MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2009.007a-hP*	(to be completed by ICTV officers)

Short title: 2 new species in the family Secoviridae and reassignment of 2 other species within the family Secoviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached
(modules 1 and 9 are required)

1 ☒ 2 ☐ 3 ☐ 4 ☐ 5 ☐
6 ☐ 7 ☐ 8 ☐ 9 ☒

Author(s) with e-mail address(es) of the proposer:

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Joan Wellink
Thierry Wetzel

and in consultation with Joe H. Vetten

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV: May 2009
Date of this revision (if different to above):

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	**2009.007aP**	(assigned by ICTV officers)

To create 1 new species with the name(s):

Carrot necrotic dieback virus

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	*2009.007bP*	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Fill in all that apply.

Genus:	*Sequivirus*
Subfamily:	
Family:	*Secoviridae*
Order:	*Picornavirales*

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Parsnip yellow fleck virus (PYFV) is the type species of the genus *Sequivirus* (recently reassigned to the new proposed family *Secoviridae* in the order *Picornavirales*) [5, 11]. The family *Secoviridae* was approved by the ICTV EC last year and has been posted for ratification by the ICTV membership. Two different strains of PYFV have been described: the parsnip strain and the *Anthriscus* strain [10]. Isolates of the *Anthriscus* and parsnip strains share the same aphid vector species but differ in their host ranges and in serological properties [9]. The complete sequence of an isolate of the parsnip strain (isolate P-121, GenBank accession number: D14066 and RefSeq: NC_003628) is used as the reference for the genome sequence of PYFV [13]. This was the only complete genomic sequence available for a sequivirus. Partial sequences of the RNA-dependent RNA polymerase coding region are available for *Dandelion yellow mosaic virus* (DaYMV, a second species in the genus) and lettuce mottle virus (LeMoV, a tentative species in the genus). The genomic RNAs of PYFV and possibly also LeMoV do not have a polyA tail at their 3' end. This is a unique feature in the family *Secoviridae*.

Because only one complete sequence was available for the genus *Sequivirus*, criteria for species demarcation within the genus have only been proposed based on those currently accepted for related genera in the family *Secoviridae*. The sequence between the conserved CG motif in the proteinase and the conserved GDD motif in the polymerase (Pro-Pol region) is easy to identify, even when cleavage sites are not known. The Pro-Pol region has been used to establish the relationship among viruses within the order *Picornavirales* or the family *Secoviridae* [7, 11]. A percentage of amino acid sequence identity of less than 80 % in the Pro-Pol region and less than 75 % in the coat protein(s) is generally used for species demarcation in various genera within the family *Secoviridae* [11].

The entire genomic sequence of isolate Rot2 of the *Anthriscus* strain was recently elucidated [8] (accession number: EU980442). In phylogenetic studies using the Pro-Pol region, the *Anthriscus* and parsnip strains of PYFV group together in a branch, which is distinct from other viruses in the family *Secoviridae* (see Fig. 1 in annex). The degree of amino acid sequence identity in Pro-Pol region of the two strains was 75 %. When considering the three coat proteins, the deduced amino acid sequences of the two PYFV strains showed 71-78 % amino acid identity. Based on criteria accepted for related genera, this is just below the cut-off point for species demarcation. Another difference between the two strains is that a polyA tail is present at the 3' end of the genomic RNAs of the *Anthriscus* strain but not of the parsnip strain [8] (see Fig. 2 in annex). This difference is significant as it could have implications on the mode of translation or other biological properties of these RNAs.

Based on the aforementioned differences in biological and molecular properties, it is suggested that the *Anthriscus* strain of PYFV constitutes a distinct species within the genus *Sequivirus*. The name "carrot necrotic dieback virus" is proposed for the new species.

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	**2009.007cP**	(assigned by ICTV officers)

To create 1 new species with the name:

 Black raspberry necrosis virus

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	*2009.007dP*	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Genus:	*unassigned*
Subfamily:	
Family:	*Secoviridae*
Order:	*Picornavirales*

