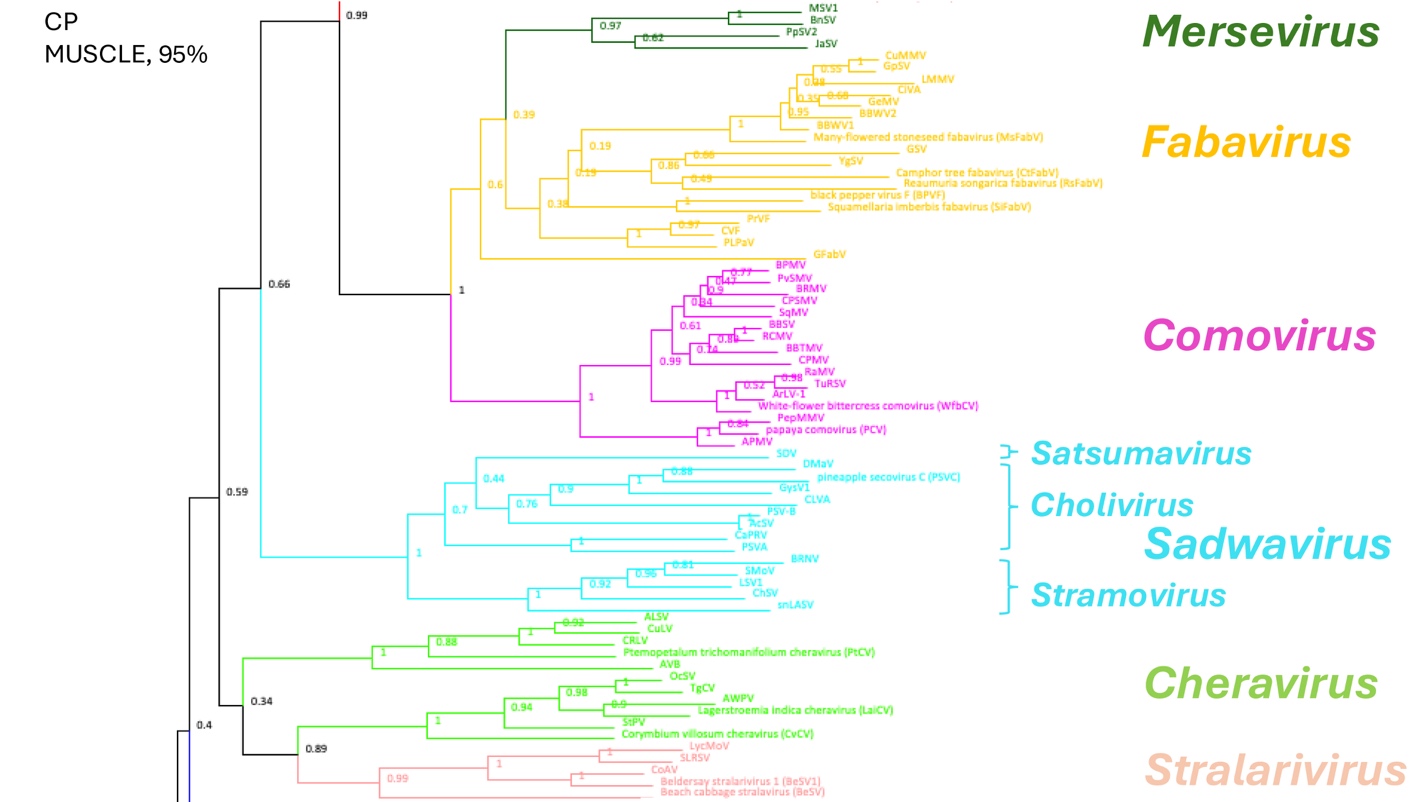
plant associated waikavirus 2 *Waikavirus duoplantae Waikavirus* OL472179 Selda Rivarez et al. 2023

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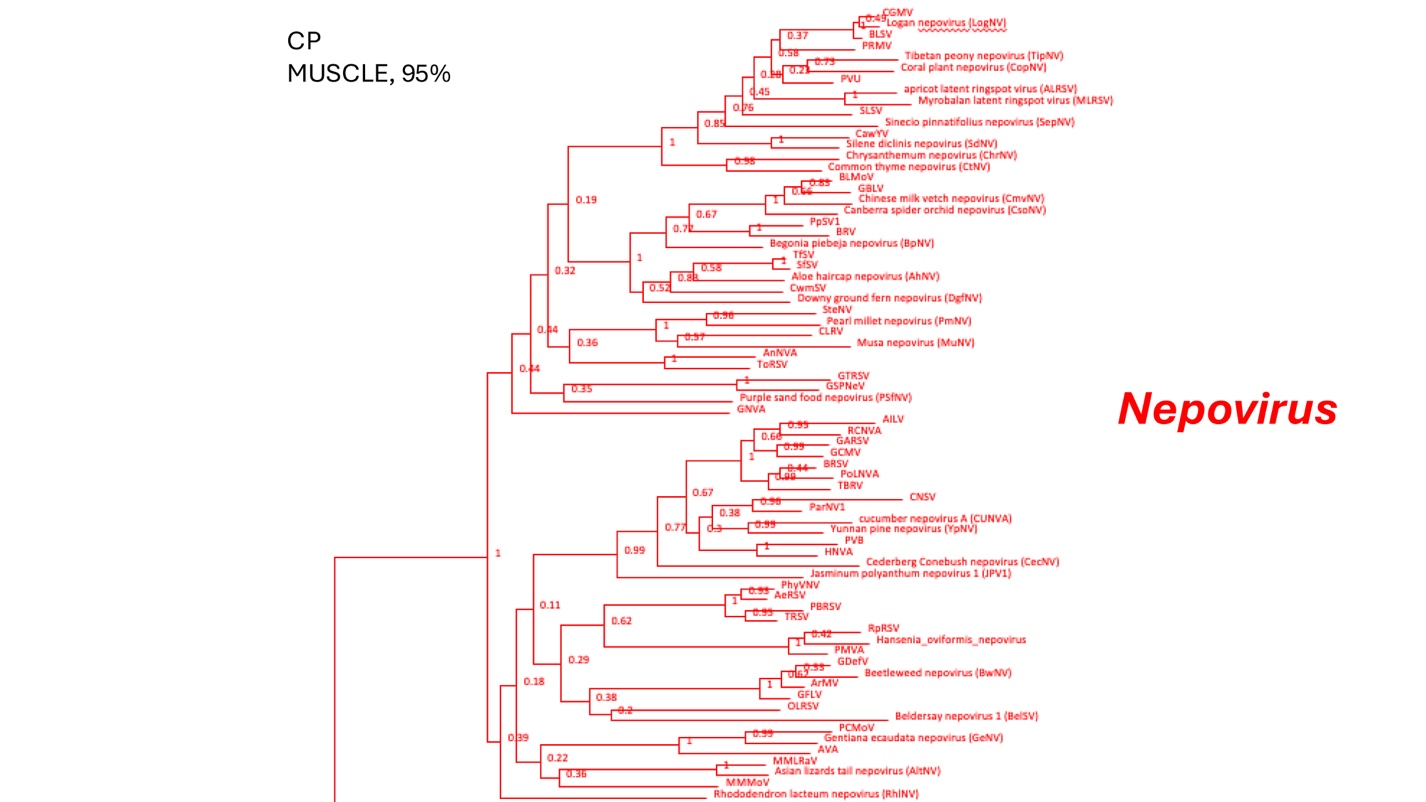
**Figure 1.** Genome organization of representative members of the 10 genera (*Comovirus*, *Fabavirus*, *Mersevirus*, *Nepovirus*, *Stralarivirus*, *Cheravirus*, *Sadwavirus*, *Torradovirus*, *Sequivirus*, *Waikavirus*) in the family *Secoviridae*. Each RNA is shown with open reading frames (ORFs) represented 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: Mercurialis secovirus 1 (exemplar isolate of the species *Mersevirus mercurialis*); 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 pastinacae*); and RTSV: rice tungro spherical virus (exemplar isolate of the species *Waikavirus oryzae*).

