This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

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

Code assigned:	***2013.001a-kkF***	(to be completed by ICTV officers)

Short title: Reorganization of family *Partitiviridae* to contain 4 new genera of plant and/or fungal viruses, with elimination of 3 current genera and creation of 16 new species
(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:

Max L. Nibert (mnibert@hms.harvard.edu), Said A. Ghabrial (saghab00@email.uky.edu), Edgar Maiss (maiss@ipp.uni-hannover.de), Till Lesker (lesker@ipp.uni-hannover.de),

List the ICTV study group(s) that have seen this proposal:

	Partitiviridae

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

Partitiviridae SG: Nobuhiro Suzuki (nsuzuki@rib.okayama-u.ac.jp) (Chair), Said A. Ghabrial (saghab00@email.uky.edu), Max L. Nibert (mnibert@hms.harvard.edu), Sead Sabanadzovic (ss501@msstate.edu), Atsuko Sasaki (sasaatu@affrc.go.jp), Eeva Vainio (eeva.vainio@metla.fi). SG members provided comments on a draft proposal, and modifications have been made to the final proposal to the agreement of all.

ICTV-EC comments: Tables 1-4: Possible members to be extracted to separate table. Do not refer to 'proposed probable'. On page 24 modules dd/ee, there is a reference to the species "Rosellinia necatrix partitivirus 1" which should be (as in the latest MSL) Rosellinia necatrix virus 1. Drop "RNA" from the names of Heterobasidion RNA virus 1, 2, etc (pages 1, 2) and replace with Heterobasidion partitivirus 1 etc. On page 28, Heterobasidion RNA virus P becomes Heterobasidion partitivirus P.

Response of Proposers: All changes indicated by ICTV-EC have been made.

Date first submitted to ICTV: April 2013
Date of this revision (if different to above):

MODULE 2.1: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.001aF***	(assigned by ICTV officers)

To create 7 new species within:

Genus:	***Alphapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	

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.

And name of the new species:	**GenBank sequence accession number(s) of reference isolate:**
Carrot cryptic virus	FJ550604, FJ550605
Cherry chlorotic rusty spot associated partitivirus	AJ781401, AJ781402
Chondrostereum purpureum cryptic virus 1	AM999771, AM999772
Flammulina velutipes browning virus	AB465308, AB465309
Heterobasidion partitivirus 1	HQ541323, HQ541324
Heterobasidion partitivirus 3	FJ816271, FJ816272
Rosellinia necatrix partitivirus 2	AB569997, AB569998

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Because genus *Alphapartitivirus* is newly proposed in Module 3.1 below, there are no pre-exisiting criteria for species demarcations within it. These criteria therefore need to be newly established here, based on the data discussed in Module 3.1 and summarized for approved species, newly proposed species, and probable species in Tables 10–21 in the Appendix. Also see Table 22 for a summary of pairwise identity score ranges in the different proposed genera.

The species demarcation criteria within genus *Alphapartitivirus* are:
- ≤ 90% aa-sequence identity in the RdRp, and/or
- ≤ 80% aa-sequence identity in the CP

Genus demarcation criteria, for assigning these proposed species to genus *Alphapartitivirus* rather than to one of the other proposed genera, are discussed and established in Module 3.1 below.

MODULE 2.2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.001bF***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***Betapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	

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.

And name of the new species:	**GenBank sequence accession number(s) of reference isolate:**
Cannabis cryptic virus	JN196536, JN196537
Crimson clover cryptic virus 2	JX971982, JX971983
Dill cryptic virus 2	JX971984, JX971985
Primula malacoides virus 1	EU195326, EU195327
Heterobasidion partitivirus 2	HM565953, HM565954
Heterobasidion partitivirus 8	JX625227, JX625228

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.

Further material in support of this proposal may be presented in the Appendix, Module 9

Because genus *Betapartitivirus* is newly proposed in Module 3.2 below, there are no pre-exisiting criteria for species demarcations within it. These criteria therefore need to be newly established here, based on the data discussed in Module 3.1 and summarized for approved species, newly proposed species, and probable species in Tables 10–21 in the Appendix. Also see Table 22 for a summary of pairwise identity score ranges in the different proposed genera.

The species demarcation criteria within genus *Betapartitivirus* are:

- ≤ 90% aa-sequence identity in the RdRp, and/or
- ≤ 80% aa-sequence identity in the CP

Genus demarcation criteria, for assigning these proposed species to genus *Betapartitivirus* rather than to one of the other proposed genera, are discussed and established in Module 3.1 below.

MODULE 2.3: NEW SPECIES

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.001cF***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Deltapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	

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.

And name of the new species:	**GenBank sequence accession number(s) of reference isolate:**
Fig cryptic virus	FR687854, FR687855
Pepper cryptic virus 1	JN117276, JN117277
Pepper cryptic virus 2	JN117278, JN117279

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.

Further material in support of this proposal may be presented in the Appendix, Module 9

Because genus *Deltapartitivirus* is newly proposed in Module 3.4 below, there are no pre-exisiting criteria for species demarcations within it. These criteria therefore need to be newly established here, based on the data discussed in Module 3.1 and summarized for approved species, newly proposed species, and probable species in Tables 10–21 in the Appendix. Also see Table 22 for a summary of pairwise identity score ranges in the different proposed genera.

The species demarcation criteria within genus *Deltapartitivirus* are:

- $\leq$ 90% aa-sequence identity in the RdRp, and/or
- $\leq$ 80% aa-sequence identity in the CP

Genus demarcation criteria, for assigning these proposed species to genus *Deltapartitivirus* rather than to one of the other proposed genera, are discussed and established in Module 3.1 below.

MODULE 3.1: NEW GENUS

creating a new genus

Code	***2013.001dF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Partitiviridae***
Order:	

naming a new genus

Code	***2013.001eF***	(assigned by ICTV officers)

To name the new genus: *Alphapartitivirus*

Assigning the type species and other species to a new genus

Code	***2013.001fF***	(assigned by ICTV officers)

To designate the following as the type species of the new genus:

White clover cryptic virus 1

Please enter here the TOTAL number of species (including the type species) that the genus will contain

11 approved or proposed species (plus 4 probable species)

Reasons to justify the creation of a new genus:

Background:

Family *Partitiviridae* currently comprises 4 approved genera: genus *Partitivirus*, containing 19 approved species; genus *Alphacryptovirus*, 16 approved species; genus *Betacryptovirus*, 4 approved species; and genus *Cryspovirus*, 1 approved species. Members of genus *Partitivirus* infect fungi, those of genera *Alphacryptovirus* and *Betacryptovirus* infect plants, and those of genus *Cryspovirus* infect protozoa. Full-length genome sequences are available for representative strains of many of these approved species in each genus. Members of all 4 genera possess 2 essential genome segments, dsRNA 1 (S1) and dsRNA2 (S2), each containing one large ORF. One segment/ORF (S1) encodes the RNA-dependent RNA polymerase (RdRp), and the other segment/ORF (S2) encodes the coat protein (CP). Virus particles are isometric, with diameters appearing to range between 25 and 40 nm by electron microscopy. Each genome segment is separately encapsidated, making these viruses not only bi-segmented but also bi-particulate.

Phylogenetic comparisons:

The available RdRp, CP, and concatenated RdRP+CP sequences of *Partitiviridae* family members, including those of representative strains of the 15 new species proposed in modules 2.1–2.3 above, define 5 phylogenetically discrete clades (Figures 1–3). Current genus *Cryspovirus* retains its identity as a distinctive clade, but current genera *Partitivirus, Alphacryptovirus,* and *Betacryptovirus* do not. Sequenced strains of the species in current genus *Partitivirus* largely distribute between 2 distinct clades, which we propose to identify as new genus *Betapartitivirus* (Table 2) and new genus *Gammapartitivirus* (Table 3). The sequenced strain of one current *Partitivirus* species, *Helicobasidium mompa virus* (see Module 8 for discussion of revised name

Helicobasidium mompa partitivirus V70), falls into a third distinct clade, which we propose to identify as new genus *Alphapartitivirus* (Table 1). Sequenced strains of the species in current genus *Alphacryptovirus* also distribute between 2 distinct clades, *Alphapartitivirus* (Table 1) and another clade that we propose to designate as new genus *Deltapartitivirus* (Table 4). Lastly, sequenced strains of the species in current genus *Betacryptovirus* fall within the clade that we propose to designate as new genus *Betapartitivirus* (Table 2). Overall, the number of approved, proposed, or probable species in the 4 proposed genera are: *Alphapartitivirus*, 14; *Betapartitivirus*, 18; *Gammapartitivirus*, 9; and *Deltapartitivirus*, 10.

Host ranges:

One notable aspect of the 4 proposed genera is that two of them, *Alphapartitivirus* and *Betapartitivirus,* comprise mixtures of viral isolates from both fungi and plants (Figures 1–3). In proposed genus *Alphapartitivirus*, 4 of the proposed species and 1 probable species are represented by fungal isolates, whereas 3 of the approved species, 2 of the proposed species, and 3 probable species are represented by plant isolates. In proposed genus *Betapartitivirus*, 6 of the approved species, 2 of the proposed species, and 2 probable species are represented by fungal isolates, whereas 3 of the approved species and 4 of the proposed species are represented by plant isolates. Based on these findings, a capacity for productive transmission of these viruses between fungal and plant hosts appears likely, at least on occasion. One possible means of such transmission may be through fungal symbionts/pathogens of plants, which mediate intimate fungus-plant contacts. A second possible means could be through animal vectors that cross-feed on both fungi and plants, and can thereby transmit the viruses between these divergent hosts. Yet another possibility is that some of the apparent plant isolates may derive instead from their fungal symbionts/pathogens; however, the extent of host admixture in both *Alphapartitivirus* and *Betapartitivirus* suggests this last explanation is unlikely to pertain to all apparent plant isolates in these two proposed genera.

