

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2021.002P** |  |
| **Short title:** Create one new genus (*Stralarivirus*) and 20 new species in the family *Secoviridae (Picornavirales*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Secoviridae* Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | May 21, 2021 |
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**ICTV-EC comments and response of the proposer**

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| The Excel file was corrected and Fig. 3 was amended |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2021.002P.R.Secoviridae\_1ng\_20ns |

**Abstract**

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| This TP considers the creation of a new genus, i.e. *Stralarivirus* (Figure 1), and the recognition of the following 20 new virus species (Table 1) in the family *Secoviridae: Comovirus PepMMV*, *Comovirus PvSMV*, and *Comovirus ArLV1* in the genus *Comovirus; Fabavirus PLPaV* in the genus *Fabavirus*; *Nepovirus RCNVA*, *Nepovirus GNVA*, *Nepovirus GSPNeV*, *Nepovirus CawYV*, *Nepovirus PCMoV*, and *Nepovirus PoLNVA* in the genus *Nepovirus*; *Sadwavirus PSVA,* and *Sadwavirus LSV1* in the genus *Sadwavirus*; *Sequivirus LSMV* in the genus *Sequivirus; Waikavirus RCaV1*, *Waikavirus BnV1*, *Waikavirus PWaiV* , *Waikavirus BCWVA*, *Waikavirus AcYV1*, and *Waikavirus PolV1* in the genus *Waikavirus*; and *Stralarivirus* *LycMoV* in the newly proposed genus *Stralarivirus* based on species demarcation criteria in the family *Secoviridae* of less than 75% and 80% amino acid sequence identity in the coat protein(s) and conserved Pro-Pol region (from the protease CG motif to the polymerase GDD motif), respectively, and/ordistinct plant hosts and biological properties. |