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Two distinct isolates of "black raspberry necrosis virus" (BRNV) have been reported in Scotland and North America (Oregon) [1]. The complete genome sequence of the North American isolate of BRNV has been determined [GeneBank accession numbers: DQ344639 (RefSeq: NC_008182) and DQ344640 (RefSeq: NC_008183)] [1]. BRNV is related to *Strawberry mottle virus* [SMoV, GeneBank accession numbers: AJ311875 (RefSeq: NC_003445) and AJ311876 (RefSeq:NC_003446)] with 63 % amino acid sequence identity in the Pro-Pol region. Relation to other viruses in the family *Secoviridae* are more distant with the closest relative being *Satsuma dwarf virus* [SDV, the type species of the genus *Sadwavirus*, GeneBank accession numbers: AB009958 (RefSeq: NC_003785) and AB009959 (RefSeq: NC_003786)] with 38 % amino acid sequence identity in the Pro-Pol region. BRNV and SMoV both share the property of having a very long 3' UTR on both genomic RNAs. This characteristic is also found in the genome of nepoviruses of subgroup C but not in the genome of SDV (see Fig. 2 in annex). Based on a criterion currently accepted within the family *Secoviridae* for species demarcation (less than 80% amino acid sequence identity in the Pro-Pol region), we propose that BRNV should be considered a distinct species in the family *Secoviridae*.

The RNA1-encoded polyprotein of BRNV contains motifs for a helicase, proteinase and polymerase and cleavage sites (Q/G, E/G, Q/N and Q/Q) separating these different domains have been identified at positions consistent with those found in the polyproteins of related viruses. However, the genomic organization of the RNA2 of BRNV is unclear. Two possible cleavage sites were identified (Q/G and E/G) in the polyprotein. These cleavage sites would define three mature proteins. The upstream protein contained sequences with some affinities with previously described movement protein motifs and had 42 % amino acid sequence identity with the corresponding protein of SMoV but very little affinity with any protein from other viruses in the family *Secoviridae*. The two other putative mature proteins delineated by the proposed cleavage sites were suggested to correspond to the large and small CP subunits. However, the size of the proteins would be very atypical for the family *Secoviridae* (102 kDa and 55 kDa). Also, the proposed CPs showed very little amino acid sequence identity with the CPs of other viruses in the family *Secoviridae*, including SDV. The only exception was a 921 amino acid region which showed 42 % amino acid sequence identity with the corresponding region of SMoV. The nature of the CPs could not be confirmed experimentally, because of the inability to purify the virus from infected plants. This situation is similar to that described with SMoV [12].

One of defining characteristics of the genus *Sadwavirus* within the family *Secoviridae* is the presence of two CPs: a large CP of 40-45 kDa and a small CP of 21-26 kDa. SMoV is currently considered a member of the genus *Sadwavirus*, based on distant sequence affinities with SDV, the type member of the genus. In a related proposal (see 2nd half of module 7), we are suggesting to remove SMoV from the genus *Sadwavirus* and define the species as an "unassigned" species within the family *Secoviridae*. Similarly, we propose that "black raspberry necrosis virus" should be defined as a new definite species within the family *Secoviridae*, but remain unassigned to a specific genus until more information becomes available on the genomic organization of RNA2.

MODULE 7: REMOVE and MOVE

Use this module whenever an existing taxon needs to be removed:
– *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
– *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2009.007eP***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Strawberry latent ringspot virus

The present taxonomic position of these taxon/taxa:

Genus:	*Sadwavirus*	
Subfamily:		Fill in all that apply.
Family:	*Secoviridae*	
Order:	*Picornavirales*	

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

See justification described in Part (b)

Part (b) re-assign to a higher taxon

Code	***2009.007fP***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

		Fill in all that apply.
Genus:	*unassigned*	• If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.
Subfamily:		
Family:	*Secoviridae*	If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Picornavirales*	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

The genus *Sadwavirus* within the proposed family *Secoviridae* currently includes three species: *Satsuma dwarf virus* (SDV, the type species which includes several closely related isolates), *Strawberry latent ringspot virus* [SLRSV, GeneBank accession numbers: AY860978 (RefSeq: NC_006964) and AY860979 (RefSeq: NC_006965)] and *Strawberry mottle virus* (SMoV). See Table 1 (annex section) for a comparison of the characteristics of these viruses with those of other viruses in the proposed family *Secoviridae*. The genus *Sadwavirus* was originally created to accommodate SDV, a bipartite plant picorna-like virus with two CPs similar to those of comoviruses (a large CP of 42 kDa and a small CP of 22 kDa) but that did not group with members of the genera *Comovirus* or *Fabavirus* in phylogenetic trees using the Pro-Pol sequence or the CP sequences [2, 3, 6].