Unlike proposed genera *Alphapartitivirus* and *Betapartitivirus*, proposed genus *Gammapartitivirus* so far comprises only viruses isolated from fungal hosts, and proposed genus *Deltapartitivirus* so far comprises only viruses isolated from plant hosts. Given the apparent mixture of both fungal and plant viruses in genera *Alphapartitivirus* and *Betapartitivirus*, however, we propose that host of isolation is no longer a strict criterion for assignment of a virus to any particular genus in the family *Partitiviridae*. Thus, in the future, for example, certain new plant isolates might be found proper to assign to genus *Gammapartitivirus*, and certain new fungal isolates to genus *Deltapartitivirus*.

Genome-segment and protein lengths:

A compilation of genome-segment and protein lengths of the fungal and plant viruses in family *Partitiviridae* (Tables 5–8) identify several additional traits that co-segregate with the 4 distinct clades defined by phylogenetic comparisons and proposed to represent the 4 new genera *Alpha-, Beta-, Gamma-,* and *Deltapartitivirus.* The summary of these findings appears in Table 9. Of particular note is that the ranges of both RdRp and RdRp+CP lengths within the 4 proposed genera are almost wholly non-overlapping, in the order *Betapartitivirus* > *Alphapartitivirus* > *Gammapartitivirus* > *Deltapartitivirus*. In addition, although the ranges of S1, S2, S1+S2, and CP lengths of genera *Gammapartitivirus* and *Deltapartitivirus* are overlapping, those ranges of genera *Alphapartitivirus* and *Betapartitivirus* are largely not, in the order *Betapartitivirus* > *Alphapartitivirus* > *Gammapartitivirus/Deltapartitivirus*. It is also worth noting that members of both genus *Alphapartitivirus* and genus *Betapartitivirus* commonly share long poly(A) tracts (≥ 10 nt) near the plus-strand 3′ terminus of one or both genome segments, whereas the members of genera *Gammapartitivirus* and genus *Deltapartitivirus* generally do not.

Pairwise comparisons:

Pairwise identity scores derived from global pairwise alignments of the RdRp, CP, and concatenated RdRP+CP sequences of the fungal and plant viruses within each of the proposed genera in family *Partitiviridae* (Tables 10–21) provide additional data points that support the proposed genus boundaries. These within-genus score are also summarized Table 22. Comparably obtained between-genus scores are summarized in Tables 23–25. Among the 4 proposed genera, the within-genus scores range from 24.6% to 90.1% for the RdRp sequences, 3.4% to 78.4% for the CP sequences, and 22.3% to 83.9% for the RdRp+CP sequences. In contrast, the between-genus scores are ≤ 26.4% for the RdRp sequences, ≤ 20.0% for the CP sequences, and ≤ 22.5% for the RdRp+CP sequences. Thus, among these pairwise identity scores, those for the RdRp sequences and the concatenated RdRp+CP sequences provide similarly good overall discrimination between genera, with RdRp scores > 24% within genera and largely < 24% between genera, and RdRp+CP sequences > 22% within genera and largely < 22% between genera. Only a few exceptions to these thresholds are found among the pairwise comparisons of certain members of genera *Alphapartitivirus* and *Betapartitivirus,* which is consistent with the finding that these 2 genera appear to be the most closely related pair among the 4 in the RdRp and RdRp+CP phylograms (Figures 1 and 3).

Summary of genus demarcation criteria:

Because of the extent of reorganization, new criteria for genus demarcations within family *Partitiviridae* need to be established and are summarized here. These criteria are based on the data discussed above and summarized in Figures 1–3 and Tables 5–25 in the Appendix. The genus demarcation criteria within family *Partitiviridae* are:

- Characteristic hosts within each genus (plants and/or fungi for genera *Alphapartitivirus, Betapartitivirus, Gammapartitivirus,* and *Deltapartitivirus*; protozoa only for genus *Cryspovirus*), and
- Genome segment and protein lengths within a characteristic size range for each genus, and
- < 24% RdRp identity in pairwise comparisons of viruses from different genera, and
- Clustering with other members of the same genus in representative phylogenetic analyses

Probable species in genus *Alphapartitivirus*:

Diuris pendunculata cryptic virus and Sclerotinia sclerotiorum partitivirus S are newly identified as probable species in proposed genus *Alphapartitivirus* (Supplemental Table S1). From their GenBank-deposited full-length sequences, both phylogenetic results (Figures 1–3) and genome-segment/protein sizes (Table 5) support their assignment to this genus, and pairwise identity scores with other genus members (Tables 10–12) support their recognition as distinct species. However, neither has yet been described in a peer-reviewed publication, and thus per SG criteria, their status must remain "probable" for now. One previously identified probable species from current genus *Alphacryptovirus*, Raphanus sativus cryptic virus 1, should also be assigned to proposed *Alphapartitivirus* (Figures 1–3; Tables 1 and 5). Although full-length RdRp and CP sequences are available for this virus, it has been reported to contain 3 genome segments, 2 of which appear to encode 2 different versions of CP, and until this issue is clarified, the status of this virus should remain "probable". One previously identified probable species from current genus *Partitivirus*, Helicobasidium mompa partitivirus V1-2, for which only a full-length S1/RdRp sequence is available (Figure 1; Tables 1 and 5), should also be assigned to proposed genus *Alphapartitivirus*.

See Tables1 and S1 for summary listings of all species and probable species, respectively, in proposed genus *Alphapartitivirus*, along with the GenBank accession numbers of their representative strains.

Origin of the new genus name:

The existing name *Partitivirus* is retained but with *Alpha*-, *Beta*-, *Gamma*-, and *Delta*- added as prefixes to designate the four new genera, with *Alpha*- and *Delta*- coming largely from division of current genus *Alphacryptovirus*, and *Beta*- and *Gamma*- coming largely from division of current genus *Partitivirus*. Use of the term "cryptovirus" in genus names of *Partitiviridae* members is discontinued for several important reasons. (i) Although previously used for designating many plant partitiviruses, many fungal partitiviruses similarly have no known disease effects on their fungal hosts and therefore are likewise "cryptic" viruses; thus, the term "cryptovirus" cannot be accurately used to differentiate plant from fungal partitiviruses. (ii) Some plant partitiviruses appear to be associated with disease symptoms and therefore are not in fact "cryptic" viruses. In addition, (iii) new genera *Alphapartitivirus* and *Betapartitivirus* contain both fungal and plant partitiviruses, and (iv) current genus *Betacryptovirus* has been subsumed into new genus *Betapartitivirus;* thus, previous use of the term "cryptovirus" to distinguish plant partitiviruses is made obsolete by phylogenetic results.

Reasons to justify the choice of type species:

White clover cryptic virus 1 is the type species of current genus *Alphacryptovirus* and was the first species of the new genus *Alphapartitivirus* for which full-length genome sequences of a representative strain were reported.

Species demarcation criteria in the new genus:

The species demarcation criteria within genus *Alphapartitivirus* are:

- ≤ 90% aa-sequence identity in the RdRp, and/or
- ≤ 80% aa-sequence identity in the CP

MODULE 3.2: NEW GENUS

creating a new genus

Code	***2013.001gF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Partitiviridae***
Order:	

naming a new genus

Code	***2013.001hF***	(assigned by ICTV officers)

To name the new genus: *Betapartitivirus*

Assigning the type species and other species to a new genus

Code	***2013.001iF***	(assigned by ICTV officers)

To designate the following as the type species of the new genus:

Atkinsonella hypoxylon virus

Please enter here the TOTAL number of species (including the type species) that the genus will contain

16 approved or proposed species (plus 3 probable species)

Reasons to justify the creation of a new genus:

See Module 3.1.

Probable species in genus *Betapartitivirus*:

Heterobasidion virus 7 and Sclerotinia sclerotiorum partitivirus 1 are newly identified as probable species in new genus *Betapartitivirus* (Table S2). From their GenBank-deposited full-length sequences, both phylogenetic results (Figures 1–3) and genome-segment/protein sizes (Table 6) support their assignment to this genus, and pairwise identity scores with other genus members (Tables 13–15) support their recognition as distinct species. However, neither of these viruses has yet been described in a peer-reviewed publication, and thus per SG criteria, their status must remain "probable" for now. One previously identified probable species in current genus *Partitivirus*, Helicobasidium mompa partitivirus V1-1, for which only a full-length S1/RdRp sequence is available (Figure 1; Tables 2 and 6), should also be assigned to proposed genus *Betapartitivirus*. One other previously identified probable species in current genus *Partitivirus*, Ceratocystis polonica partitivirus 1, for which both full-length S1/RdRp and S2/CP sequences are available, shows 96% and 88% aa-identity to the respective proteins of the reference strain of species *Ceratocystis resinifera virus 1* and should therefore be recognized as another strain of species *Ceratocystis resinifera virus 1,* not a probable species in its own right.

See Table 2 for a summary listing of all species in new genus *Betapartitivirus*, along with the GenBank accession numbers of their representative strains.

Origin of the new genus name:

See Module 3.1.

Reasons to justify the choice of type species:

Atkinsonella hypoxylon virus is the type species of current genus *Partitivirus* and was the first species in new genus *Betapartitivirus* for which full-length genome sequences of a representative strain were reported.