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**Figure 2**. Phylogenetic tree of the coat protein(s) amino acid sequences of the exemplified members of the 53 newly proposed species (identified by the full virus name and abbreviation) in the family *Secoviridae* and 155 representatives of the different genera in the family *Secoviridae.* The evolutionary history was inferred by using the Maximum Likelihood method and the model by Le and Gascuel (2008) [10]. The tree with the highest log likelihood (-136031.12) 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 the 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 = 6.3863)). The tree is drawn to scale, with branch lengths measured as the number of substitutions per site. This analysis involved 210 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 276 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [11].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), CUNVA (cucumber nepovirus A, PP376098), CtNV (common thyme nepovirus, BK065075), TipNV (Tibetan peony nepovirus, BK065119), ChrNV (chrysanthemum nepovirus, BK065073), SepNV (Senevia pinnatifolius nepovirus, BK065113), LogNV (logan nepovirus, BK065099), PsfNV (purple sand food nepovirus, BK065109), CopNV (coral plant nepovirus, BK065077), SdNV (Silene diclinis nepovirus, BK065115), BwNV (beetleweed nepovirus, 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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), PCV (papaya comovirus, MN203154), WfbCV (white-flower bittercress comovirus, BK065041), 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), BPVF (black pepper virus F, MZ648326), CtFabV (camphor tree fabavirus, BK065043), RsFabV (Reaumuria songarica fabavirus, BK065051), MsFabV (many-flowered stoneseed fabavirus, BK065049), SiFabV (Squamellatia imberbis fabavirus, BK065053), CuMMV (cucurbit mild mosaic virus, EU881937), LMMV (lamium mild mosaic virus, KC595305), GeMV (gentian mosaic virus, 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(Corymbium villosum cheravirus, BK065029), PtCV (Pternopetalum trichomanifolium, BK065037), 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), CosSV (cowslip sequivirus, BK065140), LcTV (lake cress torradovirus, BK065132), OtTV (Opisthopappus taihangensis torradovirus BK065136), LmTV (Lophophytum mirabile torradovirus, BK065134), SeTV 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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.

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**Figure 2A**. Close-up of the phylogenetic tree of the coat protein(s) amino acid sequences of the 14 newly proposed species (identified by the full virus name and abbreviation) in the genera *Fabavirus*, *Comovirus*, *Sadwavirus* (subgenera *Satsumavirus*, *Cholivirus*, *Stramovirus*) and *Cheravirus* of the family *Secoviridae*. This close-up was extracted from Figure 2. See caption of Figure 2 for details on the sequence analyses. Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in these six genera of the family *Secoviridae* are as follows: 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), PCV (papaya comovirus, MN203154), WfbCV (white-flower bittercress comovirus, BK065041), 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), BPVF (black pepper virus F, MZ648326), CtFabV (camphor tree fabavirus, BK065043), RsFabV (Reaumuria songarica fabavirus, BK065051), MsFabV (many-flowered stoneseed fabavirus, BK065049), SiFabV (Squamellatia imberbis fabavirus, BK065053), 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), PSVC (pineapple secovirus C, OP860285), ChSV (chrysanthemum sadwavirus, OR413568), ChrSV (chrysanthemum stramovirus, BK065127), 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), LaiCV (Lagerstroemia indica cheravirus, BK065035), CvCV (Corymbium villosum cheravirus, BK065029), PtCV (Pternopetalum trichomanifolium, BK065037), 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). 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.

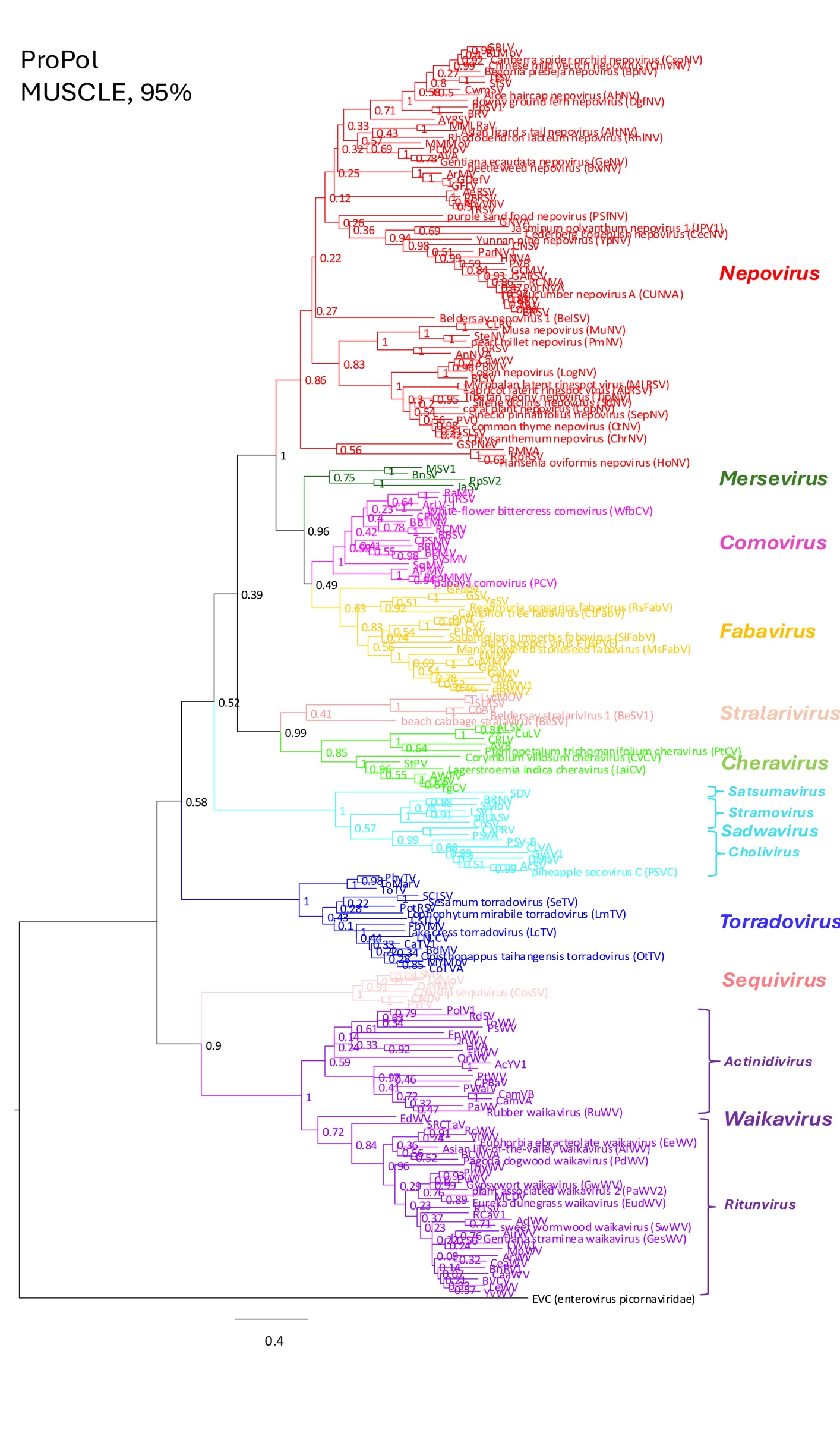


**Figure 2B**. Close-up of the phylogenetic tree of the coat protein(s) amino acid sequences of the 25 newly proposed species (identified by the full virus name and abbreviation) in the genus *Nepovirus* of the family *Secoviridae*. This close-up was extracted from Figure 2. See caption of Figure 2 for details on the sequence analyses. Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in the genus *Nepovirus* of 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), CUNVA (cucumber nepovirus A, PP376098), CtNV (common thyme nepovirus, BK065075), TipNV (Tibetan peony nepovirus, BK065119), ChrNV (chrysanthemum nepovirus, BK065073), SepNV (Senevia pinnatifolius nepovirus, BK065113), LogNV (logan nepovirus, BK065099), PsfNV (purple sand food nepovirus, BK065109), CopNV (coral plant nepovirus, BK065077), SdNV (Silene diclinis nepovirus, BK065115), BwNV (beetleweed nepovirus, BK065063), AltNV (Asian lizard’s tail nepovirus, BK065059), MuNV (Musa nepovirus, BK065103), PmNV (pearl millet nepovirus, BK065107), DgfNV (downy ground fern nepovirus, BK065079), AhNV (Aloe haircap nepovirus, BK065057), BpNV (Begonia plebeja nepovirus, BK065065), CsoNV (Canberra spider orchid nepovirus, BK065067), CmvNV (Chinese milk vectch nepovirus, BK065071), GeNV (Gentiana ecaudata nepovirus, BK065081), CecNV (Cederberg conebush nepovirus, BK065069), YpNV (Yunnan pine nepovirus, BK065121), RhiNV (Rhododendron lacteum nepvoris, BK065111), HoNV (Hansenia oviformis nepovirus, BK065089), BelSV1 (Beldersay nepovirus 1, OR912381), JPV1 (Jasminum polyanthum nepovirus 1, OQ943947), 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), and SfSV (shoestring fern secovirus, OX380478). 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 diagram of a tree

AI-generated content may be incorrect.