Similarly to SDV, SLRSV encodes two CPs (43 and 26 kDa) but does not group with comoviruses or fabaviruses in phylogenetic analyses using CP or Pro-Pol sequences [4, 14]. Although SLRSV was assigned to the genus *Sadwavirus* based on the number of CPs, it is only distantly related with SDV and groups with members of the genus *Cheravirus* in phylogenetic studies using the Pro-Pol sequence [6]. The genomic organization of SLRSV is similar to that of cheraviruses with the notable exception that cheraviruses encode three CPs of 20-27 kDa (see Fig. 2 and Table 1 in annex). One possible solution would be to reassign SLRSV to the genus *Cheravirus*, based on the similar genomic organization and the distant sequence relationships. However, this would imply redefining the genus *Cheravirus*, since the presence of three small CPs is a defining characteristic of the genus. Also the relation of SLRSV with the genus *Cheravirus* is not clear when conducting phylogenetic comparisons using the CP sequences [6]. Thus, for the time being, we propose to remove SLRSV from the genus *Sadwavirus*. We propose that SLRSV should be considered a definite species within the proposed family *Secoviridae* but unassigned to a specific genus.

MODULE 7: REMOVE and MOVE

Use this module whenever an existing taxon needs to be removed:
– *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
– *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	*2009.007gP*	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Strawberry mottle virus

The present taxonomic position of these taxon/taxa:

Genus:	*Sadwavirus*	
Subfamily:		Fill in all that apply.
Family:	*Secoviridae*	
Order:	*Picornavirales*	

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

See justification described in Part (b)

Part (b) re-assign to a higher taxon

Code	*2009.007hP*	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.
If no genus is specified, enter "**unassigned**" in the genus box.

Genus:	*unassigned*
Subfamily:	
Family:	*Secoviridae*
Order:	*Picornavirales*

Reasons to justify the re-assignment:

As mentioned in the previous module, the genus *Sadwavirus* within the proposed family *Secoviridae* currently includes three species: *Satsuma dwarf virus* (SDV, the type species which includes several closely related isolates), *Strawberry latent ringspot virus* (SLRSV) and *Strawberry mottle virus* (SMoV) (see Table 1 in Annex). A defining characteristic of the genus is the presence of two CPs with size similar with those of comoviruses (a large CP of 42 kDa and a small CP of 22 kDa) [2, 3, 6].

SMoV is distantly related to SDV in phylogenetic studies using the Pro-Pol sequence or the complete Pol sequence [6, 11, 12] (see Fig. 1 in annex). Although cleavage sites were inferred on the RNA1-polyprotein, based on conserved motifs in the replication proteins and proposed Q/G cleavage sites, the genome organization of RNA2 remains unclear. The CPs are only distantly related to those of SDV and cleavage sites delineating CPs of the expected sizes for members of the family *Secoviridae* were not identified in the sequence. Possible cleavage sites have been proposed. However, it was noted that these cleavage sites would delineate a large CP of unusual size for the family (100 kDa). Unfortunately, it was not possible to determine the size of the CPs experimentally as attempts to purify the virus and separate the CPs by SDS-PAGE were not successful [12]. A similar situation was encountered during the characterization of BRNV, a proposed new species in the family *Secoviridae* (see Module 2). In the original publication, the association of SMoV with a "SDV-lineage" was described as tentative [12]. Based on the lack of information on the nature of the CPs and the distant relationship of SMoV with SDV, we propose to remove SMoV from the genus *Sadwavirus*. We propose that SMoV should be considered a definite species within the proposed family *Secoviridae* but unassigned to a specific genus until further information on the genomic organization of RNA2 becomes available.

additional material in support of this proposal

References:

1.   Halgren A, Tzanetakis IE, Martin RR (2007) Identification, characterization and detection of Black raspberry necrosis virus. Phytopathology 97: 44-50
2.   Iwanami T, Kondo Y, Karasev AV (1999) Nucleotide sequences and taxonomy of satsuma dwarf virus. J Gen Virol 80: 793-797
3.   Karasev AV, Han SS, Iwanami T (2001) Satsuma dwarf and related viruses belong to a new lineage of plant picorna-like viruses. Virus Genes 23: 45-52
4.   Kreiah S, Strunk G, Cooper JI (1994) Sequence analysis and location of capsid proteins within RNA 2 of strawberry latent ringspot virus. J Gen Virol 75: 2527-2532
5.   Le Gall O, Iwanami T, Jones AT, Lehto K, Sanfacon H, Wellink J, Wetzel T, Yoshikawa N (2005) Sequiviridae. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U and Ball LA (eds) Virus Taxonomy, Eighth Report of the International Committee on the Taxonomy of Viruses. Elsevier/Academic Press, London, pp 793-798
6.   Le Gall O, Sanfacon H, Ikegami M, Iwanami T, Jones T, Karasev A, Lehto K, Wellink J, Wetzel T, Yoshikawa N (2007) Cheravirus and Sadwavirus: two unassigned genera of plant positive-sense single-stranded RNA viruses formerly considered atypical members of the genus Nepovirus (family Comoviridae). Arch Virol 159: 1767-1774
7.   Le Gall O, Christian P, Fauquet CM, King AM, Knowles NJ, Nakashima N, Stanway G, Gorbalenya AE (2008) Picornavirales, a proposed order of positive-sense single-stranded RNA viruses with a pseudo-T = 3 virion architecture. Arch Virol 153: 715-727
8.   Menzel W, Vetten HJ (2008) Complete nucleotide sequence of an isolate of the Anthriscus strain of Parsnip yellow fleck virus. Arch Virol 153: 2173-5
9.   Murant AF, Goold RA (1968) Purification, properties and transmission of parsnip yellow fleck virus, a semi-persistent, aphid borne virus. Ann Appl Biol 62: 123-127
10.   Murant AF (2003) Parsnip yellow fleck virus. CMI/AAB Descriptions of Plant Viruses 394
11.   Sanfacon H, Wellink J, Le Gall O, Karasev A, van der Vlugt R, Wetzel T (2009) Secoviridae: a proposed family of plant viruses within the order Picornavirales that combines the families Sequiviridae and Comoviridae, the unassigned genera Cheravirus and Sadwavirus and the proposed genus torradovirus. Arch Virol: in press
12.   Thompson JR, Leone G, Lindner JL, Jelkmann W, Schoen CD (2002) Characterization and complete nucleotide sequence of Strawberry mottle virus: a tentative member of a new family of bipartite plant picorna-like viruses. J Gen Virol 83: 229-39
13.   Turnbull-Ross AD, Reavy B, Mayo MA, Murant AF (1992) The nucleotide sequence of parsnip yellow fleck virus: a plant picorna-like virus. J Gen Virol 73: 3203-11
14.   Tzanetakis IE, Postman JD, Gergerich RC, Martin RR (2006) A virus between families: nucleotide sequence and evolution of Strawberry latent ringspot virus. Virus Res 121: 199-204

Annex:
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.