Species demarcation criteria in the new genus:

The species demarcation criteria within genus *Betapartitivirus* are:

- ≤ 90% aa-sequence identity in the RdRp, and/or
- ≤ 80% aa-sequence identity in the CP

MODULE 3.3: **NEW GENUS**

creating a new genus

Code	***2013.001jF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Partitiviridae***
Order:	

naming a new genus

Code	***2013.001kF***	(assigned by ICTV officers)

To name the new genus: ***Gammapartitivirus***

Assigning the type species and other species to a new genus

Code	***2013.001lF***	(assigned by ICTV officers)

To designate the following as the type species of the new genus:

Penicillium stoloniferum virus S

Please enter here the TOTAL number of species (including the type species) that the genus will contain

8 approved species (plus 1 probable species)

Reasons to justify the creation of a new genus:

See Module 3.1.

Probable species in genus *Gammapartitivirus*:

Botryotinia fuckeliana partitivirus 1 is identified as a probable species in new genus *Gammapartitivirus* (Table S3). From its GenBank-deposited full-length sequences, both phylogenetic results (Figures 1–3) and genome-segment/protein sizes (Table 7) support its assignment to this genus, and pairwise identity scores with other genus members (Tables 16–18) support its recognition as a distinct species. However, this virus has not yet been described in a peer-reviewed publication, and thus per SG criteria, its status must remain “probable” for now.

See Tables 3 and S3 for summary listings of all species and probable species, respectively, in new genus *Gammapartitivirus*, along with the GenBank accession numbers of their representative strains.

Origin of the new genus name:

See Module 3.1.

Reasons to justify the choice of type species:

Penicillium stoloniferum virus S was one of the first species of the new genus *Gammapartitivirus* for which full-length genome sequences of a representative strain, as well as other molecular studies, were reported. It is also one of two species from this new genus for which a 3D structure of a representative strain has been reported. *Penicillium stoloniferum virus F* would be another possible choice as type species (also early sequences, other molecular studies, and 3D structures of a representative strain), but because it is the most divergent member of the new genus, the choice of *Penicillium stoloniferum virus S* to serve as type species seems more prudent. *Fusarium solani virus 1* would be another possible choice as type species (earliest reported sequences), but it has not been studied as thoroughly as *Penicillium stoloniferum virus S.*

Species demarcation criteria in the new genus:

The species demarcation criteria within genus *Gammapartitivirus* are:

- ≤ 90% aa-sequence identity in the RdRp, and/or
- ≤ 80% aa-sequence identity in the CP

MODULE 3.4: NEW GENUS

creating a new genus

Code	***2013.001mF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Partitiviridae***
Order:	

naming a new genus

Code	***2013.001nF***	(assigned by ICTV officers)

To name the new genus: *Deltapartitivirus*

Assigning the type species and other species to a new genus

Code	***2013.001oF***	(assigned by ICTV officers)

To designate the following as the type species of the new genus:

Pepper cryptic virus 1

Please enter here the TOTAL number of species (including the type species) that the genus will contain

4 approved or proposed species (plus 9 probable species)

Reasons to justify the creation of a new genus:

See Module 3.1.

Probable species in genus *Deltapartitivirus*:

Persimmon cryptic virus is newly identified as a probable species in proposed genus *Deltapartitivirus* (Table S4). From its GenBank-deposited full-length sequences, both phylogenetic results (Figures 1–3) and genome-segment/protein sizes (Table 8) support its assignment to this genus, and pairwise identity scores with other genus members (Tables 19–21) support its recognition as a distinct species. However, it has not yet been described in a peer-reviewed publication, and thus per SG criteria, its status must remain “probable” for now. Seven previously identified probable species from current genus *Alphacryptovirus*—Black raspberry cryptic virus, Fragaria chiloensis cryptic virus, Pinus sylvestris cryptic virus, Pyrus pyrofolia cryptic virus, Raphanus sativus cryptic virus 2, Raphanus sativus cryptic virus 3, and Rose cryptic virus 1—should also be assigned to proposed genus *Deltapartitivirus* (Figure 1; Tables 4 and 8). Although full-length RdRp and CP sequences are available for Fragaria chiloensis cryptic virus, Raphanus sativus cryptic virus 2, and Rose cryptic virus 1, each has been reported to contain 3 genome segments, 2 of which appear to encode 2 different versions of CP, and until this issue is clarified, their status should remain “probable”. Similarly, although full-length RdRp and CP sequences are available for Raphanus sativus cryptic virus 3, it has not yet been described in a peer-reviewed publication, and thus per SG criteria, its status must also remain “probable” for now.

See Tables 4 and S4 for summary listings of all species and probable species, respectively, in proposed genus *Deltapartitivirus*, along with the GenBank accession numbers of their representative strains.

Origin of the new genus name:

See Module 3.1.

Reasons to justify the choice of type species:

Beet cryptic virus 2 would seem to be the more logical choice, being the first species of the new genus *Deltapartitivirus* for which full-length genome sequences of a representative strain were reported. However, it is another of the viruses that have so far been identified to contain 3 genome segments, including 2 that appear to encode 2 different versions of CP. Because of this issue, *Beet cryptic virus 2* is not an appropriate choice to serve as type species. *Beet cryptic virus 3* would be another possible choice, but only its RdRp sequence has been reported to date. *Pepper cryptic virus 1* is thus the best choice to serve as type species, being the first undisputed species of new genus *Deltapartitivirus* for which full-length genome sequences of a representative strain were reported.

Species demarcation criteria in the new genus:

The species demarcation criteria within genus *Deltapartitivirus* are:

- ≤ 90% aa-sequence identity in the RdRp, and/or
- ≤ 80% aa-sequence identity in the CP

MODULE 7.1: REMOVE and MOVE

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

Code	*2013.001pF*	(assigned by ICTV officers)

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

Species *Beet cryptic virus 1, Vicia cryptic virus, White clover cryptic virus 1*

The present taxonomic position of these taxon/taxa:

Genus:	*Alphacryptovirus*
Subfamily:	
Family:	*Partitiviridae*
Order:	

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:

These species are currently in the genus *Alphacryptovirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and assigned to the appropriate new genus, *Alphapartitivirus*.

Part (b) re-assign to a higher taxon

Code	*2013.001qF*	(assigned by ICTV officers)

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

Genus:	*Alphapartitivirus* (new)
Subfamily:	
Family:	*Partitiviridae*
Order:	
Order:	

Reasons to justify the re-assignment:

See Module 3.1.

Also see Tables 1 and S1 for a summary listing of all species and probable species, respectively, in proposed genus *Alphapartitivirus*, along with the GenBank accession numbers of their representative strains.

MODULE 7.2: **REMOVE and MOVE**

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

Code	***2013.001rF***	(assigned by ICTV officers)

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

Species *Beet cryptic virus 2, Beet cryptic virus 3*

The present taxonomic position of these taxon/taxa:

Genus:	***Alphacryptovirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

These species are currently in the genus *Alphacryptovirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and assigned to the appropriate new genus, *Deltapartitivirus*.

Part (b) re-assign to a higher taxon

Code	***2013.001sF***	(assigned by ICTV officers)

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

Genus:	***Deltapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

See Module 3.1.

Also see Tables 4 and S4 for summary listings of all species and probable species, repectively, in proposed genus *Deltapartitivirus*, along with the GenBank accession numbers of their representative strains.

MODULE 7.3: **REMOVE and MOVE**

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

Code	***2013.001tF***	(assigned by ICTV officers)

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

Species *Alfalfa cryptic virus 1, Carnation cryptic virus 1, Carrot temperate virus 1, Carrot temperate virus 3, Carrot temperate virus 4, Hop trefoil cryptic virus 1, Hop trefoil cryptic virus 3, Radish yellow edge virus, Ryegrass cryptic virus, Spinach temperate virus, White clover cryptic virus 3*

The present taxonomic position of these taxon/taxa:

Genus:	***Alphacryptovirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

These species are currently in the genus *Alphacryptovirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and designated as "Unassigned" to a genus in the family *Partitiviridae*.

Part (b) re-assign to a higher taxon

Code	***2013.001uF***	(assigned by ICTV officers)

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

Genus:	**Unassigned**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

There are no reported sequences for these plant partitiviruses. Since we are proposing three new genera to which different plant partitiviruses have been found to belong (*Alphapartitivirus*, *Betapartitivirus*, and *Deltapartitivirus*), it is impossible to confidently assign *Alfalfa cryptic virus 1, Carnation cryptic virus 1, Carrot temperate virus 1, Carrot temperate virus 3, Carrot temperate virus 4, Hop trefoil cryptic virus 1, Hop trefoil cryptic virus 3, Radish yellow edge virus, Ryegrass cryptic virus, Spinach temperate virus*, or *White clover cryptic virus* to a particular genus in the absence of sequence data.

Probable species:

Previously identified probable species Cucumber cryptic virus in current genus *Alphacryptovirus* also has no reported sequences and should thus also be moved at this time to genus “Unassigned” in family *Partitiviridae*.

See Table 26 for a summary of all approved and probable species moved to genus “Unassigned”.

MODULE 7.4: **REMOVE and MOVE**

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

Code	***2013.001vF***	(assigned by ICTV officers)

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

Genus *Alphacryptovirus*

The present taxonomic position of these taxon/taxa:

Genus:	
Subfamily:	
Family:	***Partitiviridae***
Order:	

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

Reasons to justify the removal:
This genus will disappear in the proposed reorganization.

MODULE 7.5: **REMOVE and MOVE**

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

Code	***2013.001wF***	(assigned by ICTV officers)

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

Species *Hop trefoil cryptic virus 2, Red clover cryptic virus 2, White clover cryptic virus 2*

The present taxonomic position of these taxon/taxa:

Genus:	***Betacryptovirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

These species are currently in the genus *Betacryptovirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and assigned to the appropriate new genus, *Betapartitivirus*.