**Text of proposal**

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| |  | | --- | | **Creation of a new genus in the family *Secoviridae*.** Recent determination of the complete genome sequence of five strawberry latent ringspot virus (SLRSV) isolates and the near complete genome sequence of 18 additional SLRSV isolates (Dullemans et al. 2020), as well as the characterization of lychnis mottle virus (LycMoV) (Yoo et al. 2015) yielded new amino acid sequence information of the large and small coat proteins (CPs) and conserved protease-polymerase (Pro-Pol) region. SLRSV has a bipartite RNA genome with a viral genome-linked protein (VPg) at the 5' end and a poly(A) tail at the 3' end (Figure 1). SLRSV was one of the founding members of the genus *Nepovirus*, mostly based on its transmission by nematodes, a characteristic common to many nepoviruses. It was later recognized to be significantly different from other nepoviruses and was reclassified in the newly created genus *Sadwavirus* in 2004. However, as more members of the family *Secoviridae* were characterized, SLRSV was recognized as distinct from other sadwaviruses and was removed from the genus *Sadwavirus* in 2009. It has been an unclassified species within the family *Secoviridae* since then (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017). The new sequence information of SLRSV and LycMoV prompted a proposal for the creation of a new genus tentatively named *Stralarivirus* (Figure 1) in the family *Secoviridae* (Dullemans et al. 2020). The genome organization of members of the proposed genus *Stralarivirus* is typical of members of the family *Secoviridae* that have a bipartite genome.The RNA1-encoded polyprotein contains proteins with conserved motifs for a protease co-factor (Pro-co), a helicase (Hel), a viral genome-linked protein (VPg), a protease (Pro) and an RNA-dependent RNA polymerase (Pol) (Figure 1). The RNA2-encoded polyprotein contains proteins with conserved motifs for a movement protein (MP) and two coat proteins (CPs) (Figure 1). Phylogenetic analyses using CP and Pro-Pol amino acid sequences showed that all SLRSV and LycMoV isolates form a distinct clade that is clearly separated from the other clades corresponding to the eight recognized genera (*Nepovirus*, *Fabavirus*, *Comovirus*, *Sadwavirus*, *Torradovirus*, *Cheravirus*, *Sequivirus*, *Waikavirus*) in the family *Secoviridae.* A multiple sequence alignment in ClustalW revealed 21-37.9% amino acid identity in the conserved Pro-Pol region of SLRSV and LycMoV isolates with other members of the family *Secoviridae*.At the CPs level, the overall amino acid sequence identity of SLRSV and LycMoV isolates with other members of the family *Secoviridae* is 7-14%. Maximum Likelihood phylogenetic trees using the amino acid sequence of the CP (Figure 2) and conserved Pro-Pol region (Figure 3) revealed the grouping of SLRSV and LycMoV into a clearly distinct clade. Based on low levels of sequence identity in the two taxonomic demarcation genomic regions (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), and distant relatedness of SLRSV and LycMoV with other members of the family *Secoviridae*, we propose the creation of a new genus named *Stralarivirus* in the family *Secoviridae*. The proposed genus *Stralarivirus* consists of two species: *Stralarivirus* *SLRSV* and *Stralarivirus LycMoV*. The name *Stralarivirus* derives from *stra*wberry *la*tent *ri*ngspot virus.  **Creation of a novel species in the proposed new genus *Stralarivirus* of the family *Secoviridae*.** A novel virus was identified in *Lychnis cognate* displaying virus-like symptoms in An-dong, Korea (Yoo et al. 2015). The virus was tentatively named lychnis mottle virus (LycMoV) (Table 1). Total RNA was isolated from symptomatic lychnis samples and a library was prepared after ribosomal RNA depletion for library construction and Illumina sequencing. Sequence reads were trimmed and assembled *de novo,* and sequence contigs were annotated. The complete genome sequence was obtained by RT-PCR with specific primers and 5' RACE and Sanger sequencing. The 3' end sequence was obtained by RT-PCR using an oligo(dT) primer and LycMoV specific primers followed by Sanger sequencing. The complete LycMoV genome sequence consists of two single-stranded RNAs of 7,428 (RNA1, GenBank accession number KR011032) and 3,724 (RNA2, GenBank accession number KR011033) nucleotides in size, excluding the poly(A) tail (Figure 4). The 5' and 3' untranslated regions of RNA1 are 232 and 413 nucleotides long, respectively, while those of RNA2 are 325 and 424 nucleotides long, respectively. The genome organization of LyCMoV is similar to that of strawberry latent ringspot virus (SLRSV) (Yoo et al. 2015). The LycMoV RNA1 encodes a polyprotein of 2,260 amino acids (253 kDa) which is predicted to be cleaved into a protease cofactor (Pro-co, 84 kDa), a helicase (Hel, 61 kDa), a genome-linked viral protein (VPg, 3 kDa), a protease (Pro, 29 kDa) and an RNA-dependent RNA polymerase (Pol, 76 kDa) (Figure 4). The LycMoV RNA2 encodes a polyprotein of 994 amino acids (110 kDa) which is predicted to be cleaved into a movement protein (MP, 40 kDa), a large coat protein (CP-L, 43 kDa) and a small coat protein (CP-S, 27 kDa) (Figure 4). The polyproteins encoded by the two genomic LycMoV RNAs are predicted to be cleaved by the viral 3C-like protease at Ser-Gly sites (Yoo et al. 2015). The CP and conserved Pro-Pol region of LycMoV have 63% and 92% amino acid sequence identity with SRLSV, the closest related virus in the proposed new genus *Stralarivirus*, respectively. Based on the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* LyCMoV could be considered as a novel virus based on its CP region but not on the Pro-Pol region. This situation is similar to BRSV and TBRV that are closely related in the Pro-Pol sequence (89% amino acid identity) but are much more divergent in the CP sequence (62% amino acid identity). ML phylogenetic trees generated using the CP (Figure 2) and conserved Pro-Pol sequences (Figure 3) of LyCMoV and representative members of the family *Secoviridae* revealed the clustering of LycMoV with SRLSV in a clearly separate clade, confirming that LycMoV is closely related to SRLSV in the genus *Stralarivirus*. Considering the species demarcation criteria for the family *Secoviridae* and acknowledging thatthe two major demarcation criteria (less than 75% amino acid sequence in the CP and less than 80% amino acid sequence in the conserved Pro-Pol region) do not need to be simultaneously met (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify lychnis mottle virus as a member of a novel species named *Stralarivirus LycMoV* in the proposed new genus *Stralarivirus* of the family *Secoviridae*.  **Creation of a first novel species in the genus *Sadwavirus* of the family *Secoviridae*.** A novel virus was identified in pineapple. The virus was tentatively named pineapple secovirus A (PSVA) (Larrea-Sarmiento et al. 2020) (Table 1). Total RNA was isolated from asymptomatic pineapple accession HANA 187 from a germplasm repository in Hilo, Hawaii, USA (Larrea-Sarmiento et al. 2020). Following ribosomal RNA depletion, a cDNA library was prepared and subjected to Illumina sequencing. After adapter trimming, sequence reads were assembled *de novo* and sequence contigs were annotated. Two sequence contigs suggested the presence of a putative new member of the family *Secoviridae*. The sequence of the 5' and 3' termini of RNA1 and RNA2 of PSVA was determined using RACE and Sanger sequencing. The complete sequence of the two genomic RNAs was 6,128 nucleotides for RNA1 (GenBank accession number MN809923) and 4,161 nucleotides for RNA2 (GenBank accession number MN809924) (Figure 5). RNA1 contains a large open reading frame encoding a polyprotein of 1,865 amino acids (210 kDa) that is predicted to be cleaved into a protease co-factor (49 kDa), a helicase (Hel, 52 kDa), a viral genome-linked protein (VPg, 3 kDa), a protease (Pro, 14 kDa), and an RNA-dependent RNA polymerase (Pol, 92 kDa) (Figure 5). RNA2 encodes a polyprotein of 1,119 amino acids (124 kDa) that is predicted to be cleaved into a movement protein (MP, 35 kDa), and a coat protein (CP, 89 kDa) (Figure 5). Predicted cleavage sites of the RNA1- and RNA2-encoded polyproteins are similar to those of other members of the genus *Sadwavirus* (Larrea-Sarmiento et al. 2020). Diagnostic primers designed in the RNA1-encoded Pol segment, and the RNA2-encoded CP coding region used in RT-PCR revealed the presence of PSVA in additional pineapple samples from commercial fields that exhibited virus-like symptoms (Larrea-Sarmiento et al. 2020). Amino acid alignments of PSVA CP (Figure 2) and Pro-Pol (Figure 3) sequences and those of members of the family *Secoviridae* alongside ML phylogenetic trees showed clustering of PSVA in the subgenus *Cholivirus* of the genus *Sadwavirus*,family *Secoviridae*, and the close relationship of PSVA with dioscorea mosaic-associated virus (DMaV) and chocolate lily virus A (CLVA), two members of the subgenus *Cholivirus* in the genus *Sadwavirus*. Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify pineapple secovirus A as a member of a novel species named *Sadwavirus PSVA* in the genus *Sadwavirus*, subgenus *Cholivirus*, of the *family Secoviridae*.  **Creation of a second novel species in the genus *Sadwavirus* of the family *Secoviridae*.** A near complete genome sequence of a bipartite RNA virus tentatively named lettuce secovirus 1 (LSV1) (Table 1)was submitted to GenBank as accession numbers KX925437 (RNA1) and KX925438 (RNA2) (Micali et al. 2016). The lettuce (*Lactuca sativa*) sample from which the viral sequence is derived was collected in the United Kingdom in 2015. The genome of LSC1 was determined by high throughput sequencing (Micali et al. 2016). The genome organization and predicted expression suggested LSV1 as a member of the family *Secoviridae* (Figure 6).The partial sequences of LSV1 RNA1 and RNA2 consist of 6,001 and 6,553 nucleotides and encode a large polyprotein of 1,979 and 1,740 amino acids, respectively. The RNA1-encoded polyprotein has typical conserved helicase and RNA-dependent RNA polymerase motifs (Micali et al. 2016) (Figure 6). The RNA2-encoded polyprotein contains the MP and CP domains, as well two predicted domains in the C-terminal region of the polyprotein, the first of which contains signature motifs for a glutamic protease domain similar to that characterized for strawberry mottle virus (SMoV) and also identified in black raspberry necrotic virus (BRNV) from the genus *Sadwavirus,* subgenus *Stramovirus,* in the family *Secoviridae* (Mann et al. 2019). The CP and conserved Pro-Pol regions share amino acid sequence identity of 38-42% and 26-61%, respectively, with orthologs of strawberry mottle virus (SMoV) and black raspberry necrotic virus (BRNV) from the genus *Sadwavirus,* subgenus *Stramovirus,* in the family *Secoviridae*. ML phylogenetic trees using CP (Figure 2) and Pro-Pol (Figure 3) amino acid sequences showed clustering of LSV1 in the subgenus *Stramovirus* of the genus *Sadwavirus*,and the close relationship of LSV1 with SMoV and BRNV. Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify lettuce secovirus 1 as a member of a novel species named *Sadwavirus LSV1* in the genus *Sadwavirus*, subgenus *Stramovirus*, of the family *Secoviridae*.  **Creation of one novel species in the genus *Sequivirus* of the family *Secoviridae*.** The complete genome of a monopartite RNA virus tentatively named lettuce star mosaic virus (LSMV) (Table 1)was determined by Illumina sequencing from a lettuce (*Lactuca sativa*) sample in France and was submitted to GenBank as accession number MT348706. The viral genome is 10,183 nucleotides in size and encodes a single large polyprotein of 3,017 amino acids (Svanella-Dumas et al. 2020). The polyprotein is predicted to be cleaved into a hypothetical protein P1 (P1, 42 kDa), a coat protein 1 (CP1, 21 kDa), a coat protein 2 (CP2, 24 kDa), a coat protein 3 (CP3, 26 kDa), a helicase (Hel), a protease (Pro) and an RNA-dependent RNA polymerase (Pol) (Figure 7). The genome structure is similar to that of sequiviruses. The CP and conserved Pro-Pol regions share amino acid sequence identity of 16-53% and 72%, respectively, with orthologs of parsnip yellow fleck virus (PYFV) and carrot necrotic dieback virus (CNDV) from the genus *Sequivirus* in the family *Secoviridae*. ML phylogenetic trees using CP (Figure 2) and Pro-Pol (Figure 3) amino acid sequences showed clustering of LSMV in the genus *Sequivirus*,and the close relationship of LSMV with PYFV and CNDV. Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify lettuce start mosaic virus as a member of a novel species named *Sequivirus LSMV* in the genus *Sequivirus*, of the family *Secoviridae*.  **Creation of a novel species in the genus *Fabavirus* of the family *Secoviridae.*** Total RNA isolated from leaves of a peach tree (XJ-6) in Wuhan, Hubei province, in China were used for small RNA Illumina sequencing (He et al. 2017). Raw reads were trimmed and assembled. After removal of noncoding RNAs and host genomic RNAs, sequence contigs were used to query GenBank databases using BLAST. Analyses revealed high amino acid sequence similarities with members of the subfamily *Comovirinae* in the family *Secoviridae*. The new virus was tentatively named peach leaf pitting-associated virus (PLPaV) (He et al. 2017) (Table 1). Sequence gaps of the PLPaV genome were filled by RT-PCR using specific primers and Sanger sequencing. The 5' and 3' terminal sequences of the two genomic viral RNAs were determined by RACE. The siRNA-assembled PLPaV genome sequences were validated by Sanger sequencing of RT-PCR products covering the entire genome. The complete bipartite RNA genome of PLPaV was 6,357 nucleotides (RNA1, GenBank accession number KY867750) and 3,834 nucleotides (RNA2, KY8677751) long, excluding the poly(A) tails (He et al. 2017). The genome organization of PLPaV is similar to that of fabaviruses (Figure 8). The 5' and 3' untranslated regions of PLPaV RNA1 are 238 and 308 nucleotides in size, respectively. RNA1 contains a single large open reading frame of 1,919 amino acids (217 kDa) predicted to be cleaved into a proteinase co-factor (Pro-co, 46 kDa), a helicase (Hel, 66 kDa), a genome-linked protein (VPg, 3 kDa), and protease (Pro, 23 kDa) and an RNA-dependent RNA polymerase (Pol, 80 kDa) (He et al. 2017) (Figure 8). The 5' and 3' untranslated regions of PLPaV RNA2 are 216 and 625 nucleotides in size, respectively. The 5' untranslated regions of both genomic RNAs are predicted to form stem/loop structures (He et al. 2017). PLPaV RNA2 contains a single open reading frame of 996 amino acids (109 kDa) predicted to be cleaved into a movement protein (MP, 47 kDa), a large coat protein (CP-L, 40 kDa) and a small coat protein (CP-S, 22 kDa) (Figure 8). The proteolytic cleavage sites of the PLPaV polyproteins are identical to those of prunus virus F (PrVF) (He et al. 2017). A BLASTp search revealed 49% amino acid sequence identity in the CPs (large and small) of PLPaV and PrVF, its closest related viruses in the genus *Fabavirus,* and 77% in the conserved Pro-Pol region*.* Phylogenetic trees using CP (Figure 2) and Pro-Pol (Figure 3) amino acid sequences revealed clustering of PLPaV with other members of the genus *Fabavirus* in the family *Secoviridae.* Diagnostic nested RT-PCR with specific primers revealed the presence of PLPaV in GF305 peach seedlings grafted with buds of the original infected peach tree XJ-6. PLPaV was also mechanically transmitted to several herbaceous species of the families *Fabaceae*, *Solanaceae*, *Cucurbitaceae* and *Chenopodiaceae* but the virus titer was low, except in *Pisum sativum* (He et al. 2017). PLPaV was also identified in a few additional peach trees in germplasm repositories in Wuhan and Zhengzhou provinces (He et al. 2017). Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify peach leaf pitting-associated virus A as a member of a novel species named *Fabavirus PLPaV* in the genus *Fabavirus*, family *Secoviridae.*  **Creation of a first novel species in the genus *Comovirus* of the family *Secoviridae.*** Double-stranded (ds) RNAs isolated from tabasco pepper (*Capsicum frutescens*) infected with a comovirus in Honduras were treated with DNAse 1 and S1 nuclease and resolved by electrophoresis on agarose gels (Alcalá-Briseño et al. 2019). Two dsRNAs of approximately 6.0 kbp and 4.0 kbp were gel-purified, denatured at 95°C for 5 min and used to prepare cDNA libraries for Illumina sequencing. Sequence reads were trimmed and assembled *de novo*. Two sequence contigs represented the full-length sequence of RNA1 (6,028 nucleotides, GenBank accession number MK990555) and RNA2 (3,646 nucleotides, GenBank accession number MK990556) of a new comovirus, tentatively named pepper mild mosaic virus (PepMMV) (Alcalá-Briseño et al. 2019) (Table 1). RNA1 contains a single large open reading frame of 1,957 amino acids (215 kDa) predicted to be cleaved into a protease co-factor (Pro-co, 43 kDa), a helicase (Hel, 66 kDa), a viral protein genome-linked (VPg, 3 kDa), a protease (Pro, 23 kDa) and an RNA-dependent RNA polymerase (Pol, 81 kDa) (Figure 9). The 5' and 3' untranslated RNA1 sequences are 90 and 157 nucleotides long, respectively (Alcalá-Briseño et al. 2019). RNA2 contains a single large open reading frame of 1,003 amino acids (110 kDa) predicted to be cleaved into a movement protein (MP, 46 kDa), a large coat protein (CP-L, 42 kDa) and a small coat protein (CP-S, 22 kDa) (Figure 9). The 5' and 3' untranslated RNA2 sequences are 460 and 177 nucleotides long, respectively (Alcalá-Briseño et al. 2019). Pairwise amino acid sequence alignment of the conserved Pol-Pro region revealed that PepMMV shares the closest identity with broad bean true mosaic virus (BBTMV, 56%) and cowpea mosaic virus (CPMV, 54%). Pairwise amino acid sequence alignment of the CP revealed that PepMMV shares the closest identity with Andean potato mottle virus (APMV, 54%) and red clover mottle virus (RCMV, 41%) from the genus *Comoviru*s in the family *Secoviridae*. A ML phylogenetic tree using the amino acid sequence of the CP (Figure 2) and conserved Pro-Pol region (Figure 3) revealed that PepMMV clusters with other members of the genus *Comovirus*. A diagnostic RT-PCR assay showed the occurrence of PepMMV in pepper in several locations in Honduras and Nicaragua (Alcalá-Briseño et al. 2019). Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify pepper mild mosaic virus as a member of a novel species named *Comovirus PepMMV* in the genus *Comovirus,* family *Secoviridae*.  **Creation of a second novel species in the genus *Comovirus* of the family *Secoviridae.*** Total RNA was isolated from a common bean plant exhibiting necrotic lesions, mosaic, local and apical necrosis in Mexico and enriched in small RNA to prepare a cDNA library that was sequenced on an Illumina platform (Chiquito-Almanza et al. 2020). Two large viral sequence contigs were identified and the complete viral genome sequence was obtained by RT-PCR with six pairs of primers and Sanger sequencing. The 5' and 3' sequences were obtained using RACE and Sanger sequencing. The novel virus tentatively named Phaseolus vulgaris severe mosaic virus (PvSMV) (Table 1)shows a typical genome organization of comoviruses (Chiquito-Almanza et al. 2020). RNA1 consists of 5,947 nucleotides (GenBank accession number MN837498) and contains a polyprotein of 1,856 amino acids (210 kDa) that is predicted to be cleaved into a putative protease cofactor (Pro-co, 34 kDa), a helicase (Hel, 68 kDa), a viral genome-linked protein (VPg, 3 kDa) and an RNA-dependent RNA polymerase (Pol, 81 kDa) (Figure 10). RNA2 consists of 3,721 nucleotides (GenBank accession number MN837499) and contains a polyprotein of 1,024 amino acids (114 kDa) that is predicted to be cleaved into a movement protein (MP, 50 kDa), a large coat protein (CP-L, 41 kDa) and a small coat protein (CP-S, 22 kDa) (Figure 10). The 5' and 3' untranslated region of RNA1 is 260 and 116 nucleotides long, respectively, and those of RNA2 is 245 and 401 nucleotides long, respectively (Chiquito-Almanza et al. 2020). The highest amino acid sequence identity in the CP (65%) and conserved Pro-Pol region (75%) was obtained with those of bean pod mottle virus (BPMV) from the genus *Comovirus* in the family *Secoviridae*. Phylogenetic trees using CP (Figure 2) and conserved Pro-Pol (Figure 3) amino acid sequences showed PvSMV and BPMV on the same branch in a cluster containing comoviruses. Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify Phaseolus vulgaris severe mosaic virus as a member of a novel species named *Comovirus PvSMV* in the genus *Comovirus,* family *Secoviridae*.  **Creation of a third novel species in the genus *Comovirus* of the family *Secoviridae.*** A novel virus species was isolated from *Arabidopsis thaliana* in The Netherlands (van der Vlugt et al. 2018). A transcriptome analysis of several *Arabidopsis* ecotypes by RNA-Seq analysis and BLASTn and BLASTx analyses of the RNA-Seq datasets showed high levels of sequence identities with radish mosaic virus (RaMV) from the genus *Comovirus,* as well as the unclassified turnip ringspot virus (TuRSV). The new virus was tentatively named Arabidopsis latent virus 1 (ArLV-1) (Table 1). The full-length genomic sequence of ArLV-1 was deposited at NCBI as accession numbers MH899120 for RNA1 and MH899121 for RNA2. ArLV-1 does not cause any symptoms in most *Arabidopsis thaliana* ecotypes, but the virus is mechanically transmitted to *Nicotiana benthamiana* and *N. occidentalis* P1, onto which mosaic and leaf crinkling symptoms are apparent (van der Vlugt, unpublished). ArLV1 is seed transmitted. Spherical particles typical of comoviruses were observed in preparations of infected *N. benthamiana* by transmission electron microscopy. Diagnostic RT-qPCR using specific primers designed on RNA1 and RNA2 was developed for quantification of ArLV1 in plant tissue (van der Vlugt, unpublished). RNA1 consists of 5,940 nucleotides and contains a large open reading frame encoding a polyprotein of 1,850 amino acids. The polyprotein is predicted to be cleaved into a protease co-factor (Pro-co), a helicase (Hel), a viral-genome linked protein (VPg), a protease (Pro), and an RNA-dependent RNA polymerase (Pol) (Figure 11). RNA2 consists of 3,588 nucleotides and contains one large open reading frame encoding a polyprotein of 1,046 amino acids with a putative movement protein (MP), a large coat protein (CP-L), and a small coat protein (CP-S) (Figure 11). ArLV1 shares 21.0-63.3% and 47.7-85.5% amino acid sequence identity in the CP and Pro-Pol % aa sequence identity with other comoviruses. ML trees using the amino acid sequence of the CP (Figure 2) and conserved Pro-Pol region (Figure 3) clearly group ArLV within the genus *Comovirus*. Considering the species demarcation criteria for the family *Secoviridae* and acknowledging thatthe two major demarcation criteria (less than 75% amino acid sequence in the CP and less than 80% amino acid sequence in the conserved Pro-Pol region) do not need to be simultaneously met (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify Arabidopsis latent virus-1 as a member of a novel species named *Comovirus ArLV1* in the genus *Comovirus,* family *Secoviridae*.  **Creation of a first novel species in the genus *Nepovirus* of the family *Secoviridae.*** A new virus was isolated from red clover in the Czech Republic (Koloniuk et al. 2018). The virus was tentatively named red clover nepovirus A (RCNVA) (Table 1). Double-stranded RNA was isolated from a red clover plant (B46) exhibiting stunted growth, and irregular vein clearing and chlorotic spots of leaves, and processed for the construction of a cDNA library for Illumina sequencing (Koloniuk et al. 2018). Sequence reads were quality trimmed and assembled *de novo*. Several sequence contigs related to a new nepovirus were identified. The complete RCNVA genome was obtained using 5' and 3' RACE and Sanger sequencing. RNA1 consists of 7,326 nucleotides (GenBank accession number MG253828) and encodes a polyprotein (254 kDa) that is putatively cleaved into a X1 protein (X1, 49 kDa), a X2 protein (X2, 17 kDa), a helicase (Hel, 68 kDa), a viral genome-linked protein (VPg, 3kDa), a protease (Pro, 23 kDa) and an RNA-dependent RNA polymerase (Pol, 91 kDa) (Figure 12). RNA2 consists of 4,682 nucleotides (GenBank accession MG253829) and encodes a polyprotein (152 kDa) that is putatively cleaved into a 2A protein (2A, 48 kDa), a movement protein (MP, 46 kDa) and a coat protein (CP, 58 kDa) (Figure 12). Pairwise CP (48%-65% identity) and Pro-Pol (81%-93% identity) amino acid sequence alignments demonstrated the relatedness of RCNVA with tomato black ring virus (TBRV), beet ringspot virus (BRSV) and artichoke latent Italian virus (AILV) from the formerly recognized subgroup B in the genus *Nepovirus*. Phylogenetic analyses of amino acid sequences of the CP (Figure 2) and conserved Pro-Pol (Figure 3) regions of RCNVA and members of the family *Secoviridae* revealed the relatedness of RCNVA with nepoviruses from formerly recognized subgroup B. Considering the species demarcation criteria for the family *Secoviridae* and acknowledging thatthe two major demarcation criteria (less than 75% amino acid sequence in the CP and less than 80% amino acid sequence in the conserved Pro-Pol region) do not need to be simultaneously met (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify red clover nepovirus A as a member of a novel species named *Nepovirus RCNVA* in the genus *Nepovirus* of the family *Secoviridae*.  **Creation of a second novel species in the genus *Nepovirus* of the family *Secoviridae.*** A novel virus was isolated from symptomatic bluegrass (*Poa trivalis*) in Belgium (Maclot et al. 2021). The virus was tentatively named poaceae Liege nepovirus A (PoLNVA) (Table 1). Leaf and stem samples of 50 bluegrass plants were pooled and virus particle enrichments was performed by virion-associated nucleic acids extraction. Following library preparation, sequencing was performed on a NextSeq 500 platform. Sequencing reads were trimmed assembled *de novo,* and sequence contigs were analyzed by BLASTx. Several contigs presented similarities with tomato black ring virus (TBRV) and beet ringspot virus (BRSV) from the genus *Nepovirus*, formerly recognized subgroup B, in the family *Secoviridae*. The sequence of the 5' and 3' ends were determined by RACE and Sanger sequencing. The complete PoLNVA genome was 7,298 nucleotides long for RNA1 (GenBank accession number MW289235) and 4,263 nucleotide long for RNA2 (GenBank accession number MW289236) (Figure 13). The 5' and 3' untranslated regions were 157 and 295 nucleotides for RNA1, and 196 and 287 nucleotides for RNA2 (Maclot et al. 2021). ML trees using amino acid sequences of the conserved Pro-Pol region (Figure 3) showed that PoLNVA cluster with formerly recognized subgroup B nepoviruses with TRBV (91%) and BRSV (87%) being the closest relatives. However, the PoLNVA CP showed lower amino acid sequence identities with TBVV (57%) and BRV (67%) but phylogenetic relationships confirmed PoLNVA with subgroup B nepoviruses (Figure 2). Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* PoLNVA could be considered as a novel virus based on its CP region but not on the Pro-Pol region. This situation is similar to BRSV and TBRV that are closely related in the Pro-Pol sequence (89% amino acid sequence identity) but are much more divergent in the CP sequence (62% amino acid sequence identity). Diagnostic RT-PCR using specific primers designed in the RNA1 and RNA2 revealed the presence of PoLNVA in the majority (78%) of samples tested, including additional perennial and annual Poaceae species with a prevalence in meadow soft grass and ryegrass (Maclot et al. 2021). PoLNVA is seed transmitted in ryegrass. Considering the species demarcation criteria for the family *Secoviridae* and acknowledging thatthe two major demarcation criteria (less than 75% amino acid sequence in the CP and less than 80% amino acid sequence in the conserved Pro-Pol region) do not need to be simultaneously met (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify poaceae Liege nepovirus A as a member of a novel species named *Nepovirus PoLNVA* in the genus *Nepovirus* of the family *Secoviridae*.  **Creation of a third novel species in the genus *Nepovirus* of the family *Secoviridae.***  A novel virus was identified in an asymptomatic *Vitis vinifera* from France (Al Rwahnih et al. 2021). This virus was tentatively named grapevine nepovirus A (GNVA) (Table 1). None of the conventional *Vitis* indicators exhibited disease symptoms following chi bud inoculation, but the virus was mechanically transmissible to *Chenopodium amaranticolor* and *Chenopodium quinoa*, onto which chlorotic ringspots developed. Transmission electron microscopy of virus preparations from symptomatic *C. quinoa* revealed spherical virions of 27 nm in diameter (Al Rwahnih et al. 2021). Total RNA was isolated from symptomatic *C. quinoa* and the source *Vitis vinifera,* depleted of ribosomal RNA and used for cDNA library construction for Illumina sequencing. High throughput sequencing showed the presence of nepovirus-like sequence contigs in symptomatic *C. quinoa* and the source *V. vinifera*. A bipartite RNA genome was assembled from the contigs and the 5' and 3' terminal sequences were obtained by RACE and Sanger sequencing (Al Rwahnih et al. 2021). RNA1 consists of 7,186 nucleotides (GenBank accession number MT507290) encoding a large polyprotein (231 kDa) (Figure 14). RNA2 consists of 4,460 nucleotides (GenBank accession number MT507291) encoding a large polyproptein (140 kDa) (Figure 14). The 5' and 3' untranslated regions are 156 and 834 nucleotides long for RNA1, and 170 and 261 nucleotides long for RNA2, respectively (Al Rwahnih et al. 2021). ML phylogenetic analyses of the CP (Figure 2) and conserved Pro-Pol (Figure 3) amino acid sequences revealed clustering of GNVA within the genus *Nepovirus* in the family *Secoviridae*. The ML phylogenetic tree generated with CP sequences showed clustering of GNVA with formerly recognized subgroup B nepoviruses while the ML phylogenetic tree generated with Pro-Pol sequences showed clustering of GNVA with formerly recognized subgroup C nepoviruses. No recombination event was found within the GNVA genomic sequences (Al Rwahnih et al. 2021). Diagnostic RT-PCR revealed the presence of GNVA in the source grapevine but in none of the additional 1,644 samples tested (Al Rwahnih et al. 2021). Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017)*,* we propose to classify grapevine nepovirus A as a member of a novel species named *Nepovirus GNVA* in the genus *Nepovirus* of the family *Secoviridae*.  **Creation of a fourth novel species in the genus *Nepovirus* of the family *Secoviridae.*** A novel virus was identified and characterized from caraway (*Carum carvi* L.) in Germany (Gaafar et al. 2019). The virus was mechanically transmissible to *Nicotiana benthamiana* onto which chlorotic local lesions developed (Gaafar et al. 2019). Isomeric virus particles of about 30 nm in diameter were observed in infected caraway tissue by electron microscopy. In addition, tubules containing virus-like particles were observed by electron microscopy in tissue of infected *N. benthamiana* (Gaafar et al. 2019). The virus was tentatively named caraway yellows virus (CawYV) (Table 1). Double-stranded RNA was isolated from infected *N. benthamiana* and used for cDNA library preparation and high throughput sequencing on an Illumina platform. Sequence reads were trimmed, normalized and assembled *de novo*. The sequence of the 5' ends of both RNA segments were obtained by RACE and Sanger sequencing, and the 3' end sequences were obtained by RT-PCR using an oligo(dT) primer and specific primers (Gaafar et al. 2019). The full-length genome of CawYV consists of 8,026 nucleotides for RNA1 (GenBank accession number MK492273) and 6,405 nucleotides for RNA2 (GenBank accession number MK492274), excluding the poly(A) tails. The 5’ untranslated region is 91 nucleotides long for RNA1 and 94 nucleotides long for RNA2. The 3' untranslated region is 1,293 nucleotides long for RNA1 and 1,289 nucleotides long for RNA2 (Gaafar et al. 2019). RNA1 contains a large open reading frame encoding a polyprotein of 2,213 amino acids (247 kDa) that is predicted to be cleaved into a X1 protein (X1, 46 kDa), a protease cofactor (Pro-co, 18 kDa), a helicase (Hel, 73 kDa), a viral genome-linked protein (VPg, 3 kDa), a protease (Pro, 27 kDa), and an RNA-dependent RNA polymerase (Pol, 82 kDa) (Figure 15). RNA2 contains a large open reading frame encoding a polyprotein of 1,673 amino acids (185 kDa) that is predicted to be cleaved into a N-terminal protein (2A, 82 kDa), a movement protein (MP, 43 kDa), and a coat protein (CP, 59 kDa) (Figure 15). A diagnostic RT-PCR confirmed the presence of CawYV in infected plants (Gaafar et al. 2019). The CawYV amino acid sequence shares the highest identities with those of formerly recognized subgroup C nepoviruses such as peach rosette mosaic virus (PRMV) (80.1% in the conserved Pro-Pol region) and soybean latent spherical virus (SLSV) (39.6% in the CP). Phylogenetic analysis of the CawYV CP (Figure 2) and Pro-Pol (Figure 3) amino acid sequences provided additional evidence of its association with formerly recognized subgroup C nepoviruses. Based on particle morphology and considering the species demarcation criteria for the family *Secoviridae* while acknowledging that the two major criteria (less than 75% amino acid sequence in the CP and less than 80% amino acid sequence in the conserved Pro-Pol region) do not need to be simultaneously met (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify caraway yellows virus as a member of a novel species named *Nepovirus CawYV* in the genus *Nepovirus* in the family *Secoviridae*.  **Creation of a fifth novel species in the genus *Nepovirus* of the family *Secoviridae.*** A novel virus was identified in green Sichuan pepper(*Zanthoxylum armatum* v*. novemfolius*)displaying short internodes, leaf curling pistil abortion and yellow stamen, and a progressive degeneration and tree death in Chongqing province in China (Cao et al. 2019). Total RNA was isolated from symptomatic trees and enriched in small RNA. After depletion of ribosomal RNAs, cDNA libraries were constructed and subjected to RNA-Seq. Small RNA libraries were obtained and sequenced on an Illumina platform. Sequences reads were trimmed and assembled *de novo* to identify sequence contigs with moderate similarities to virus sequences by BLASTx search of NCBI databases. Some contigs showed similarities to a potential novel virus tentatively named green Sichuan pepper nepovirus (GSPNeV) (Table 1). The nearly complete viral genome was obtained by RT-PCR with specific primers. The GSPNeV genome consists of RNA1 (7,082 nucleotides, GenBank accession number MH323435) and RNA2 (7,083 nucleotides, GenBank accession number MH323434) (Figure 16). The 5' untranslated regions of RNA1 and RNA2 are both 54 nucleotides long, and the 3' untranslated regions are 1,358 nucleotides long for RNA1 and 1,443 nucleotides long for RNA2 (Cao et al. 2019). RNA1 encodes a polyprotein of 2,152 amino acids (242 kDa) that is predicted to be cleaved into a protease co-factor (Pro-Co), a helicase (Hel), a viral genome-linked protein (VPg), a protease (Pro), and an RNA-dependent RNA polymerase (Pol) (Figure 16). RNA2 contains one open reading frame encoding a polyprotein of 1,822 amino acids (208 kDa) that is predicted to be cleaved into a movement protein (MP), and a coat protein (CP) (Figure 16). The highest amino acid sequence was identified between the conserved Pro-Pol region of GSPNeV and petunia chlorotic mottle virus (PCMoV), a formerly recognized subgroup A nepovirus (42%), and between the CP of GSPNeV and mulberry mosaic leafroll-associated virus (MMLRaV), another formerly recognized subgroup A nepovirus (23%) in the family *Secoviridae*. A phylogenetic tree analysis using the Pro-Pol amino acid sequence placed GSPNeV and known formerly recognized subgroup A nepoviruses in the same cluster (Figure 3), while a phylogenetic tree using the CP amino acid sequence placed GSPNeV as monophyletic (Figure 2). Diagnostic RT-PCR using specific primers identified GSPNeV in 34 of 145 (23%) green Sichuan pepper trees tested, in particular in symptomatic trees (34 of 41, 83%) (Cao et al. 2019). GSPNeV is graft transmissible to healthy green Sichuan pepper seedlings using bark chips of infected green Sichuan pepper trees, as shown by RT-PCR (Cao et al. 2019). Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify green Sichuan pepper nepovirus as a member of a novel species named *Nepovirus GSPNeV* in the genus *Nepovirus*, family *Secoviridae*.  **Creation of a sixth novel species in the genus *Nepovirus* of the family *Secoviridae.*** A novel virus was identified in *Petunia hybrida* displaying foliar interveinal chlorosis and mottling (Bartsch et al. 2017). Icosahedral particles of 28 nm in diameter were observed by electron microscopy in preparations of partially purified virions from infected *P. hybrida* leaf tissue. The virus was mechanically transmissible from infected to healthy petunias (Bartsch et al. 2017). The virus was tentatively named petunia chlorotic mottle virus (PCMoV) (Table 1). Two RNA species were isolated from purified virions as shown by gel electrophoresis analysis. Total RNA was isolated from symptomatic leaves containing spherical virus particles and used for cDNA preparation and RNA-Seq. The 5' and 3' sequences were obtained by RACE and Sanger sequencing. RNA1 is 7,615 nucleotides (GenBank accession number KX812815) long excluding the poly(A) tail and encodes a single open reading frame of 2,315 amino acids. The 5' and 3' untranslated regions of PCMoV RNA1 are 114 and 565 nucleotides long, respectively. The RNA1 polyprotein is predicted to be cleaved into a protease co-factor, (Pro-co), a helicase (Hel), a viral genome-linked protein (VPg), a protease (Pro), and an RNA-dependent RNA polymerase (Pol) (Figure 17). RNA2 is 3,804 nucleotides (GenBank accession number KX812816) long excluding the poly(A) tail and encodes a single open reading frame of 1,890 amino acids. The 5' and 3' untranslated regions of PCMoV RNA2 are 118 and 326 nucleotides long, respectively. The RNA2 polyprotein is predicted to be cleaved into a N-terminal protein (2A), a movement protein (MP) and a coat protein (CP) (Figure 17). Multiple amino acid sequence alignments showed low identity between the CP (19%-25%) and conserved Pro-Pol region (41%-50%) of PCMoV and other nepoviruses of formerly recognized subgroup A in the family S*ecoviridae*. ML phylogenetic analysis using the CP (Figure 3) and conserved Pro-Pol (Figure 3) sequences of PCMoV revealed a close similarity to formerly recognized subgroup A nepoviruses such as arabis mosaic virus (ArMV) and tobacco ringspot virus (TRSV). Based on the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify petunia chlorotic mottle virus as a member of a novel species named *Nepovirus PCMoV* in the genus *Nepovirus* of the family *Secoviridae*.  **Creation of a first novel species in the genus *Waikavirus* of the family *Secoviridae.*** A novel virus tentatively named persimmon waikavirus (PWaiV) (Table 1)was detected from Japanese persimmon (*Diospyros kaki*) ‘Reigyoku’ 794 showing poor growth (Ito and Sato 2020). Total RNA was isolated from leave samples of symptomatic persimmon ‘Reigyoku’ trees. After ribosomal RNA depletion, random priming was performed for cDNA synthesis and a library constructed for Illumina sequencing. Sequence reads were trimmed and assembled *de novo*. Sequence contigs were analyzed by BLASTN and BLASTx. Sequence gaps were filled by RT-PCR using specific primers and Sanger sequencing. The 5' and 3' terminal sequences were obtained by RACE and Sanger sequencing. PWaiV has the highest amino acid sequence identity (42%) in the conserved Pro-Pol region with rice tungro spherical virus (RTSV) from the genus *Waikavirus.* A diagnostic RT-PCR with specific primers was developed (Ito and Sato 2020). The complete genome of PWaiV is 12,117 nucleotides long (GenBank accession number LC488189). The 5' and 3' untranslated sequences are 587 and 505 nucleotides long, respectively. The genome encodes of large open reading frame of 3,674 amino acids (411 kDa) (Figure 18). A Pfam search identified motifs for coat protein 1 (CP1), a helicase (Hel), and an RNA-dependent RNA polymerase (Pol) (Figure 18). A phylogenetic tree using the CP (Figure 2) and conserved Pro-Pol region (Figure 3) revealed the clustering of PWaiV in the genus *Waikavirus*. The CP and Pro-Pol amino acid sequences of PWaiV share 18-23% and 38-42% identities with those of waikaviruses, respectively. A diagnostic RT-PCR with specific primers detected PWaiV in 11 of the 20 persimmon trees tested. PWaiV was graft-transmissible to ‘Fuyu’ rootstock seedings after side grafting of buds of infected ‘Reigyoku’ 794, as shown by RT-PCR (Ito and Sato 2020). Based on the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify persimmon waikavirus as a member of a novel species named *Waikavirus PWaiV* in the genus *Waikavirus* of the family *Secoviridae*.  **Creation of a second novel species in the genus *Waikavirus* of the family *Secoviridae***. A novel virus was identified in a red clover (*Trifolium pratense* L.) plant displaying stunted growth and irregular foliar vein clearing and chlorotic spots in South Bohemia, Czech Republic (Koloniuk and Fránová 2018). The virus was tentatively named red clover-associated virus 1 (RCaV1) (Table 1). Total RNA was extracted from leaf tissue and ribosomal RNA was depleted for the construction of a cDNA library for Illumina processing. Raw reads were trimmed and then assembled *de novo* into contigs. A BLASTx analysis revealed several contigs of a nearly complete new viral genome sequence. The 5' and 3' terminal sequences were determined by RACE and Sanger sequencing (Koloniuk and Fránová 2018). The genome of RCaV1 is 11,875 nucleotides in length (GenBank accession number MH325329), excluding the poly(A) tail (Figure 19). The viral genome contains a single large open reading frame of 3,536 amino acids (402 kDa). The 5' and 3' untranslated regions are 541 and 703 nucleotides long, respectively (Koloniuk and Fránová 2018). Six putative cleavage sites were deduced from the polyprotein amino acid sequence to produce a P1 protein (P1, 89 kDa), three coat proteins (CP1, 23 kDa; CP2, 22 kDa; CP3, 34 kDa), a helicase (Hel, 130 kDa), a protease (Pro, 34 kDa), and an RNA-dependent RNA polymerase (Pol, 69 kDa) (Figure 19). RCaV1 shared sequence similarity with other waikaviruses in the CP (37-68%) and conserved Pro-Pol region (34-47%). Phylogenetic analysis of the CP (Figure 2) and conserved Pro-Pol region (Figure 3) revealed the clustering of RCaV1 with other waikaviruses. Based on the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify red clover-associated virus 1 as a member of a novel species named *Waikavirus RCaV1* in the genus *Waikavirus* of the family *Secoviridae*.  **Creation of a third novel species in the genus *Waikavirus* of the family *Secoviridae.*** A novel virus was identified in rapeseed (*Brassica napus*). This virus was tentatively named Brassica napus RNA virus 1 (BnRV1) (Park and Hahn 2019) (Table 1). Total RNA was isolated from young floral buds of rapeseed plants and used for RNA-Seq. Sequence data were downloaded from Sequence Read Archive SRR2052475, trimmed and assembled *de novo* into sequence contigs. The genome of BnRV1 is 12,293 nucleotides long (GenBank accession number MH844554), excluding the poly(A) tail (Figure 20). The 5' and 3' untranslated regions are 630 and 1,247 nucleotides long (Park and Hahn 2019). Predictions of open reading frames (ORF) revealed a large ORF (ORF1) of 3,471 amino acids and an overlapping smaller ORF (ORFX) of 87 amino acid. ORF1 encodes a protein P1 (P1, 77 kDa), a coat protein 1 (23 kDa), a coat protein 2 (22 kDa), a coat protein 3 (32 kDa), a helicase (126 kDa), a protease (34 kDa) and an RNA-dependent RNA polymerase (Pol, 68 kDa) (Figure 20). A BLASTp search showed moderate sequence similarly of the BnRV1 conserved Pro-Pol region with members of the genus *Waikavirus* (57-67%). The CP and Pro-Pol amino acid sequences of BnRV1 share 24.8-65.3% and 42.5-77.9% identities with those of waikaviruses, respectively. A multiple sequence alignment of the CP (Figure 2) and conserved Pro-Pol (Figure 3) sequences of BnRV1 and members of the family *Secoviridae* showed the clustering of BnRV1 within the genus *Waikavirus.* Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify Brassica napus RNA virus 1 as a member of a novel species named *Waikavirus BnRV1* in the genus *Waikavirus* of thefamily *Secoviridae*.  **Creation of a fourth novel species in the genus *Waikavirus* of the family *Secoviridae.*** A novel virus was identified from American blackcurrant (*Ribes americanum*) accession PI 617879 with virus-like symptoms at the National Clonal Germplasm Repository in Corvallis, Oregon (Thekke-Veetil et al. 2020). The virus was tentatively named blackcurrant waikavirus A (BCWVA)(Table 1). Double-stranded RNA was isolated from the symptomatic American blackcurrant and subjected to degenerate oligonucleotide-primed reversed transcription polymerase chain reaction followed by high throughput sequencing. The completed genome sequence was determined by RT-PCR using specific primers and Sanger sequencing. The 5' and 3' terminal genome sequences were obtained by RACE using total RNA extracted from the infected plant and Sanger sequencing (Thekke-Veetil et al. 2020). The BVWVA genome is 11,833 nucleotide long (GenBank accession number MN701059), excluding the poly(A) tail (Figure 21). The 5' and 3' untranslated regions are 574 and 759 nucleotides long (Thekke-Veetil et al. 2020). *In silico* analyses predicted two open reading frames: ORF1 and ORFX (Figure 21). ORF1 encodes a polyprotein of 3,499 amino acids (380 kDa) that contains structural and nonstructural proteins arranged similarly to other members of the family *Secoviridae* with a protein P1 (P1, 70 kDa), a coat protein 1 (CP1, 24 kDa), a coat protein 2 (CP2, 22 kDa), a coat protein 3 (CP3, 34 kDa), a helicase (Hel, 135 kDa), a protease (Pro, 37 kDa) and an RNA-dependent RNA polymerase (Pol, 67 kDa) (Figure 21). The predicted ORFX of BCWVA (p2) encodes a 9 kDa protein with two transmembrane domains at the N-terminus (Figure 21). The BCWVA proteins show the highest amino acid sequence identity in p2 (64% with the ortholog of bellflower vein chlorosis virus -BVCV-) followed by the RdRP (56% with ortholog of brassica napus RNA virus 1 -BNRV1-). The CP and Pro-Pol amino acid sequences of BCWVA share 20.8-41.9% and 57.0-71.3% identities with those of waikaviruses, respectively. A phylogenetic analysis using CP (Figure 2) and conserved Pro-Pol (Figure 3) amino acid sequences grouped BCWVA in a clade with waikaviruses. Based on the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify blackcurrant waikavirus A as a member of a novel species named *Waikavirus BCWVA* in the genus *Waikavirus* of the family *Secoviridae*.  **Creation of a fifth novel species in the genus *Waikavirus* of the family *Secoviridae.*** A new virus was detected in kiwifruit (*Actinidia* spp.) plants displaying virus-like symptoms in Shaavi province, China (Zhao et al. 2021). Total RNA from leaf tissue of symptomatic plants was isolated and ribosomal RNA was depleted to construct an RNA-Seq library for Illumina sequencing. Raw reads were trimmed, filtered and assembled *de novo* into sequence contigs. BLASTn and BLASTx analyses revealed contigs showing nucleotide identity with known and unknown viruses, including contigs with moderate identity with maize chlorotic dwarf virus (MCDV) from the genus *Waikavirus* in the family *Secoviridae*. The novel virus from kiwifruit was tentatively named Actinidia yellowing virus 1 (AcYV1) (Zhao et al. 2021) (Table 1). Contigs of AcYV1 were found in four of 30 kiwifruit samples subjected to RNA-Seq. The 5' and 3' terminal sequences were determined by RACE and Sanger sequencing (Zhao et al. 2021). The genome of AcYV1 consists of 12,149 nucleotides, excluding the poly(A) tail (GenBank accession number MN180070) (Figure 22). The polyprotein is 3,688 amino acid long with conserved motifs typically organized for a waikavirus genome. The genome was not annotated by Zhao et al. (2021) but correspondence with Dr. Yunfeng Wu, Northwest A&F University in Yangling, China clarified the CP and conserved Pro-Pol amino acid sequences. The CP sequence of AcYV1 shares 14-17% amino acid sequence identity with orthologs of members of the genus *Waikavirus.* The CP and Pro-Pol amino acid sequences of AcYV1 share 26.4-45.2% and 42.2-61.0% identities with those of waikaviruses, respectively. A phylogenetic analysis using the CP (Figure 2) and conserved Pro-Pol (Figure 3) amino acid sequences revealed that AcYV1 clusters with members of the genus *Waikavirus*. Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify Actinidia yellowing virus 1 as a member of a novel species named *Waikavirus AcYV1* in the genus *Waikavirus* of the family *Secoviridae*.  **Creation of a sixth novel species in the genus *Waikavirus* of the family *Secoviridae.*** A novel virus was identified in bluegrass (*Poa trivalis* L.) in Belgium (Maclot et al. 2021). This virus was tentatively named poaceae Liege virus 1 (PoLV1) (Table 1). Leaf and stem samples of 50 bluegrass plants were pooled and virus particle enrichments was performed by virion-associated nucleic acids extraction. Following library preparation, sequencing was performed on a NextSeq 500 platform. Sequencing reads were trimmed assembled *de novo,* and sequence contigs were analyzed by BLASTx. Several contigs presented similarities with maize chlorotic virus (MCDV) and brassica napus RNA virus 1 (BnRV1) from the genus *Waikavirus* in the family *Secoviridae*. The sequence of the 5' and 3' ends were determined by RACE. The complete PoLV1 genome was 11,623 nucleotides long (GenBank accession number MW289237), excluding the poly(A) tail (Figure 23). The 5' and 3' untranslated regions were 664 and 534 nucleotides long, respectively (Maclot et al. 2021). The amino acid sequence identity between the coat protein (CP) and RNA-dependent RNA polymerase (Pol) of PoLV1 and waikaviruses was 39.1-62.4% and 21.2-35.4%, respectively. The CP and Pro-Pol amino acid sequences of PoLV1 share 21.1-35.4% and 58.4-62.4% identities with those of waikaviruses, respectively. ML trees using amino acid sequences of the CP (Figure 2) and conserved Pro-Pol region (Figure 3) showed that PoLV1 clustering with waikaviruses. Diagnostic RT-PCR using specific primers revealed the presence of PoLV1 in 38% of bluegrass samples tested, including additional perennial and annual Poaceae species (Maclot et al. 2021). Considering the species demarcation criteria for the family *Secoviridae* (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify poaceae Liege virus 1 as a member of a novel species named *Waikavirus* *PoLV1* in the genus *Waikavirus* of the family *Secoviridae*. | |  | |