The use of Figures and Tables is strongly recommended.

Figure 1: Hierarchical clustering of members of the family *Secoviridae* based on the Pro-Pol amino acid sequence. Family (Secoviridae), sub-family (Comovirinae) and genera are shown on the right. Viruses outlined in yellow are discussed in this proposal. The current taxonomy is shown (the same tree with the proposed new taxonomy is shown in Fig. 3). PYFV-anthriscus is proposed as a new species under the name Carrot necrotic dieback virus. Circles indicate nodes supported by bootstrap values above 80% (closed circles) or 60% (open circles); nodes without circles are not supported to these levels. The bar represents a p-distance of 0.1. The amino-acid sequence clustering is based on the region between the Pro (CG) and the Pol (GDD) sequence motifs. The accession numbers used for each virus were as follows with the GeneBank number listed first, followed by the RefSeq number when applicable: potato virus Y (PVY, X12456, NC 001616), Norwalk virus (NV, M87661, NC 001959), poliovirus (PV, V01149, NC 002058), Heterosigma akashiwo RNA virus (HaRNV, AY337486, NC 005281), infectious flacherie virus (IFV, AB000906, NC 003781), cricket paralysis virus (CrPV, AF218039, NC 003924), parsnip yellow fleck virus (PYFV, D14066, NC 003628), maize chlorotic dwarf virus (MCDV, U67839, NC 003626), rice tungro spherical virus (RTSV, M95497, NC 001632), tomato torrado virus (ToTV, DQ388879, NC 009013), tomato marchitez virus (ToMarV, EF681764, NC 010987), Satsuma dwarf virus (SDV, AB009958, NC 003785), strawberry mottle virus (SMoV, AJ311875, NC 003445), black raspberry necrosis virus (BRNV, DQ344639, NC 008182), strawberry latent ringspot virus (SLRSV, AY860978, NC 006964), stocky prune virus (StPV, AAZ76594), apple latent spherical virus (ALSV, AB030940, NC 003787), cherry rasp leaf virus (CRLV, AJ621357, NC 006271), broad bean wilt virus 1 (BBWV1, AB084450, NC 005289), BBWV2 (AF225953, NC 003003), gentian mosaic virus (GeMV, BAD99001), squash mosaic virus (SqMV, AB054688, NC 003799), radish mosaic virus (RaMV, AB295643), cowpea mosaic virus (CPMV, X00206, NC 003549), red clover mottle virus (RCMV, X64886, NC 003741), bean pod mottle virus (BPMV, U70866, NC 003496), cowpea severe mosaic virus (CPSMV, M83830, NC 003545), raspberry ringspot virus (RpRSV, AY303787, NC 005266), tomato ringspot virus (ToRSV, L19655, NC 003840), peach rosette mosaic virus (PRMV, AAB69867), cycas necrosis stunt virus (CNSV, AB073147, NC 003791), grapevine chrome mosaic virus (GCMV, X15346, NC 003622), beet ringspot virus (BRSV, D00322, NC 003693), tomato black ring virus (TBRV, AY157993, NC 004439), arabis mosaic virus (ArMV, AY303786, NC 006057), grapevine fanleaf virus (GFLV, D00915, NC 003615), tobacco ringspot virus (TRSV, U50869, NC 005097), artichoke yellow ringspot virus (AYRSV, AM087671), blackcurrant reversion virus (BRV, AF368272, NC 003509).