Part (b) re-assign to a higher taxon

Code	***2013.001xF***	(assigned by ICTV officers)

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

Genus:	***Betapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

See Module 3.1.

Also see Tables 2 and S2 for summary listings of all species and probable species, respectively, in proposed genus *Betapartitivirus*, along with the GenBank accession numbers of their representative strains.

MODULE 7.6: **REMOVE and MOVE**

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

Code	***2013.001yF***	(assigned by ICTV officers)

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

Species *Carrot temperate virus 2*

The present taxonomic position of these taxon/taxa:

Genus:	***Betacryptovirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

This species is currently in the genus *Betacryptovirus*. As that genus will disappear in the proposed reorganization, this species needs to be removed and designated as "unassigned" in the family *Partitiviridae*.

Part (b) re-assign to a higher taxon

Code	***2013.001zF***	(assigned by ICTV officers)

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

Genus:	**Unassigned**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

There are no reported sequences for this plant partitivirus. Since we are proposing three new genera to which different plant partitiviruses have been found to belong (*Alphapartitivirus*, *Betapartitivirus*, and *Deltapartitivirus*), it is impossible to confidently assign *Carrot temperate virus 2* to a particular genus in the absence of sequence data.

Probable species:

Previously identified probable species Alfalfa cryptic virus 2 in current genus *Betacryptovirus* also has no reported sequences and should thus also be moved at this time to genus "Unassigned" in family *Partitiviridae*.

See Table 26 for a summary of all approved and probable species moved to genus "Unassigned".

MODULE 7.7: **REMOVE and MOVE**

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

Code	***2013.001aaF***	(assigned by ICTV officers)

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

Genus *Betacryptovirus*

The present taxonomic position of these taxon/taxa:

Genus:	
Subfamily:	
Family:	***Partitiviridae***
Order:	

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

Reasons to justify the removal:
This genus will disappear in the proposed reorganization.

MODULE 7.8: **REMOVE and MOVE**

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

Code	***2013.001bbF***	(assigned by ICTV officers)

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

Species *Helicobasidium mompa virus*

The present taxonomic position of these taxon/taxa:

Genus:	***Partitivirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

This species is currently in the genus *Partitivirus*. As that genus will disappear in the proposed reorganization, this species needs to be removed and assigned to the appropriate new genus, *Alphapartitivirus*.

Part (b) re-assign to a higher taxon

Code	***2013.001ccF***	(assigned by ICTV officers)

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

Genus:	***Alphapartitivirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

See Module 3.1.

Also see Tables 1 and S1 for summary listings of all species and probable species, respectively, in proposed genus *Alphapartitivirus*, along with the GenBank accession numbers of their representative strains.

MODULE 7.9: **REMOVE and MOVE**

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

Code	***2013.001ddF***	(assigned by ICTV officers)

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

Species *Atkinsonella hypoxylon virus, Ceratocystis resinifera virus 1, Fusarium poae virus 1, Heterobasidion annosum virus, Pleurotus ostreatus virus 1, Rhizoctonia solani virus 717, Rosellinia necatrix partitivirus 1*

The present taxonomic position of these taxon/taxa:

Genus:	***Partitivirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

These species are currently in the genus *Partitivirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and assigned to the appropriate new genus, *Betapartitivirus.*

Part (b) re-assign to a higher taxon

Code	***2013.001eeF***	(assigned by ICTV officers)

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

Genus:	***Betapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

See Module 3.1.

Also see Tables 2 and S2 for summary listings of all species and probable species, respectively, in proposed genus *Betapartitivirus*, along with the GenBank accession numbers of their representative strains.

MODULE 7.10: **REMOVE and MOVE**

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

Code	***2013.001ffF***	(assigned by ICTV officers)

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

Species Aspergillus ochraceous virus, Discula destructiva virus 1, Discula destructiva virus 2, Fusarium solani virus 1, Gremmeniella abietina RNA virus MS1, Ophiostoma partitivirus 1, Penicillium stoloniferum virus F, Penicillium stoloniferum virus S

The present taxonomic position of these taxon/taxa:

Genus:	***Partitivirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

These species are currently in the genus *Partitivirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and assigned to the appropriate new genus, *Gammapartitivirus*.

Part (b) re-assign to a higher taxon

Code	***2013.001ggF***	(assigned by ICTV officers)

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

Genus:	***Gammapartitivirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

See Module 3.1.

Also see Tables 3 and S3 for summary listings of all species and probable species, respectively, in proposed genus *Gammapartitivirus*, along with the GenBank accession numbers of their representative strains.

MODULE 7.11: **REMOVE and MOVE**

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

Code	***2013.001hhF***	(assigned by ICTV officers)

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

Species *Agaricus bisporus virus 4, Gaeumannomyces graminis virus 019/6-A, Gaeumannomyces graminis virus T1-A*

The present taxonomic position of these taxon/taxa:

Genus:	***Partitivirus***
Subfamily:	
Family:	***Partitiviridae***
Order:	

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:

These species are currently in the genus *Partitivirus*. As that genus will disappear in the proposed reorganization, these species need to be removed and designated as "Unassigned" in the family *Partitiviridae*.

Part (b) re-assign to a higher taxon

Code	***2013.001iiF***	(assigned by ICTV officers)

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

Genus:	**Unassigned**
Subfamily:	
Family:	***Partitiviridae***
Order:	
Order:	

Reasons to justify the re-assignment:

There are no reported sequences for these fungal partitiviruses. Since we propose three new genera to which different fungal partitiviruses have been found to belong (*Alphapartitivirus*, *Betapartitivirus*, and *Gammapartitivirus*), it is impossible to confidently assign *Agaricus bisporus virus 4, Gaeumannomyces graminis virus 019/6-A,* or *Gaeumannomyces graminis virus T1-A* to a particular genus in the absence of sequence data.

See Table 26 for a summary of all approved and probable species moved to genus "Unassigned".

MODULE 7.12: **REMOVE and MOVE**

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

Code	***2013.001jjF***	(assigned by ICTV officers)

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

Genus *Partitivirus*

The present taxonomic position of these taxon/taxa:

Genus:	
Subfamily:	
Family:	***Partitiviridae***
Order:	

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

Reasons to justify the removal:
This genus will disappear in the proposed reorganization.

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	***2013.001kkF***	(assigned by ICTV officers)

Title of proposal: Change the names of 3 existing species in proposed new genera *Alphapartitivirus* and *Betapartitivirus* (current genus *Partitivirus*), as follows: *Heterobasidion annosum virus* to *Heterobasidion partitivirus P*, *Helicobasidium mompa virus* to *Helicobasidium mompa partitivirus V70*, and *Rosellinia necatrix virus 1* to *Rosellinia necatrix partitivirus 1*.

Text of proposal:

We propose to change the names of three existing species in in proposed new genera *Alphapartitivirus* and *Betapartitivirus* (current genus *Partitivirus*) for consistency with related names, and also to distinguish them from several related species, as explained below.

Heterobasidion annosum virus. Eeva Vainio and colleagues have agreed to the nomenclature "Heterobasidion virus 1, 2, etc." for viruses they have isolated from different *Heterobasidion* fungal species. In support of this nomenclature is evidence that these viruses can readily cross between different *Heterobasidion* species (Vainio et al, 2011), suggesting that the host genus but not the host species name should be included in the virus species name. Several of these viruses are proposed as new species in Modules 2.1 and 2.2, above. Predating this more recent work, a partitivirus was isolated from fungus *Heterobasidion annosum* and designated as the reference strain of species *Heterobasidion annosum virus.* To bring the nomenclature of this older species in line with the newer nomenclature, we propose to change its species name to *Heterobasidion partitivirus P*, the *P* modifier being used because the reference strain was identified as having been obtained from *Heterobasidion annosum* P-type fungus. In addition to being consistent with the nomenclature agreed to by Vainio and colleagues, the new species name *Heterobasidion partitivirus P* helps to distinguish this species and reference strain from another, partial but phylogenetically distinct RdRp sequence in GenBank that is attributed to Heterobasidion annosum virus.

Helicobasidium mompa virus. There is a species in family *Totiviridae* named *Helicobasidium mompa totivirus 1-17.* In order to more clearly differentiate the species *Helicobasidium mompa virus* in family *Partitiviridae* from that totivirus species, we first propose to change its name to *Helicobasidium mompa partitivirus.* In addition, because there are currently two other, probable species of partitiviruses isolated from *Helicobasidium mompa*, Helicobasidium mompa partitivirus V1-1 and Helicobasidium mompa partitivirus V1-2, it is necessary to add a modifier to the species name *Helicobasidium mompa partitivirus* to distinguish it from these probable species. The modifier suggested by Atsuko Sasaki, one of the original discoverers of this virus is *V70*. Thus, we finally propose to change the name of current species *Helicobasidium mompa virus* to *Helicobasidium mompa partitivirus V70.*

Rosellinia necatrix virus 1. There is a species in genus *Megabirnavirus* named *Rosellinia necatrix megabirnavirus 1* and another species in genus *Quadrivirus* named *Rosellinia necatrix quadrivirus 1.* In order to more clearly differentiate the species *Rosellinia necatrix virus 1* in family *Partitiviridae* from those megabirnavirus and quadrivirus species, we propose to change its name to *Rosellinia necatrix partitivirus 1.* This nomenclature change is also consistent with the name of new species *Rosellinia necatrix partitivirus 2* proposed in Module 2.1, above.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

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Magae Y, Sunagawa M. 2010. Characterization of a mycovirus associated with the brown discoloration of edible mushroom, *Flammulina velutipes*. *Virol J* **7,** 342.