**Supporting evidence**

**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 accession number

Pepper mild mosaic virus *Comovirus* PepMMV *Comovirus* RNA1 MK990555

RNA2 MK990556

Phaseolus vulgaris severe mosaic virus *Comovirus PvSMV Comovirus* RNA1 MN837498

RNA2 MN837499

Arabidopsis latent virus 1 *Comovirus ArLV1 Comovirus* RNA1 MH899120

RNA2 MH899121

Peach leaf pitting-associated virus *Fabavirus PLPaV Fabavirus* RNA1 KY867750

RNA2 KY867751

Red clover nepovirus A *Nepovirus RCNVA Nepovirus* RNA1 MG253828

RNA2 MG253829

Grapevine nepovirus A *Nepovirus GNVA Nepovirus* RNA1 MT507290

RNA2 MT507291

Green Sichuan pepper nepovirus *Nepovirus GSPNeV Nepovirus* RNA1 MH323435

RNA2 MH323434

Caraway yellows virus *Nepovirus CawYV Nepovirus* RNA1 MK492273

RNA2 MK492274

Petunia chlorotic mottle virus *Nepovirus PCMoV Nepovirus* RNA1 KX812815

RNA2 KX812816

Poaceae Liege nepovirus A *Nepovirus PoLNVA Nepovirus* RNA1 MW289235

RNA2 MW289236

Pineapple secovirus A *Sadwavirus PSVA Sadwavirus* RNA1 MN809923

RNA2 MN809924

Lettuce secovirus 1 *Sadwavirus LSV1 Sadwavirus* RNA1 KX925437

RNA2 KX925438

Lychnis mottle virus *Stralarivirus* *LycMoV Stralarivirus* RNA1 KR011032

RNA2 KR011033

Lettuce star mosaic virus *Sequivirus LSMV Sequivirus* MT348706

Red clover-associated virus 1 *Waikavirus RCaV1 Waikavirus* MH325329

Brassica napus RNA virus 1 *Waikavirus BnRV1 Waikavirus* MH844554

Persimmon waikavirus *Waikavirus PWaiV Waikavirus* LC488189

Blackcurrant waikavirus A *Waikavirus BCWVA Waikavirus* MN701059

Actinidia yellowing virus 1 *Waikavirus AcYV1 Waikavirus* MN180070

Poaceae Liege virus 1 *Waikavirus PolV1 Waikavirus* MW289237

**Chart

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**Figure 1**. Genome organization of representative members of the nine genera (*Comovirus*, *Fabavirus*, *Nepovirus*, *Stralarivirus*, *Cheravirus*, *Sadwavirus*, *Torradovirus*, *Sequivirus*, *Waikavirus*) in the family *Secoviridae*, including the newly proposed *Stralarivirus* (in red). Strawberry latent ringspot virus and lychnis mottle virus are two members of the newly proposed genus *Stralarivirus*. 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 (dPro, ark blue), RNA-dependent RNA polymerase (Pol, light blue), 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 formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