**Figure 2C**.Close-up of the phylogenetic tree of the coat protein(s) amino acid sequences of the 14 newly proposed species (identified by the full virus name and abbreviation) in the genera *Torradovirus*, *Sequivirus*, and *Waikavirus* of the family *Secoviridae*. This close-up was extracted from Figure 2. See caption of Figure 2 for details on the sequence analyses. Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in these three genera of the family *Secoviridae* are as follows: LycMoV (lychnis mottle virus, KR011032), CoAV (cohombrillo-associated virus, OP019481), SLRSV (strawberry latent ringspot virus, AY860978), BCSV (beach cabbage stralarivirus, BK065130), BeSV1 (Berldersay stralarivirus 1, OR912383), 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), CosSV (cowslip sequivirus, BK065140), LcTV (lake cress torradovirus, BK065132), OtTV (Opisthopappus taihangensis torradovirus, BK065136), LmTV (Lophophytum mirabile torradovirus, BK065134), SeTV (Sesamum torradovirus, BK065140), 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 (BesV1 (Beldersay stralarivirus 1, OR912383), BCSV (cabbage stralarivirus, BK065130), 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 (Mercurialis 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), 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), AlWV (Asian lily-of-the-valley waikavirus, BK065141), EeWV (Euphorbia ebracteolate waikavirus, BK065142 ), EudWV (Eureka dunegrass waikavirus, BK065143), GesWV (Gentiana straminae waikavirus, BK065144), GwWV (Gypsywort waikavirus, BK065145), PdWV (Pagoda dogwood waikavirus, BK065147), RuWV (Rubber waikavirus, BK065149), SwWV (Sweet wormwood waikavirus, BK065150), SwWV (Plant associated waikavirus 2, OL472179).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.

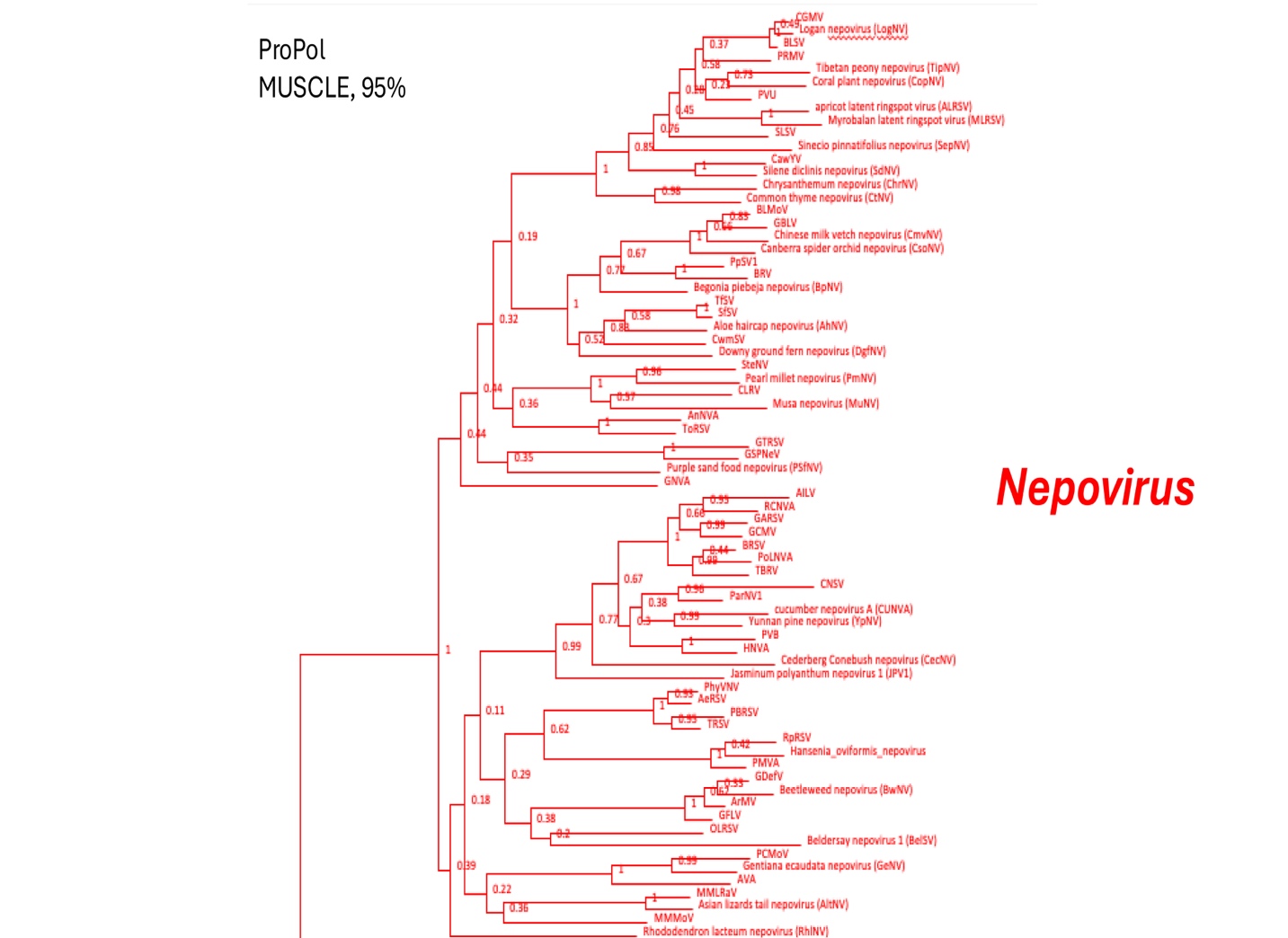
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**Figure 3.** Phylogenetic tree of the amino acid sequences of the conserved protease-polymerase (Pro-Pol) region (from the protease CG motif to the polymerase GDD motif) of the exemplified members of the 53 newly proposed species (identified by the full virus names and abbreviations) in the family *Secoviridae* and 155 representatives of the different genera in the family *Secoviridae.* The evolutionary history was inferred by using the Maximum Likelihood method and the model by Le and Gascuel (2008) [10]. The tree with the highest log likelihood (-66175.16) 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 the 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 = 1.5418)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 2.94% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 208 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 272 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [11]. 