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Figure 1. Maximum-likelihood tree of the RdRp sequences of *Partitiviridae* family members, highlighting the existence of 4 discrete clades of fungal and/or plant partitiviruses distinct from current genera. Alignments were conducted using MAFFT version 6.85 as implemented at http://www.ebi.ac.uk/Tools/msa/mafft/ with default settings except for refinement with 10 iterations. Trees were generated with PhyML 3.0 as implemented at http://www.hiv.lanl.gov/content/sequence/PHYML/interface.html using the LG substitution model, empirical equilibrium frequencies, program-estimated invariant-proportion value (0.013) and gamma-shape value (1.509), and 4 rate categories. The starting tree was obtained by BioNJ and optimized by both branch length and tree topology. Tree improvement was performed according to the best of nearest neighbor interchange and subtree pruning and regrafting. Branch support values (%) were estimated by the approximate likelihood ratio test (aLRT) with SH-like criteria; branches with values ≥ 90% are not labeled, and branches with values < 50% are collapsed. Two picobirnavirus sequences were used as outgroup. Color and shading are explained in the figure. The putative host of each virus is shown at right: F, fungus; P, plant; Pr, Protozoan; and V, vertebrate.

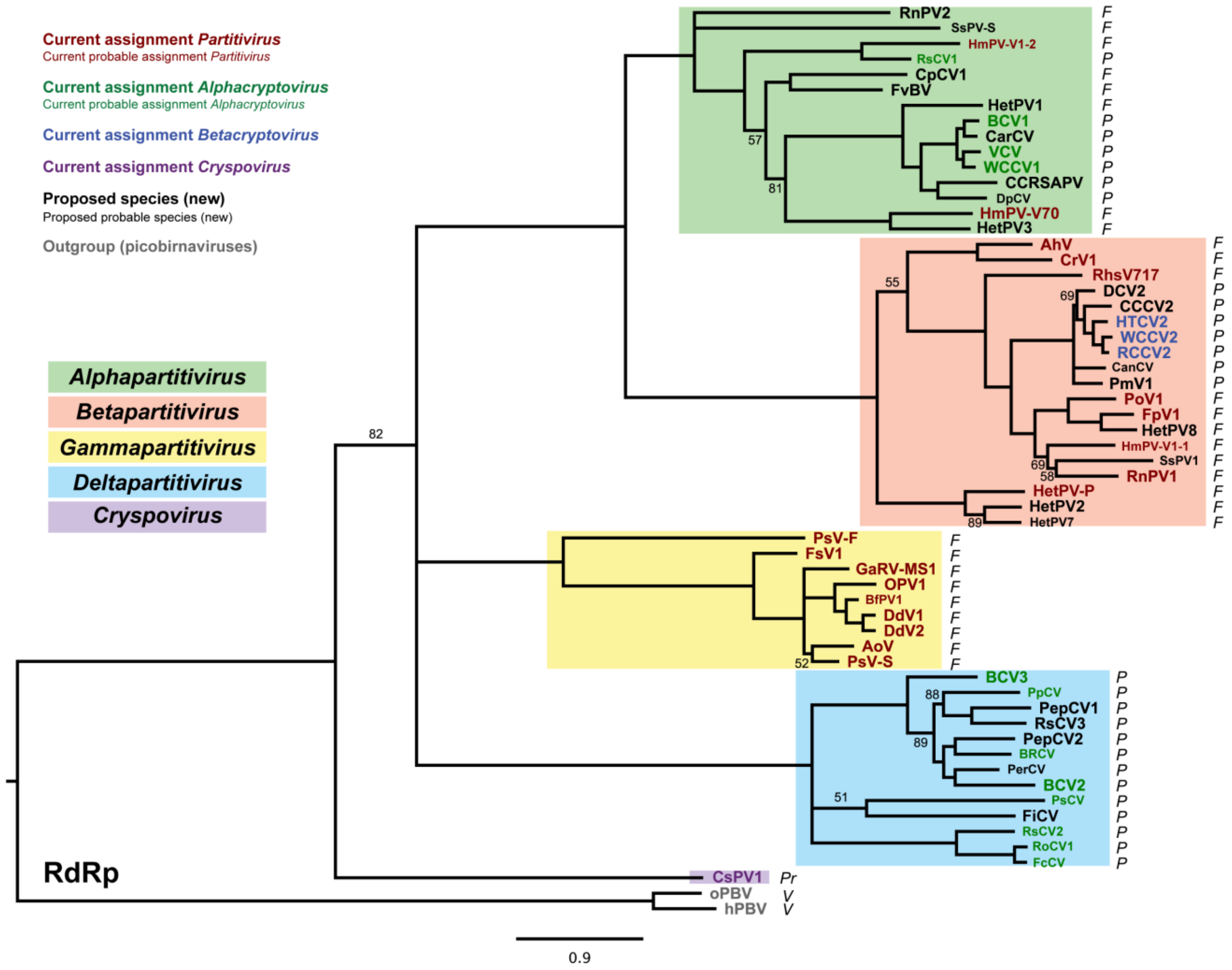

Figure 2. Maximum-likelihood tree of the CP sequences of *Partitiviridae* family members, highlighting the existence of 4 discrete clades of fungal and/or plant partitiviruses distinct from current genera. Methods were the same as those described for RdRp in Figure 1, including the use of program-estimated invariant-proportion value (0.002) and gamma-shape value (4.980). Color and shading are explained in the figure. The putative host of each virus is shown at right: F, fungus; P, plant; Pr, Protozoan; and V, vertebrate.

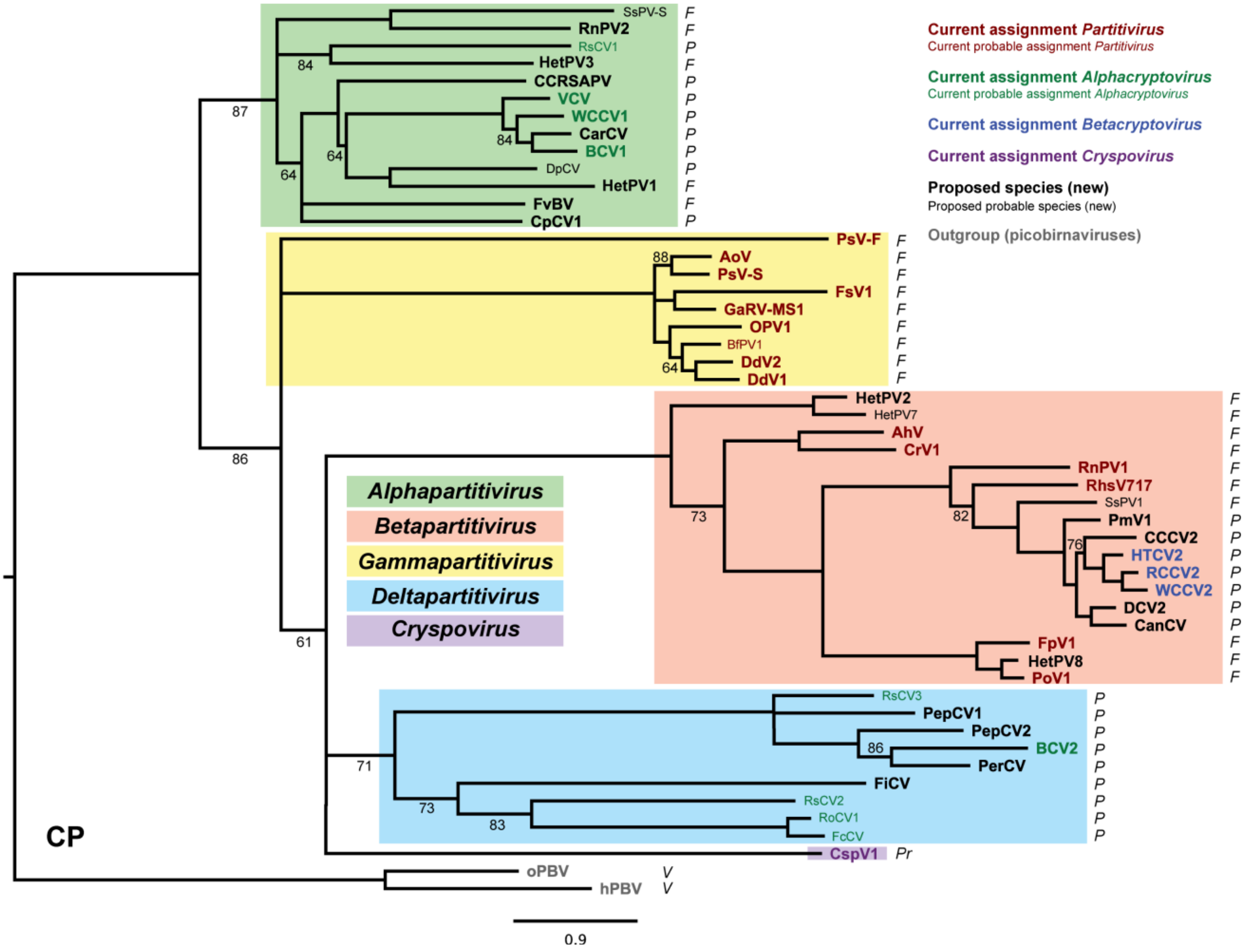

Figure 3. Maximum-likelihood tree of the concatenated RDRP and CP sequences of *Partitiviridae* family members, highlighting the existence of 4 discrete clades of fungal and/or plant partitiviruses distinct from current genera. Methods were the same as those described for RdRp in Figure 1, including the use of program-estimated invariant-proportion value (0.008) and gamma-shape value (1.770). Color and shading are explained in the figure. The putative host of each virus is shown at right: F, fungus; P, plant; Pr, Protozoan; and V, vertebrate.