**Diagram

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**Figure 2.** Phylogenetic tree of the coat protein amino acid sequence of the 20 newly proposed species (depicted by a star) in the family *Secoviridae* and 60 representatives of the different genera in the family *Secoviridae.* Alignments were performed by MUSCLE with default parameters implemented in MEGA X (Kumar et al. 2018). The evolutionary history was inferred by using the Maximum Likelihood method described by Le and Gascue (2008). The tree with the highest log likelihood (-100452.91) 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-joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+*G*, parameter = 3.1203)]. The tree is drawn to scale with branch lengths indicating the number of substitutions per site. A total of 81 amino acid sequences were with 1,346 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018).The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Sequence accession numbers are as follows: ToRSV (tomato ringspot virus, D12477), BRV (blackcurrant reversion virus, AF020051), GBLV (grapevine Bulgarian latent virus, FN691935), BLSV (blueberry latent spherical virus, AB649297), SLSV (soybean latent spherical virus, KX424572), PRMV (peach rosette mosaic virus, (KJ572573), CawYV (caraway yellow virus, MK492274), CLRV (cherry leaf roll virus, FR851462), GNVA (grapevine nepovirus A, MT507291), MMMoV (melon mild mottle virus, AB518486), RpRSV (raspberry ringspot virus, AY303788), PoLNVA (poaceae Liege nepovirus A, MW289236), MMLRaV (mulberry mosaic leaf roll-associated virus, KC904084), AeRSV (Aeonium ringspot virus, JQ670669), PBRSV (potato black ringspot virus, KC832892), TRSV (tobacco ringspot virus, AY363727), GDefV (grapevine deformation virus, AY291208), ArMV (Arabis mosaic virus, AY017339), GFLV (grapevine fanleaf virus, X16907), OLRSV (olive latent ringspot virus, AJ277435), PCMoV (petunia chlorotic mottle virus, KX812816), BRSV (beet ringspot virus, X04062), RCNA (red clover nepovirus A, MG253829), TBRV (tomato black ring virus, AY157994), AILV (artichoke Italian latent virus, LT608396), GARSV (grapevine Anatolian ringspot virus, AY291207), GCMV (grapevine chrome mosaic virus, X15163), CNSV (cycas necrotic stunt virus, AB073148), PVB (potato virus B, KX656671), GSPNeV (green Sichuan pepper nepovirus, MH323434), 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), CPMV (cowpea mosaic virus, X00729), ArLV1 (Arabidopsis latent virus 1, MH899121), RCMV (red clover mottle virus, M14913), BBTMV (broad bean true mosaic virus, GU810904), SqMV (squash mosaic virus, AB054689), PepMMV (pepper mild mosaic virus, MK990556), GFabV (grapevine fabavirus, KX241485), PrVF (prunus virus F, KX269871), CuMMV (cucurbit mild mosaic virus, EU881937), LMMV (lamium mild mosaic virus, KC595305), GeMV (gentian mosaic virus, AB084453), BBWV2 (broad bean wilt virus 2, AF225954), PLPaV (peach latent pitting-associated virus, KY867751), BBWV1 (black raspberry necrosis virus, AB084451), BRNV (black raspberry necrosis virus, DQ344640), SMoV (strawberry mottle virus, AJ311876), LSV1 (lettuce secovirus 1, KX925438), SDV (satsuma dwarf virus, AB009959), DMaV (dioscorea mosaic-associated virus, KU215539), PSVA (pineapple secovirus A, MN809924), CLVA (chocolate lily virus A, JN052074), ALSV (apple latent spherical virus, AB030941), CuLV (currant latent virus, KT692953), CRLV (cherry leafroll virus, AJ621358), AVB (arracacha virus B, JQ581051), ToTV (tomato torrado virus, DQ388880), ToMarV (tomato marchitez virus, EF681765), MYMoV (motherwort yellow mottle virus, KM229701), LNLCV (lettuce necrotic leaf curl virus, KC855267), CaTV1 (carrot torradovirus 1, KF533720), SCLSV (squash chlorotic leaf spot virus, KU052531), LSMV (lettuce star mosaic virus, MT348706), PYFV (parsnip yellow fleck virus, D14066), AcYV1 (Actinidia yellowing virus 1, MN180070), PWaiV (persimmon waikavirus, LC488189), 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), LycMoV (lychnis mottle virus, KR011033), and SLRSV (strawberry latent ringspot virus, AY860979). 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. The CP sequence of poliovirus (EVC, *Enterovirus C*, accession number 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 sequence of the conserved protease-polymerase (Pro-Pol) region (from the protease CG motif to the polymerase GDD motif) of the 20 newly proposed species (depicted by a star) in the family *Secoviridae* and 61 representatives of the different genera in the family *Secoviridae.* Alignments were performed by MUSCLE with default parameters implemented in MEGA X (Kumar et al. 2018). The evolutionary history was inferred by using the Maximum Likelihood method and the model described by Le and Gascuel (2008). The tree with the highest log likelihood (-53540.69) 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-joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories [+*G*, parameter = 1.1592)]. The rate variation model allowed for some sites to be evolutionarily invariable ([+*I*], 1.14% sites). The tree is drawn to scale with branch lengths indicating the number of substitutions per site. A total of 82 amino acid sequences were used with 837 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018). The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Sequence accession numbers are as follows: ToRSV (tomato ringspot virus, L19655), BRV (blackcurrant reversion virus, AF368272), GBLV (grapevine Bulgarian latent virus, FN691934), CawYV (caraway yellow virus, MK494273), BLSV (blueberry latent spherical virus, AB649296), SLSV (soybean latent spherical virus, KX424571), PRMV (peach rosette mosaic virus, AF016626), CLRV (cherry leaf roll virus, FR851461), AYRSV (artichoke yellow ringspot virus, AM087671), GNVA (grapevine nepovirus A, MT507290), MMMoV (melon mild mottle virus, AB518485), RpRSV (raspberry ringspot virus, AY303787), PoLNVA (poaceae Liege nepovirus A, MW289235), MMLRaV (mulberry mosaic leaf roll-associated virus, KC904083), AeRSV (Aeonium ringspot virus, JX304792), PBRSV (potato black ringspot virus, KC832890), TRSV (tobacco ringspot virus, U50869), GDefF (grapevine deformation virus, [HE613269](https://www.ncbi.nlm.nih.gov/nuccore/HE613269)), ArMV (Arabis mosaic virus, AY303786), GFLV (grapevine fanleaf virus, [D00915](https://www.ncbi.nlm.nih.gov/nuccore/D00915)), PCMoV (petunia chlorotic mottle virus, KX812815), BRSV (beet ringspot virus, [D00322](https://www.ncbi.nlm.nih.gov/nuccore/D00322)), RCNA (red clover nepovirus A, MG253828), TBRV (tomato black ring virus, AY157993), AILV (artichoke Italian latent virus, LT608395), GARSV (grapevine Anatolian ringspot virus, [HE774604](https://www.ncbi.nlm.nih.gov/nuccore/HE774604)), GCMV (grapevine chrome mosaic virus, [X15346](https://www.ncbi.nlm.nih.gov/nuccore/X15346)), CNSV (cycas necrotic stunt virus, AB073147), PVB (potato virus B, [KX656670](https://www.ncbi.nlm.nih.gov/nuccore/KX656670)), GSPNeV (green Sichuan pepper nepovirus, MH323435), APMV (Andean potato mottle virus, MN148891), CPSMV (cowpea severe mosaic virus, M83830), PvSMV (phaseolus vulgaris severe mosaic virus, MN837498), BRMV (bean rugose mosaic virus, KP404602), BPMV (bean pod mosaic virus, U70866), CPMV (cowpea mosaic virus, [X00206](https://www.ncbi.nlm.nih.gov/nuccore/X00206)), ArLV1 (Arabidopsis latent virus 1, MH899120), RCMV (red clover mottle virus, X64886), BBTMV (broad bean true mosaic virus, GU810903), SqMV (squash mosaic virus, AB054688), PepMMV (pepper mild mosaic virus, MK990555), GFabV (grapevine fabavirus, KX241484), PcSMV (phaseolus vulgaris severe mosaic virus, MN837498), PrVF (prunus virus F, KX269870), CuMMV (cucurbit mild mosaic virus, EU881936), LMMV (lamium mild mosaic virus, KC595304), GeMV (gentian mosaic virus, AB084452), BBWV2 (broad bean wilt virus 2, AF225953), PLPaV (peach latent pitting-associated virus, KY867750), BBWV1 (broad bean wilt virus 1, AB084450), StPV (stocky prune virus, DQ143874), 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), CLVA (chocolate lily virus A, JN052073), ALSV (apple latent spherical virus, AB030940), CuLV (currant latent virus, KT692952), CRLV (cherry leafroll virus, AJ621357), AVB (arracacha virus B, JQ437415), ToTV (tomato torrado virus, DQ388879), ToMarV (tomato marchitez virus, EF681764), MYMoV (motherwort yellow mottle virus, KM229700), LNLCV (lettuce necrotic leaf curl virus, KC855266), CaTV1 (carrot torradovirus 1, KF533719), SCLSV (squash chlorotic leaf spot virus, KU052530), LSMV (lettuce star mosaic virus, MT348706), PYFV (parsnip yellow fleck virus, D14066), AcYV1 (Actinidia yellowing virus 1, MN180070), PWaiV (persimmon waikavirus, LC488189), 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), LycMoV (lychnis mottle virus, KR011032), and SLRSV (strawberry latent ringspot virus, AY860978). 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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**Figure 4.** Genome organization of lychnis mottle virus (LycMoV) from the genus *Stralarivirus* in the family *Secoviridae*. The genome structure of LycMoV is similar to that of strawberry latent ringspot virus (SLRSV), the type member of the genus *Stralarivirus*. The 5' end of the LycMoV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3’ end is polyadenylated. 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), movement protein (MP, orange) and two coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 5.** Genome organization of pineapple secovirus A (PSVA) from the genus *Sadwavirus*, subgenus *Cholivirus*, in the family S*ecoviridae*. The genome structure of LycMoV is similar to that of chocolate lily virus A (CLVA), the type member of the subgenus C*holivirus*, in the genus *Sadwavirus*. The 5' end of the PSVA genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. Protein domains with conserved motifs for the putative NTP-binding domain protein (Hel, green), VPg (peach), 3C-like proteinase (dark blue), RNA-dependent RNA polymerase (Pol, light blue), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 6.** Genome organization and expression of lettuce secovirus 1 (LSC1) from the genus *Sadwavirus*, subgenus *Stramovirus*, in the family S*ecoviridae*. The genome structure of LSC1 is similar to that of strawberry mottle virus (SoMV), the type member of the subgenus *Stramovirus*, in the genus *Sadwavirus*. The 5' end of the LSC1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3’ end is polyadenylated. Protein domains with conserved motifs for the NTP-binding domain protein (Hel, green), VPg (peach), 3C-like proteinase (Pro, dark blue), RNA-dependent RNA polymerase (lPol, ight blue), protease co-factor (Pro-co, white), movement protein (MP, orange), coat protein (CP, red), and protease (grey) are shown. The dark grey domain in the C-terminal region of the RNA2-encoded polyprotein contains signature motifs for the glutamic protease characterized in strawberry mottle virus. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. In stramoviruses, the two cleavage sites downstream of the CP domain are cleaved by the RNA2-encoded glutamic protease. Other cleavage sites are cleaved by the 3C-like proteinase. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 7.** Genome organization and expression of lettuce star mosaic virus (LSMV) from the genus *Sequivirus* in the family *Secoviridae*. The genome structure of LSMV is similar to that of parsnip yellow fleck virus (PYFV), the type member of the genus *Sequivirus*. The 5' end of the LSC1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3’ end is polyadenylated. 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), movement protein (MP, orange) and three coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 8:** Genome organization and expression of peach leaf pitting-associated virus (PLPaV) from the genus *Fabavirus* in the family *Secoviridae*. The genome structure of PLPaV is similar to that of broad bean wilt virus 2 (BBWV2), the type member of the genus *Fabavirus*. The 5' end of the LSC1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), movement protein (MP, orange) and two coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.A screenshot of a computer