PVY   *Potyviridae*
NV   *Caliciviridae*
IFV   *Iflavirus*
          HaRNAV *Marnaviridae*
CrPV   *Dicistroviridae*
PV   *Picornaviridae*
PYFV   ⎱
PYFV anthriscus ⎰ *Sequivirus*
MCDV   ⎱ *Waikavirus*
RTSV   ⎰
RpRSV   ⎱
ArMV
GFLV
     TRSV
AYRSV
BRV
     CNSV   *Nepovirus*
GCMV
BRSV
TBRV
ToRSV
PRMV   ⎰
SqMV   ⎱
RaMV
CPMV
RCMV   *Comovirus*
BPMV
CPSMV   ⎰
BBWV1   ⎱
BBWV2   *Fabavirus*
GeMV   ⎰
SLRSV   *Sadwavirus*
StPV   ⎱
ALSV   *Cheravirus*
CRLV   ⎰
ToTV   ⎱ *Torradovirus*
ToMarV   ⎰
SDV   ⎱
SMoV   *Sadwavirus*
BRNV   ⎰
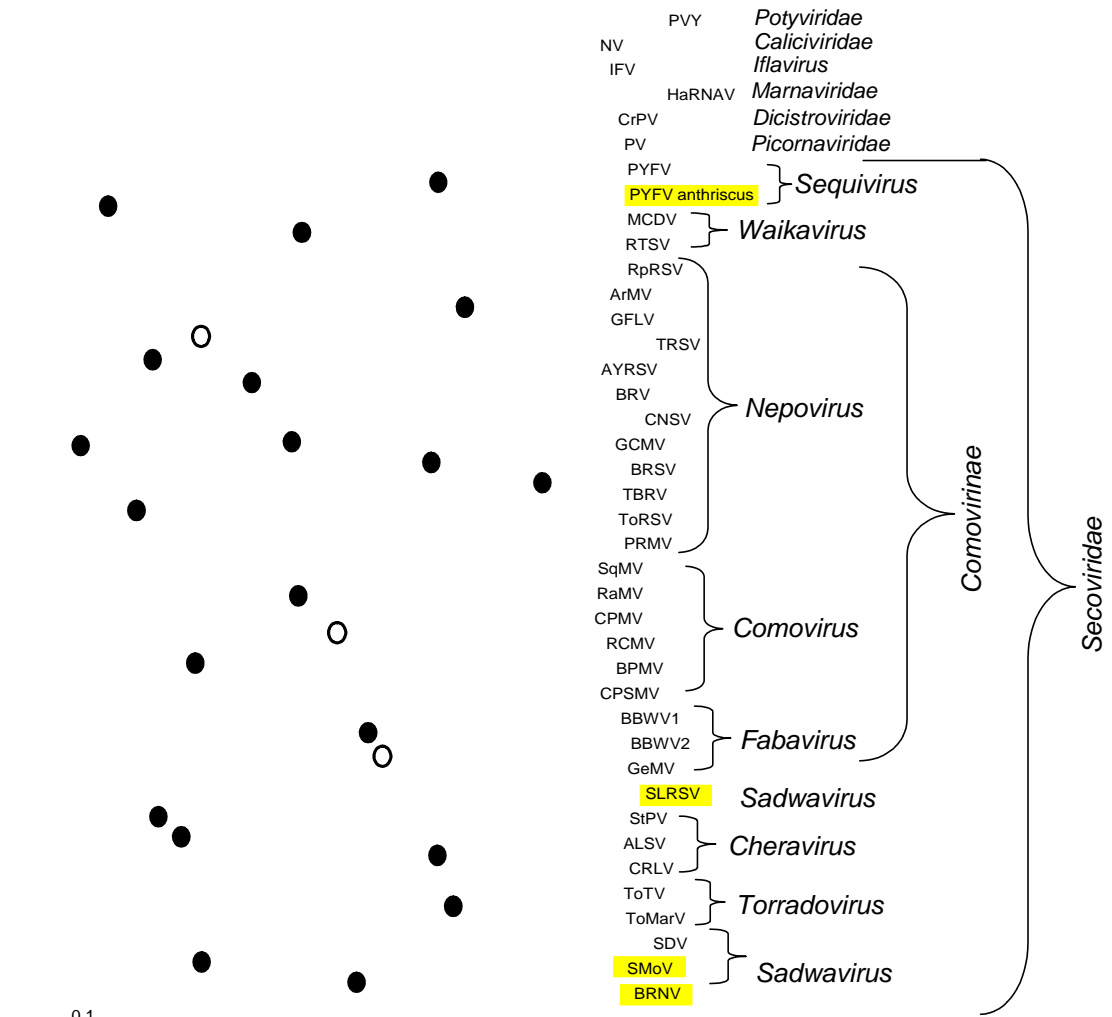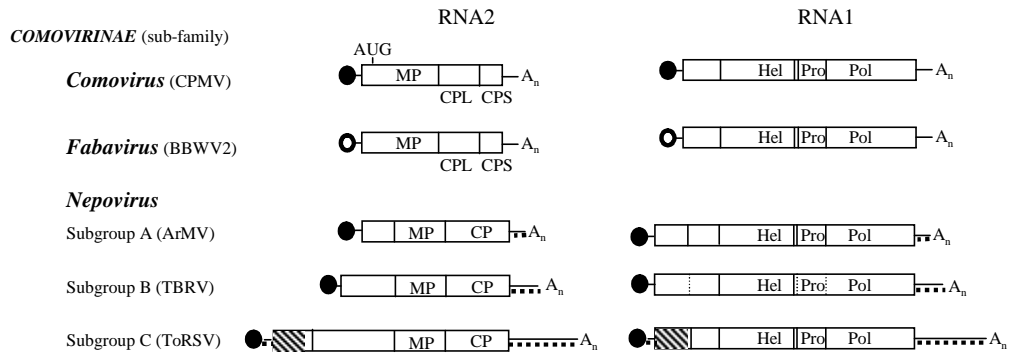
Comovirinae