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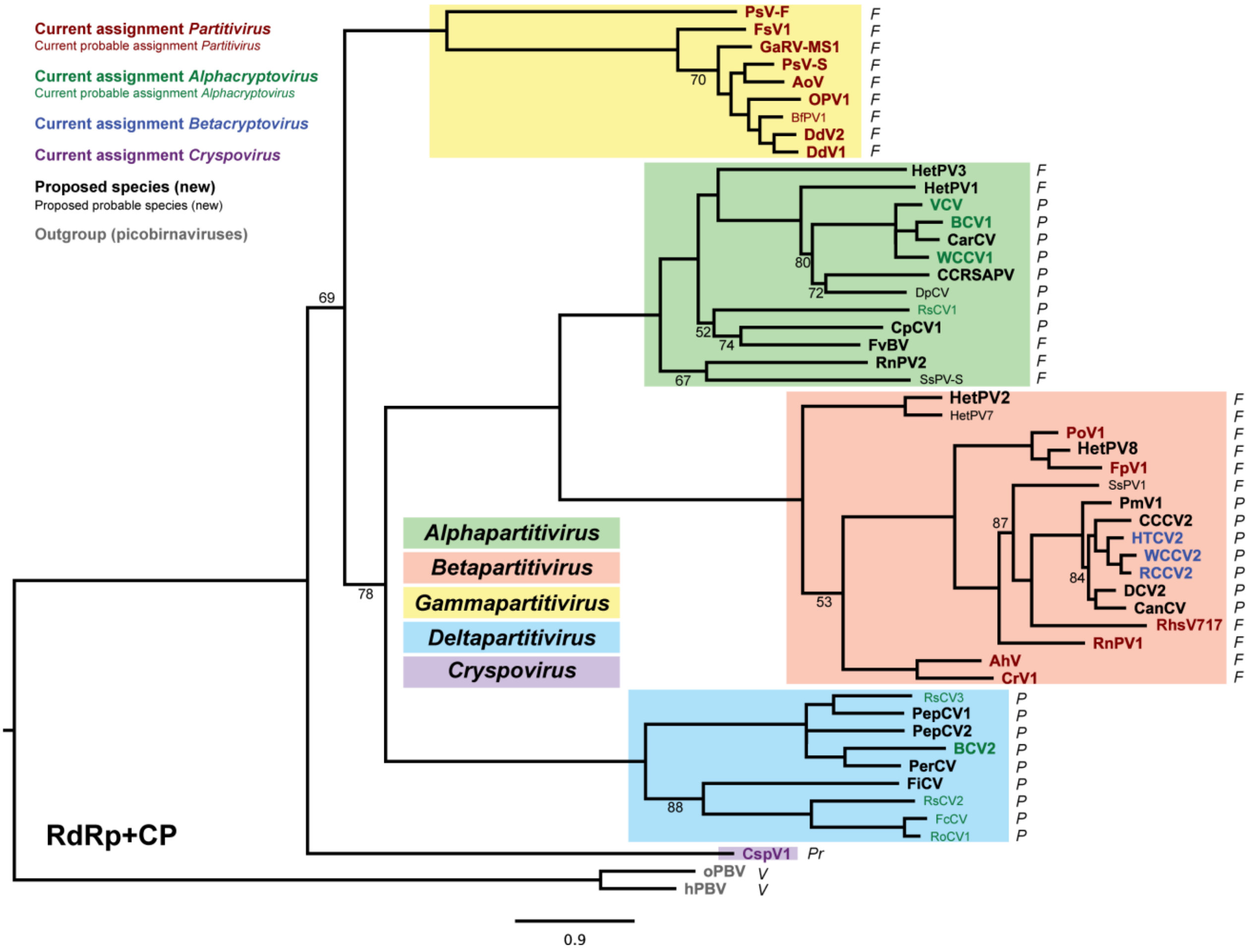

Table 1. Summary of species in proposed genus *Alphapartitivirus*, including GenBank accession numbers for their representative strains

Species	Taxonomic status	Current genus	S1/RdRp	S2/CP
Beet cryptic virus 1	Approved	*Alphacryptovirus*	EU489061	EU489062
Vicia cryptic virus	Approved	*Alphacryptovirus*	AY751737	AY751738
*White clover cryptic virus 1**	Approved	*Alphacryptovirus*	AY705784	AY705785
Helicobasidium mompa partitivirus V70†	Approved	*Partitivirus*	AB025903	na
Carrot cryptic virus	Proposed (new)	None	FJ550604	FJ550605
Cherry chlorotic rusty spot associated partitivirus	Proposed (new)	None	AJ781401	AJ781402
Chondrostereum purpureum cryptic virus 1	Proposed (new)	None	AM999771	AM999772
Flammulina velutipes browning virus	Proposed (new)	None	AB465308	AB465309
Heterobasidion partitivirus 1	Proposed (new)	None	HQ541323	HQ541324
Heterobasidion partitivirus 3	Proposed (new)	None	FJ816271	FJ816272
Rosellinia necatrix partitivirus 2	Proposed (new)	None	AB569997	AB569998

* Type species

† Revised name as discussed in Module 8

Table S1. List of probable species in proposed genus *Alphapartitivirus*, including GenBank accession numbers for their representative strains

Probable species	Taxonomic status	*Current genus*	S1/RdRp	S2/CP
Helicobasidium mompa partitivirus V1-2	Probable	*Partitivirus*	AB110980	na
Raphanus sativus cryptic virus 1	Probable	*Alphacryptovirus*	AY949985	DQ181926‡, DQ181927
Diuris pendunculata cryptic virus	Probable (new)	None	JX156424	JX891460
Sclerotinia sclerotiorum partitivirus S	Probable (new)	None	GQ280377	GQ280378

‡ Segment encoding the larger version of CP

Table 2. Summary of species in proposed genus *Betapartitivirus*, including GenBank accession nos. for their representative strains

Species	Taxonomic status	Current genus	S1/RdRp	S2/CP
*Atkinsonella hypoxylon virus**	Approved	*Partitivirus*	L39125	L39126
Ceratocystis resinifera virus 1	Approved	*Partitivirus*	AY603052	AY603051
Fusarium poae virus 1	Approved	*Partitivirus*	AF047013	AF015924
Heterobasidion partitivirus P†	Approved	*Partitivirus*	AF473549	na
Pleurotus ostreatus virus 1	Approved	*Partitivirus*	AY533038	AY533036
Rhizoctonia solani virus 717	Approved	*Partitivirus*	AF133290	AF133291
Rosellinia necatrix partitivirus 1†	Approved	*Partitivirus*	AB113347	AB113348
Hop trefoil cryptic virus 2	Approved	*Betacryptovirus*	JX971980	JX971981
Red clover cryptic virus 2	Approved	*Betacryptovirus*	JX971984	JX971985
White clover cryptic virus 2	Approved	*Betacryptovirus*	JX971976	JX971977
Cannabis cryptic virus	Proposed (new)	None	JN196536	JN196537
Crimson clover cryptic virus 2	Proposed (new)	None	JX971982	JX971983
Dill cryptic virus 2	Proposed (new)	None	JX971984	JX971985
Heterobasidion partitivirus 2	Proposed (new)	None	HM565953	HM565954
Heterobasidion partitivirus 8	Proposed (new)	None	JX625227	JX625228
Primula malacoides virus 1	Proposed (new)	None	EU195326	EU195327

* Type species

† Revised name as discussed in Module 8

Table S2. List of probable species **in proposed genus *Betapartitivirus*, including GenBank accession nos. for their representative strains**

Probable species	Taxonomic status	*Current genus*	S1/RdRp	S2/CP
Helicobasidium mompa partitivirus V1-1	Probable	*Partitivirus*	AB110979	na
Heterobasidion partitivirus 7†	Probable (new)	None	JN606091	JN606090
Sclerotinia sclerotiorum partitivirus 1	Probable (new)	None	JX297511	JX297510

† Revised name as discussed in Module 8

Table 3. Summary of species in proposed genus *Gammapartitivirus*, including GenBank accession numbers for their representative strains

Species	Taxonomic status	Current genus	S1/RdRp	S2/CP
Aspergillus ochraceous virus	Approved	*Partitivirus*	EU118277	EU118278
Discula destructiva virus 1	Approved	*Partitivirus*	AF316992	AF316993
Discula destructiva virus 2	Approved	*Partitivirus*	AY033436	AY033437
Fusarium solani virus 1	Approved	*Partitivirus*	D55668	D55669
Gremmeniella abietina RNA virus MS1	Approved	*Partitivirus*	AY089993	AY089994
Ophiostoma partitivirus 1	Approved	*Partitivirus*	AM087202	AM087203
Penicillium stoloniferum virus F	Approved	*Partitivirus*	AY738336	AY738337
*Penicillium stoloniferum virus S**	Approved	*Partitivirus*	AY156521	AY156522

* Type species

Table S3. List of probable species in proposed genus *Gammapartitivirus*, including GenBank accession numbers for their representative strains

Probable species	Taxonomic status	*Current genus*	S1/RdRp	S2/CP
Botryotinia fuckeliana partitivirus 1	Probable	*Partitivirus*	AM491609	AM491610

Table 4. Summary of species in proposed genus *Deltapartitivirus*, including GenBank accession numbers for their representative strains

Species	Taxonomic status	Current genus	S1/RdRp	S2/CP
Beet cryptic virus 2	Approved	*Alphacryptovirus*	HM560702	HM560703†, HM560704
Beet cryptic virus 3	Approved	*Alphacryptovirus*	S63913	Na
Fig cryptic virus	Proposed (new)	None	FR687854	FR687855
*Pepper cryptic virus 1**	Proposed (new)	None	JN117276	JN117277
Pepper cryptic virus 2	Proposed (new)	None	JN117278	JN117279