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), CUNVA (cucumber nepovirus A, PP376097), CtNV (common thyme nepovirus, BK065074), TipNV (Tibetan peony nepovirus, BK065118), ChrNV (chrysanthemum nepovirus, BK065072), SepNV (Senecio pinnatifolius nepovirus, BK065112), LogNV (logan nepovirus, BK065100), PsfNV (purple sand food nepovirus, BK065108), CopNV (coral plant nepovirus, BK065076), SdNV (Silene diclinis nepovirus, BK065114), BwNV (beetleweed nepovirus, BK065062), AltNV (Asian lizard’s tail nepovirus, BK065058), MuNV (Musa nepovirus, BK065102), PmNV (pearl millet nepovirus, BK065106), DgfNV (downy ground fern nepovirus, BK065078), AhNV (Aloe haircap nepovirus, BK065056), BpNV (Begonia plebeja nepovirus, BK065064), CsoNV (Canberra spider orchid nepovirus, BK065066), CmvNV (Chinese mild vectch nepovirus, BK065070), GeNV (Gentiana ecaudata nepovirus, BK065080), CecNV (Cederberg cone bush nepovirus, BK065089), YpNV (Yunnan pine nepovirus, BK065120), RhiNV (Rhododendron lacteum nepovirus, BK065110), HoNV (Hansenia oviformis nepovirus, BK065088), BelSV1 (Beldersay nepovirus 1, OR912380), JPV1 (Jasminum polyanthum nepovirus 1, OQ943946), 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)), PCV (papaya comovirus, MN203153), WfbCV (white-flower bittercress comovirus, BK065040), 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), BPVF (black pepper virus F, MZ648325), CtFabV (camphor tree fabavirus, BK065044), RsFabV (Reaumuria songarica fabavirus, BK065050), MsFabV (Mmany-flowered stoneseed fabavirus, BK065048), SiFabV (Squamellaria imberbis fabavirus, BK065052), 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), LaiCV (Lagerstoemia indica cheravirus, BK065034), CvCV (Corymbium villosum cheravirus, BK065028), PtCV (Pternopetalum trichomanifoliun cheravirus, BK065036), 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), CosSV (cowslip sequivirus, BK065140), 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 (Mercurialis 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), PSVC (pineapple secovirus C, OP860260), ChrSV (chrysanthemum stramovirus, BK065126), BesV1 (Berdersay stralarivirus, OR912382), BCSV (beach cabbage stralarivirus, BK065129), PhyTV (physalis torrado virus, MZ357183), LcTV (lake cress torradovirus, BK065131), OtTV (Opisthopappus taihangensis torradovirus, BK065135), LmTV (Lophophytum mirabile torradovirus, BK065133), SeTV (Sesamum torradovirus, BK065139), 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), AlWV (Asian lily-of-the-valley waikavirus, BK065141), EeWV (Euphorbia ebracteolate waikavirus, BK065142 ), EudWV (Eureka dunegrass waikavirus, BK065143), GesWV (Gentiana straminea waikavirus, BK065144), GwWV (Gypsywort waikavirus, BK065145), PdWV (Pagoda dogwood waikavirus, BK065147), RuWV (Rubber waikavirus, BK065149), SwWV (sweet wormwood waikavirus, BK065150), SwWV (plant associated waikavirus 2, OL472179), 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.