Secoviridae

0.1

Figure 2: Genome organization of members of the family *Secoviridae*. The abbreviations are Hel: Helicase, Pro: 3C-like Proteinase, Pol: RNA-dependent RNA polymerase, CP: capsid protein, MP: movement protein, An: poly(A). The open reading frames are shown by the boxes. Proteinase cleavage sites identified experimentally or deduced by sequence comparison are shown by the solid or dotted vertical lines, respectively. The VPg is shown with a circle (open circle: no experimental evidence for a VPg; a sequence homologous to the VPg of comoviruses is found in the RNA1 of fabaviruses). The RNA2 of comoviruses (and possibly fabaviruses) encodes two polyproteins differing by their translation initiation site as indicated by the second AUG above the CPMV polyprotein. Dashed lines below the 3' or 5' UTR represent areas of sequence identity between RNA1 and RNA2. Similarly, the shaded areas in the N-terminus region of the subgroup C nepovirus and sadwavirus polyproteins represent areas of sequence identity. Possible subgenomic RNAs are represented by the arrows below the waikavirus 3' UTR. Virus acronyms are as defined in Figure 1. Viruses under consideration in this proposal are outlined in yellow.

RNA2 RNA1

COMOVIRINAE (sub-family)

AUG

Comovirus (CPMV) MP CPL CPS A_n Hel Pro Pol A_n

Fabavirus (BBWV2) MP CPL CPS A_n Hel Pro Pol A_n

Nepovirus

Subgroup A (ArMV) MP CP A_n Hel Pro Pol A_n

Subgroup B (TBRV) MP CP A_n Hel Pro Pol A_n

Subgroup C (ToRSV) MP CP A_n Hel Pro Pol A_n

ADDITIONAL GENERA

Sadwavirus MP CPL CPS A_n Hel Pro Pol A_n
(Type species: SDV)

SMoV and BRNV MP? CP ? A_n Hel Pro Pol A_n

SLRSV MP CPL CPS A_n Hel Pro Pol A_n

CP2

Cheravirus (CRLV and ALSV) MP CP1 CP3 A_n Hel Pro Pol A_n

CP2

Torradovirus (ToTV) MP? CP1 CP3 A_n Hel Pro Pol A_n

CP2

Sequivirus (PYFV) CP1 CP3 Hel Pro Pol

CP2

PYFV-Anthriscus CP1 CP3 Hel Pro Pol A_n

CP2

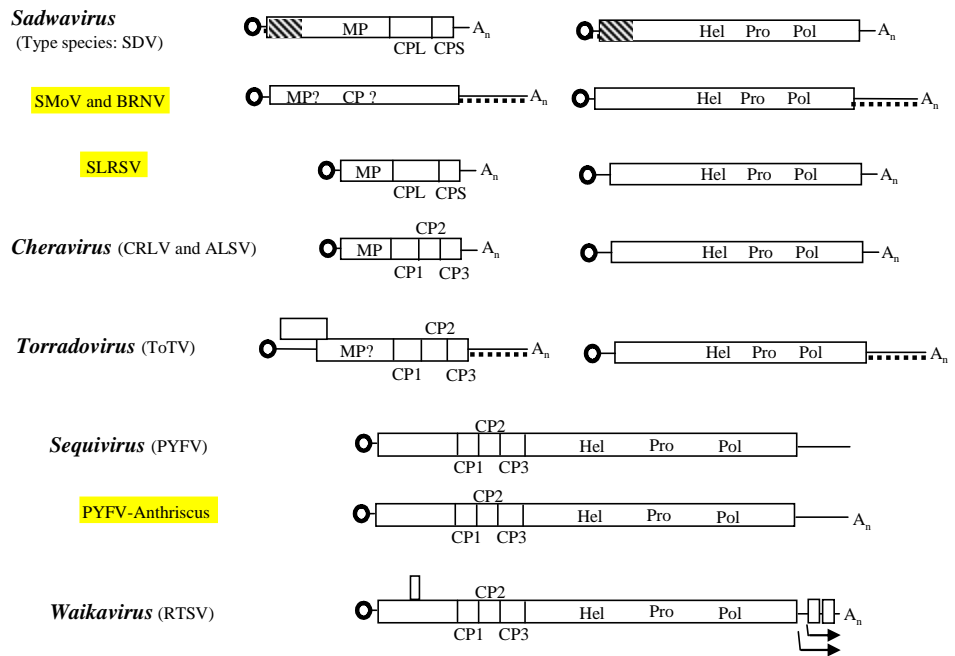*Waikavirus* (RTSV) CP1 CP3 Hel Pro Pol A_n