* Type species

Table S4. List of probable species in proposed genus *Deltapartitivirus*, including GenBank accession numbers for their representative strains

Probable species	Taxonomic status	*Current genus*	S1/RdRp	S2/CP
Black raspberry cryptic virus	Probable	*Alphacryptovirus*	EU082132	na
Fragaria chiloensis cryptic virus	Probable	*Alphacryptovirus*	DQ093961	DQ355440†, DQ355439
Pinus sylvestris cryptic virus	Probable	*Alphacryptovirus*	AY973825	na
Pyrus pyrofolia cryptic virus	Probable	*Alphacryptovirus*	AB012616	na
Raphanus sativus cryptic virus 2	Probable	*Alphacryptovirus*	DQ218036	DQ218037†, DQ218038
Raphanus sativus cryptic virus 3	Probable	*Alphacryptovirus*	FJ461349	FJ461350
Rose cryptic virus 1	Probable	*Alphacryptovirus*	EU413666	EU413667†, EU413668
Persimmon cryptic virus	Probable (new)	None	HE805113	HE805114

† Segment encoding the larger version of CP

Table 5. Genome-segment and protein lengths of representative strains of species in proposed genus *Alphapartitivirus*

Species or probable species	S1	S2	S1+S2	RdRp	CP	RdRp+CP
Beet cryptic virus 1	2008	1783	3791	616	489	1105
Vicia cryptic virus	1950	1732	3682	616	487	1103
White clover cryptic virus 1	1955	1708	3663	616	487	1103
Helicobasidium mompa partitivirus V70†	1928	na	na	598	na	na
Carrot cryptic virus	1971	1776	3747	616	490	1106
Cherry chlorotic rusty spot associated partitivirus	2021	1841	3862	621	504	1125
Chondrostereum purpureum cryptic virus 1	1920	1757	3677	587	480	1067
Flammulina velutipes browning virus	1915	1730	3645	580	463	1043
Heterobasidion partitivirus 1	2027	1866	3893	621	510	1131
Heterobasidion partitivirus 3	1885	1826	3711	585	521	1106
Rosellinia necatrix partitivirus 2	1985	1828	3813	603	483	1086
Helicobasidium mompa partitivirus V1-2	1776‡	na	na	538	na	na
Raphanus sativus cryptic virus 1	1866	1791*	3657	573	505*	1078
Diuris pendunculata cryptic virus	2010	1806	3816	621	496	1117
Sclerotinia sclerotiorum partitivirus S	1874	1852	3726	580	508	1088
mean	**1939**	**1792**	**3745**	**598**	**494**	**1097**
SD	**67**	**48**	**79**	**23**	**15**	**23**
range	**1776-2027**	**1708-1866**	**3645-3893**	**538-621**	**463-521**	**1043-1131**

* Larger of the 2 apparent CP-encoding segments and encoded CPs are shown. Values for the smaller ones are: Raphanus sativus cryptic virus 1, 1778/502.

† Revised name as discussed in Module 8.

‡ Values for probable species are included in means, etc.

Table 6. Genome-segment and protein lengths of representative strains of species in proposed genus *Betapartitivirus*

Species or probable species	S1	S2	S1+S2	RdRp	CP	RdRp+CP
Atkinsonella hypoxylon virus	2180	2135	4315	665	662	1327
Ceratocystis resinifera virus 1	2305	2207	4512	663	661	1324
Fusarium poae virus 1	2203	2185	4388	673	637	1310
Heterobasidion partitivirus *P†*	2325	na	na	734	na	na
Pleurotus ostreatus virus 1	2296	2223	4519	706	636	1342
Rhizoctonia solani virus 717	2363	2206	4569	730	683	1413
Rosellinia necatrix partitivirus 1†	2299	2279	4578	709	686	1395
Hop trefoil cryptic virus 2	2431	2349	4780	746	673	1419
Red clover cryptic virus 2	2430	2353	4783	745	673	1418
White clover cryptic virus 2	2435	2348	4783	746	673	1419
Cannabis cryptic virus	2420	2290	4710	745	672	1417
Crimson clover cryptic virus 2	2444	2354	4798	746	674	1420
Dill cryptic virus 2	2430	2354	4784	745	673	1418
Heterobasidion partitivirus *2*	2290	2238	4528	722	659	1381
Heterobasidion partitivirus *8*	2281	2235	4516	704	638	1342
Primula malacoides virus 1	2390	2344	4734	723	673	1396
Helicobasidium mompa partitivirus V1-1	2247*	na	na	706	na	na
Heterobasidion partitivirus 7	2297	2231	4528	724	654	1378
Sclerotinia sclerotiorum partitivirus 1	2334	2292	4626	704	678	1382
Mean	**2337**	**2272**	**4615**	**718**	**665**	**1382**
SD	**79**	**68**	**145**	**27**	**15**	**38**
Range	**2180-2444**	**2135-2354**	**4315-4798**	**663-746**	**636-686**	**1310-1420**

* Values of probable species are included in means, etc.

† Revised name as discussed in Module 8.

Table 7. Genome-segment and protein lengths of representative strains of species in proposed genus *Gammapartitivirus*

Species or probable species	S1	S2	S1+S2	RdRp	CP	RdRp+CP
Aspergillus ochraceous virus	1754	1555	3309	539	433	972
Discula destructiva virus 1	1787	1585	3372	539	436	975
Discula destructiva virus 2	1781	1611	3392	539	442	981
Fusarium solani virus 1	1645	1445	3090	519	413	932
Gremmeniella abietina RNA virus MS1	1782	1586	3368	539	443	982
Ophiostoma partitivirus 1	1744	1567	3311	539	430	969
Penicillium stoloniferum virus F	1677	1500	3177	538	420	958
Penicillium stoloniferum virus S	1754	1582	3336	539	434	973
Botryotinia fuckeliana partitivirus 1	1793*	1566	3359	540	436	976
Mean	**1746**	**1555**	**3302**	**537**	**432**	**969**
SD	**49**	**48**	**96**	**6**	**9**	**15**
Range	**1645-1793**	**1445-1611**	**3090-3392**	**519-540**	**413-443**	**932-982**

* Values for probable species are included in means, etc.

Table 8. Genome-segment and protein lengths of representative strains of species in proposed genus *Deltapartitivirus*

Species or probable species	S1	S2	S1+S2	RdRp	CP	RdRp+CP
Beet cryptic virus 2	1598	1575*	3173	475	426*	901
Beet cryptic virus 3	1607	na	na	478	na	na
Fig cryptic virus	1696	1415	3111	472	337	809
Pepper cryptic virus 1	1563	1512	3075	479	412	891
Pepper cryptic virus 2	1609	1525*	3134	478	430	908
Black raspberry cryptic virus	partial	na	na	partial	na	na
Fragaria chiloensis cryptic virus	1734†	1479*	3213	479	348*	827
Pinus sylvestris cryptic virus	partial	na	na	partial	na	na
Pyrus pyrofolia cryptic virus	1592	na	na	477	na	Na
Raphanus sativus cryptic virus 2	1717	1521*	3238	477	347*	824
Raphanus sativus cryptic virus 3	1609	1581	3190	481	374	855
Rose cryptic virus 1	1749	1485*	3234	479	348*	827
Persimmon cryptic virus	1577	1491	3068	477	415	892
mean	**1646**	**1509**	**3160**	**478**	**382**	**859**
SD	**66**	**48**	**62**	**2**	**36**	**37**
range	**1563-1734**	**1415-1581**	**3068-3238**	**472-481**	**337-430**	**809-908**

* Larger of the 2 apparent CP-encoding segments and encoded CPs are shown. Values for the smaller ones are: *Beet cryptic virus 2*, 1522/393; Fragaria chiloensis cryptic virus, 1465/346; Raphanus sativus cryptic virus 2, 1485/347; and Rose cryptic virus 1, 1446/346.

† Values for probable species are included in means, etc.

Table 9. Ranges of genome-segment and protein lengths within proposed genera of fungal and plant viruses in family *Partitiviridae*

Genus*	S1	S2	S1+S2	RdRp	CP	RdRp+CP
Betapartitivirus	**2180-2444†**	**2135-2354**	**4315-4798**	**663-746**	**636-686**	**1310-1420**
Alphapartitivirus	**1776-2027**	**1708-1866**	**3645-3893**	**538-621**	**463-521**	**1043-1131**
Gammapartitivirus	1645-1793	1445-1611	3090-3392	**519-540**	413-443	**932-982**
Deltapartitivirus	1563-1734	1415-1581	3068-3238	**472-481**	337-430	**809-908**

* Genera listed in decreasing order of RdRp size range

† Bold lettering indicates that the range overlaps only minimally, if at all, with that of another genus.

Tables 10–21. These tables contain pairwise identity scores from global alignments of pairs of sequences from each of the proposed genera. The scores were generated using EMBOSS 6.3.1: needelall as implemented at mobile.pasteur.fr/ with default settings (Blosum62 matrix) plus gap opening extension penalties of 10 and 0.5. The highest and lowest scores in each table are highlighted.