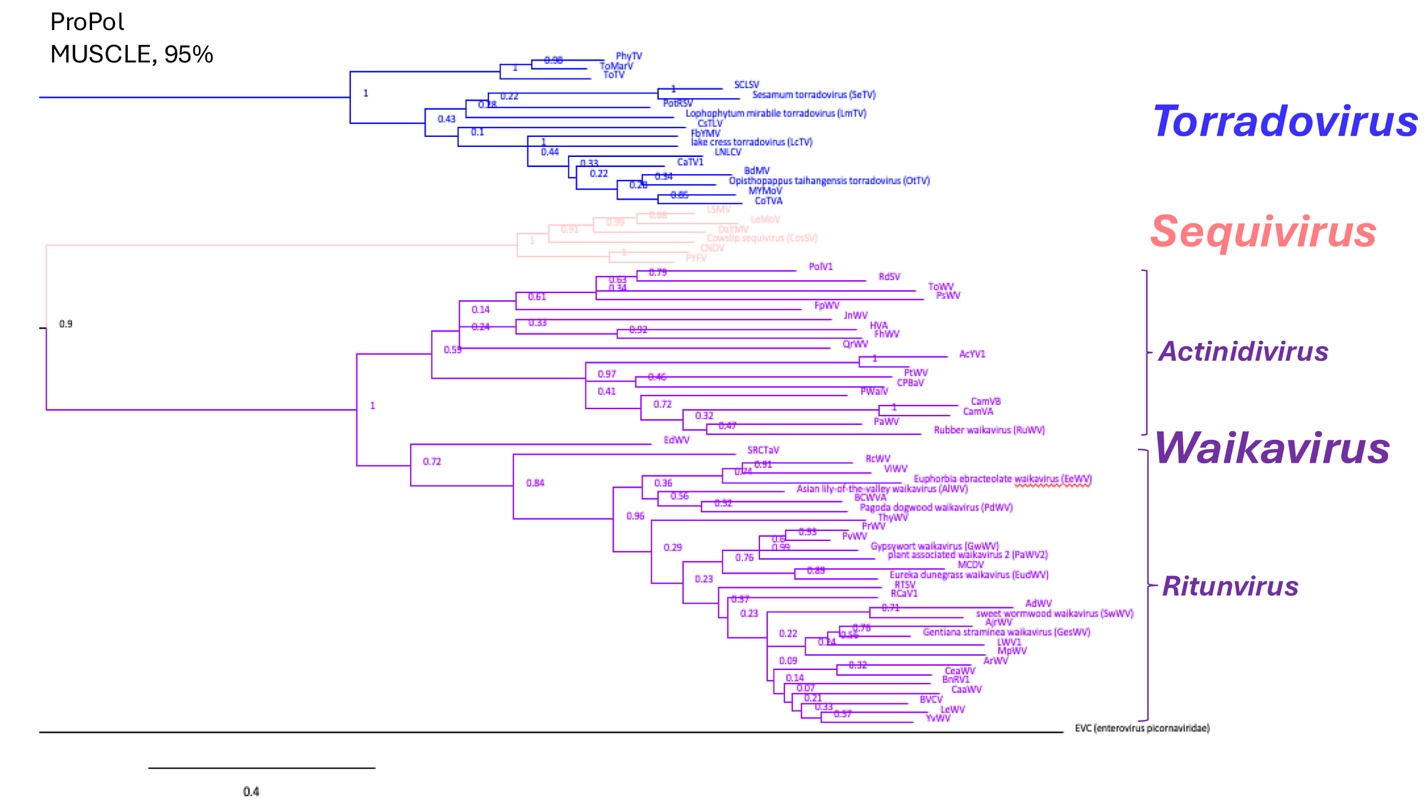
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AI-generated content may be incorrect.

**Figure 3A**.Close-up of the phylogenetic tree of the conserved protease-polymerase (Pro-Pol) region (from the protease CG motif to the polymerase GDD motif) of the 14 newly proposed species (identified by the full virus names and abbreviations) in the genera *Comovirus*, *Fabavirus*, *Sadwavirus*, *Stralarivirus* and *Cheravirus* of the family *Secoviridae*. This close-up was extracted from Figure 3. See caption of Figure 3 for details on the sequence analyses. Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in these three genera of the family *Secoviridae* are as follows: MSV1 (Mercurialis secovirus 1, OR544055), PpSV2 (Paris polyphylla secovirus 2, BK061330), BnSV (Boehmeria nivea secovirus, BK061322), JaSV (jujube-associated secovirus, QNN26328), 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)), PCV (papaya comovirus, MN203153), WfbCV (white-flower bittercress comovirus, BK065040), 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), BPVF (black pepper virus F, MZ648325), CtFabV (camphor tree fabavirus, BK065044), RsFabV (Reaumuria songarica fabavirus, BK065050), MsFabV (many-flowered stoneseed fabavirus, BK065048), SiFabV (Squamellaria imberbis fabavirus, BK065052), 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), LaiCV (Lagerstoemia indica cheravirus, BK065034), CvCV (Corymbium villosum cheravirus, BK065028), PtCV (Pternopetalum trichomanifoliun cheravirus, BK065036), CRLV (cherry rasp leaf virus, AJ621357), AVB (arracacha virus B, JQ437415), LycMoV (lychnis mottle virus, KR011032), CoAV (cohombrillo-associated virus, OP019481), SLRSV (strawberry latent ringspot virus, AY860978), 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), PSVC (pineapple secovirus C, OP860260), ChrSV (chrysanthemum stramovirus, BK065126), BesV1 (Berdersay stralarivirus, OR912382) and BCSV (beach cabbage stralarivirus, BK065129). 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.