Figure 3: Hierarchical clustering of members of the family *Secoviridae* based on the Pro-Pol amino acid sequence. Family (Secoviridae), sub-family (Comovirinae) and genera are shown on the right. Viruses outlined in yellow are discussed in this proposal. The tree is the same as that shown in Figure 1, but with the proposed new taxonomy. The proposed new species in the genus *Sequivirus* is shown with the abbreviation CNDV for carrot necrotic dieback virus.
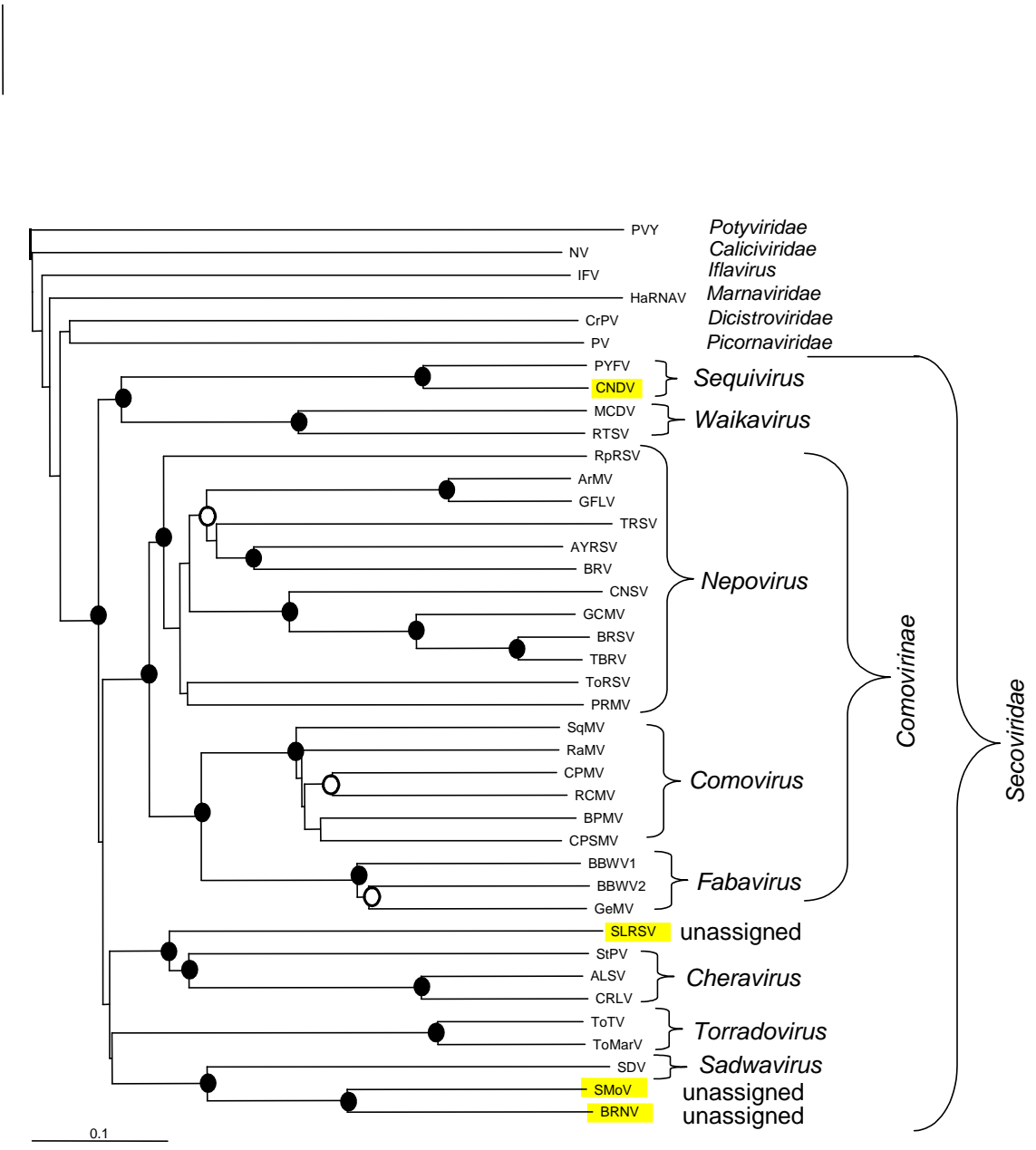
Table 1. Characteristics of members of the family *Secoviridae*

Genus or Species	N^1 RNA	N^1 CP	Proteinase substrate[2] binding pocket	Cleavage sites (a.a. at -1 position)	Vector
Sequivirus	1	3	Leu	Asp, Ser or Gln	aphid
Waikavirus	1	3	His	Gln	aphid or leafhopper
Comovirus	2	2	His	Gln	beetle
Fabavirus	2	2	His	Gln	aphid
Nepovirus	2	1	His or Leu	Gln, Asn, Asp, Arg, Lys, Cys or Gly	nematode (most) or mite (BRV) or thrips (TRSV) or no known vector
torradovirus	2	3	His	??	whitefly
Cheravirus	2	3	His	Gln or Glu	nematode
Sadwavirus SDV	2	2	Cys	Tyr or Ala	possibly nematode
<mark>SMoV, BRNV</mark>	2	?	His	Gln or Glu	aphid
<mark>SLRSV</mark>	2	2	His	Ser	nematode

[1] N: number (of RNA or of CP)

[2] The indicated amino acid in the substrate binding pocket interacts with the amino acid at the -1 position of the cleavage site. This amino acid is important in determining the cleavage site specificity of the proteinase. In the case of nepoviruses, this amino acid is His for nepoviruses of subgroup C and Leu for nepoviruses of subgroups A and B. Accordingly the cleavage sites of subgroup C nepoviruses have a Gln, Asn or Asp at the -1 position, while the cleavage sites of subgroup A or B nepoviruses have a Arg, Lys, Cys or Gly at the -1 position.

Abbreviations for viruses are as described in Figures 1 and 2. Viruses discussed in this proposal are outlined in yellow.