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**Figure 9.** Genome organization and expression of pepper mild mosaic virus (PepMMV) from the genus *Comovirus* in the family *Secoviridae*. The genome structure of PepMMV is similar to that of cowpea mosaic virus (CPMV), the type member of the genus *Comovirus*. The 5' end of the PepMMV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and two coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.A screenshot of a computer

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**Figure 10.** Genome organization and expression of phaseolus vulgaris severe mosaic virus (PvSMV) from the genus *Comovirus* in the family *Secoviridae*. The genome structure of PvSMV is similar to that of cowpea mosaic virus (CPMV), the type member of the genus *Comovirus*. The 5' end of the PvSMV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and two coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 11.** Genome organization and expression of Arabidopsis latent virus 1 (ArLV1) from the genus *Comovirus* in the family *Secoviridae*. The genome structure of PvSMV is similar to that of cowpea mosaic virus (CPMV), the type member of the genus *Comovirus*. The 5' end of the ArLV1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and two coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.Chart

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**Figure 12.** Genome organization and expression of red clover nepovirus A (RCNVA) from the genus *Nepovirus* in the family *Secoviridae*. The genome structure of RCNVA is similar to that of tomato black ring virus (TBRV), a representative of formerly recognized subgroup B in the genus *Nepovirus*. The 5' end of the RCNVA genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.Chart

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**Figure 13.** Genome organization and expression of poaceae Liege nepovirus A (PoLNVA) from the genus *Nepovirus* in the family *Secoviridae*. The genome structure of PolNVA is similar to that of tomato black ring virus (TBRV), a representative of formerly recognized subgroup B in the genus *Nepovirus*. The 5' end of the PolNVA genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 14.** Genome organization and expression of grapevine nepovirus A (GNVA) from the genus *Nepovirus* in the family *Secoviridae*. The genome structure of GNVA is similar to that of tomato black ring virus (TBRV), a representative of formerly recognized subgroup B in the genus *Nepovirus.* The 5' end of the GNVA genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 15.** Genome organization and expression of caraway yellows virus (CawYV) from the genus *Nepovirus* in the family *Secoviridae*. The genome structure of CawYV is similar to that of tomato ringspot virus (ToRSV), a representative of formerly recognized subgroup C in the genus *Nepovirus*. The 5' end of the CawYV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), X3 protein (X3, pink), X4 protein (X4, white), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 16.** Genome organization and expression of green Sichuan pepper nepovirus (GSPNeV) from the genus *Nepovirus* in the family *Secoviridae*. The genome structure of GSPNeV is similar to that of arabis mosaic virus (ArMV), a representative of formerly recognized subgroup A in the genus *Nepovirus*. The 5' end of the GSPNeV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, white), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 17.** Genome organization and expression of petunia chlorotic mottle virus (PCMoV) from the genus *Nepovirus* in the family *Secoviridae*. The genome structure of PCMoV is similar to that of arabis mosaic virus (ArMV), a representative of formerly recognized subgroup A in the genus *Nepovirus*. The 5' end of the PCMoV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), protease co-factor (Pro-co, yellow), movement protein (MP, orange) and coat protein (CP, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 18.** Genome organization and expression of persimmon waikavirus (PWaiV) from the genus *Waikavirus* in the family *Secoviridae*. The genome structure of PWaiV is similar to that of rice trungro virus (RTSV), the type member of the genus *Waikavirus*. The 5' end of the PWaiV genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), and three coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 19.** Genome organization and expression of red clover-associated virus 1 (RCaV1) from the *Waikavirus* in the family *Secoviridae*. The genome structure of RCaV1 is similar to that of rice trungro virus (RTSV), the type member of the genus *Waikavirus*. The 5' end of the RCaV1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), movement protein (MP, orange) and three coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 20.** Genome organization and expression of brassica napus RNA virus 1 (BnRV1) from the *Waikavirus* in the family *Secoviridae*. The genome structure of BnRV1 is similar to that of rice trungro virus (RTSV), the type member of the genus *Waikavirus*. The 5' end of the BnRV1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), movement protein (MP, orange) and three coat proteins (CPS, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 21.** Genome organization and expression of blackcurrant waikavirus A (BCWVA) from the *Waikavirus* in the family *Secoviridae*. The genome structure of BCWVA is similar to that of rice trungro virus (RTSV), the type member of the genus *Waikavirus*. The 5' end of the BCWVA genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), movement protein (MP, orange) and three coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 22.** Genome organization and expression of Actinidia yellowing virus 1 (AcYV1) from the *Waikavirus* in the family *Secoviridae*. The genome structure of AcYV1 is similar to that of rice trungro virus (RTSV), the type member of the genus *Waikavirus*. The 5' end of the AcYV1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3’ end is polyadenylated. 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), movement protein (MP, orange) and three coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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**Figure 23.** Genome organization and expression of poaceae Liege virus 1 (PoLV1) from the *Waikavirus* in the family *Secoviridae*. The genome structure of PoLV1 is similar to that of rice trungro virus (RTSV), the type member of the genus *Waikavirus*. The 5' end of the PoLV1 genomic RNAs is predicted to be bound to a viral genome-linked protein (VPg, black circle) and the 3' end is polyadenylated. 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), movement protein (MP, orange) and three coat proteins (CPs, red) are shown. Proteinase cleavage sites predicted by sequence comparisons are indicated by solid vertical lines. The three formerly recognized subgroups of nepoviruses and the three sub-genera of sadwaviruses are indicated. Additional virus acronyms are: CPMV: cowpea mosaic virus; BBWV2: ArMV: Arabis mosaic virus; TBRV: tomato black ring virus; ToRSV: tomato ringspot virus; SLRSV: strawberry latent ringspot virus; LycMoV: lychnis mottle virus; CLRV: cherry rasp leaf virus: SMoV: strawberry mottle virus; CLVA: chocolate lily virus A; DMaV: dioscorea mosaic-associated virus; SDV: satsuma dwarf virus: ToTV: tomato torradovirus; PYVF: parsnip yellow fleck virus: RTSV: rice tungro spherical virus.

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