**Figure 3B**. Close-up of the phylogenetic tree of the conserved protease-polymerase (Pro-Pol) region (from the protease CG motif to the polymerase GDD motif) of the 25 newly proposed species (identified by the full virus name and abbreviation) in the genus *Nepovirus* of the family *Secoviridae*. This close-up was extracted from Figure 3. See caption of Figure 3 for details on the sequence analyses. Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in the genus *Nepovirus* of 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), CUNVA (cucumber nepovirus A, PP376098), CtNV (common thyme nepovirus, BK065075), TipNV (Tibetan peony nepovirus, BK065119), ChrNV (chrysanthemum nepovirus, BK065073), SepNV (Senevia pinnatifolius nepovirus, BK065113), LogNV (logan nepovirus, BK065099), PsfNV (purple sand food nepovirus, BK065109), CopNV (coral plant nepovirus, BK065077), SdNV (Silene diclinis nepovirus, BK065115), BwNV (Beetleweed nepovirus, BK065063), AltNV (Asian lizard’s tail nepovirus, BK065059), MuNV (Musa nepovirus, BK065103), PmNV (pearl millet nepovirus, BK065107), DgfNV (downy ground fern nepovirus, BK065079), AhNV (Aloe haircap nepovirus, BK065057), BpNV (Begonia plebeja nepovirus, BK065065), CsoNV (Canberra spider orchid nepovirus, BK065067), CmvNV (Chinese milk vectch nepovirus, BK065071), GeNV (Gentiana ecaudata nepovirus, BK065081), CecNV (Cederberg conebush nepovirus, BK065069), YpNV (Yunnan pine nepovirus, BK065121), RhiNV (rhododendron lacteum nepvoris, BK065111), HoNV (Hansenia oviformis nepovirus, BK065089), BelSV1 (Beldersay nepovirus 1, OR912381), JPV1 (Jasminum polyanthum nepovirus 1, OQ943947), 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), and SfSV (shoestring fern secovirus, OX380478). 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.



**Figure 3C**.Close-up of the phylogenetic tree of the conserved protease-polymerase (Pro-Pol) region (from the protease CG motif to the polymerase GDD motif) of the 14 newly proposed species (identified by the full virus name and abbreviation) in the genera *Torradovirus*, *Sequivirus*, and *Waikavirus* of the family *Secoviridae*. This close-up was extracted from Figure 3. See caption of Figure 3 for details on the sequence analyses. Sequence accession numbers of exemplar isolates of recognized species and of viruses proposed as exemplar isolates of new species in these three genera of the family *Secoviridae* are as follows: 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), CosSV (cowslip sequivirus, BK065140), LcTV (lake cress torradovirus, BK065132), OtTV (Opisthopappus taihangensis torradovirus, BK065136), LmTV (Lophophytum mirabile torradovirus, BK065134), SeTV (Sesamum torradovirus, BK065140), 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 (BesV1 (Beldersay stralarivirus 1, OR912383), BCSV (beach cabbage stralarivirus, BK065130), 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 (Mercurialis 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), 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), AlWV (Asian lily-of-the-valley waikavirus, BK065141), EeWV (Euphorbia ebracteolate waikavirus, BK065142 ), EudWV (Eureka dunegrass waikavirus, BK065143), GesWV (Gentiana straminae waikavirus, BK065144), GwWV (gypsywort waikavirus, BK065145), PdWV (Pagoda dogwood waikavirus, BK065147), RuWV (rubber waikavirus, BK065149), SwWV (sweet wormwood waikavirus, BK065150), SwWV (plant associated waikavirus 2, OL472179).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.