Table 10. Pairwise identity scores within genus *Alphapartitivirus* (new): RdRp

Viruses	BCV1	VCV	WCCV1	HmPV-V70	CarCV	CCRSAPV	CpCV1	FvBV	HetPV1	HetPV3	RnPV2	RsCV1	DpCV	SsPV-S
BCV1	100%													
VCV	81%	100%												
WCCV1	83%	**84.6%**	100%											
HmPV-V70	28%	29%	29%	100%										
CarCV	85%	82%	83%	29%	100%									
CCRSAPV	57%	59%	59%	27%	58%	100%								
CpCV1	34%	35%	37%	34%	35%	34%	100%							
FvBV	34%	35%	36%	39%	36%	34%	46%	100%						
HetPV1	52%	52%	52%	29%	52%	51%	34%	34%	100%					
HetPV3	32%	32%	33%	50%	33%	31%	34%	36%	31%	100%				
RnPV2	27%	29%	29%	29%	29%	31%	33%	31%	27%	30%	100%			
RsCV1	31%	29%	31%	33%	31%	28%	35%	37%	28%	32%	32%	100%		
DpCV	60%	61%	61%	27%	61%	61%	34%	33%	53%	32%	30%	29%	100%	
SsPV-S	29%	28%	28%	29%	28%	28%	33%	33%	**26.1%**	28%	33%	30%	27%	100%

Table 11. Pairwise identity scores within genus *Alphapartitivirus* (new): CP

Viruses	BCV1	VCV	WCCV1	CarCV	CCRSAPV	CpCV1	FvBV	HetPV1	HetPV3	RnPV2	RsCV1	DpCV	SsPV-S
BCV1	100%												
VCV	56%	100%											
WCCV1	58%	56%	100%										
CarCV	**62.2%**	58%	58%	100%									
CCRSAPV	25%	25%	26%	26%	100%								
CpCV1	25%	24%	22%	25%	22%	100%							
FvBV	24%	21%	24%	21%	22%	25%	100%						
HetPV1	25%	23%	26%	25%	23%	21%	22%	100%					
HetPV3	21%	23%	22%	21%	22%	22%	20%	22%	100%				
RnPV2	19%	20%	20%	**17.9%**	19%	23%	19%	19%	22%	100%			
RsCV1	22%	26%	24%	23%	20%	21%	20%	21%	21%	20%	100%		
DpCV	27%	26%	24%	26%	22%	25%	24%	29%	20%	19%	23%	100%	
SsPV-S	20%	19%	19%	20%	20%	21%	18%	20%	20%	24%	22%	20%	100%

Table 12. Pairwise identity scores within genus *Alphapartitivirus* (new): RdRp+CP

Viruses	BCV1	VCV	WCCV1	CarCV	CCRSAPV	CpCV1	FvBV	HetPV1	HetPV3	RnPV2	RsCV1	DpCV	SsPV-S
BCV1	100%												
VCV	70%	100%											
WCCV1	72%	72%	100%										
CarCV	**74.9%**	71%	72%	100%									
CCRSAPV	42%	43%	43%	43%	100%								
CpCV1	30%	30%	30%	30%	29%	100%							
FvBV	30%	28%	30%	29%	28%	37%	100%						
HetPV1	39%	38%	40%	39%	38%	28%	29%	100%					
HetPV3	27%	28%	28%	27%	26%	28%	28%	27%	100%				
RnPV2	24%	26%	25%	24%	26%	28%	25%	23%	27%	100%			
RsCV1	27%	28%	28%	28%	24%	28%	29%	25%	26%	26%	100%		
DpCV	45%	44%	44%	45%	43%	30%	29%	42%	27%	25%	26%	100%	
SsPV-S	25%	24%	24%	25%	25%	28%	26%	**23.3%**	25%	29%	26%	25%	100%

Table 13. Pairwise identity scores within genus *Betapartitivirus* (new): RdRp

Viruses	AhV	CrV1	FpV1	HetPV-P	PoV1	RhsV717	RnPV1	HTCV2	RCCV2	WCCV2	CanCV	CCCV2	DCV2	HetPV2	HetPV8	PmV1	HetPV7	SsPV1
AhV	100%																	
CrV1	55%	100%																
FpV1	34%	33%	100%															
HetPV-P	33%	35%	29%	100%														
PoV1	35%	34%	58%	29%	100%													
RhsV717	36%	33%	44%	31%	43%	100%												
RnPV1	34%	33%	48%	31%	53%	45%	100%											
HTCV2	32%	31%	43%	30%	46%	44%	48%	100%										
RCCV2	32%	31%	42%	30%	46%	43%	49%	84%	100%									
WCCV2	31%	31%	43%	30%	44%	43%	48%	82%	**90.1%**	100%								
CanCV	32%	29%	42%	30%	45%	42%	48%	74%	74%	74%	100%							
CCCV2	31%	30%	43%	30%	44%	44%	48%	77%	77%	76%	73%	100%						
DCV2	32%	31%	43%	30%	48%	45%	48%	79%	78%	77%	76%	77%	100%					
HetPV2	35%	33%	30%	57%	30%	32%	31%	31%	32%	31%	29%	32%	31%	100%				
HetPV8	34%	34%	66%	30%	58%	45%	47%	45%	43%	44%	44%	42%	45%	30%	100%			
PmV1	33%	30%	45%	29%	46%	44%	48%	74%	75%	74%	71%	73%	75%	31%	45%	100%		
HetPV7	34%	34%	31%	57%	33%	34%	32%	30%	31%	30%	**29.0%**	31%	30%	67%	31%	31%	100%	
SsPV1	33%	30%	45%	28%	47%	42%	49%	41%	41%	40%	39%	40%	39%	30%	45%	40%	30%	100%

Table 14. Pairwise identity scores within genus *Betapartitivirus* (new): CP

Viruses	AhV	CrV1	FpV1	PoV1	RhsV717	RnPV1	HTCV2	RCCV2	WCCV2	CanCV	CCCV2	DCV2	HetPV2	HetPV8	PmV1	HetPV7	SsPV1
AhV	100%																
CrV1	40%	100%															
FpV1	22%	21%	100%														
PoV1	20%	24%	58%	100%													
RhsV717	18%	18%	22%	21%	100%												
RnPV1	18%	**16.8%**	20%	21%	32%	100%											
HTCV2	20%	22%	22%	24%	36%	30%	100%										
RCCV2	19%	20%	23%	24%	34%	29%	73%	100%									
WCCV2	19%	21%	24%	23%	33%	27%	68%	77%	100%								
CanCV	20%	19%	23%	22%	36%	29%	61%	59%	60%	100%							
CCCV2	19%	21%	22%	21%	33%	28%	61%	59%	57%	57%	100%						
DCV2	21%	19%	23%	25%	36%	29%	64%	60%	59%	70%	59%	100%					
HetPV2	25%	23%	20%	20%	20%	20%	19%	19%	22%	21%	18%	19%	100%				
HetPV8	22%	24%	60%	**78.4%**	23%	21%	22%	23%	22%	23%	22%	22%	22%	100%			
PmV1	20%	20%	23%	22%	35%	31%	61%	56%	57%	60%	58%	62%	21%	23%	100%		
HetPV7	26%	24%	19%	21%	19%	18%	19%	19%	20%	21%	18%	21%	60%	21%	19%	100%	
SsPV1	18%	18%	23%	23%	34%	30%	43%	41%	43%	42%	39%	42%	21%	25%	44%	19%	100%

Table 15. Pairwise identity scores within genus *Betapartitivirus* (new): RDRP+CP

Viruses	AhV	CrV1	FpV1	PoV1	RhsV717	RnPV1	HTCV2	RCCV2	WCCV2	CanCV	CCCV2	DCV2	HetPV2	HetPV8	PmV1	HetPV7	SsPV1
AhV	100%																
CrV1	48%	100%															
FpV1	29%	27%	100%														
PoV1	28%	29%	58%	100%													
RhsV717	27%	26%	33%	32%	100%												
RnPV1	26%	25%	34%	37%	39%	100%											
HTCV2	26%	27%	33%	35%	41%	39%	100%										
RCCV2	26%	26%	33%	35%	39%	39%	79%	100%									
WCCV2	25%	26%	34%	34%	38%	38%	76%	**83.9%**	100%								
CanCV	26%	25%	33%	34%	39%	39%	68%	67%	67%	100%							
CCCV2	25%	26%	32%	33%	39%	38%	69%	68%	67%	66%	100%						
DCV2	27%	25%	34%	37%	41%	39%	72%	70%	68%	73%	68%	100%					
HetPV2	30%	28%	25%	25%	26%	26%	25%	26%	27%	26%	25%	25%	100%				
HetPV8	28%	29%	63%	68%	35%	34%	34%	33%	33%	34%	32%	34%	26%	100%			
PmV1	26%	25%	34%	34%	39%	39%	68%	66%	66%	66%	66%	69%	26%	34%	100%		
HetPV7	31%	29%	25%	27%	26%	26%	25%	25%	25%	25%	25%	26%	63%	26%	26%	100%	
SsPV1	26%	**23.6%**	33%	35%	38%	40%	42%	41%	41%	41%	40%	40%	25%	34%	42%	25%	100%

Table 16. Pairwise identity scores within genus *Gammapartitivirus* (new): RdRp

Viruses	AoV	DdV1	DdV2	FsV1	GaRV-MS1	OPV1	PsV-F	PsV-S	BfPV1
AoV	100%								
DdV1	63%	100%							
DdV2	64%	**87.6%**	100%						
FsV1	58%	56%	57%	100%					
GaRV-MS1	67%	66%	65%	60%	100%				
OPV1	64%	72%	71%	55%	65%	100%			
PsV-F	26%	29%	28%	27%	28%	**24.6%**	100%		
PsV-S	72%	70%	68%	58%	72%	67%	28%	100%	
BfPV1	66%	82%	82%	57%	70%	74%	27%	70%	100%

Table 17. Pairwise identity scores within genus *Gammapartitivirus* (new): CP

Viruses	AoV	DdV1	DdV2	FsV1	GaRV-MS1	OPV1	PsV-F	PsV-S	BfPV1
AoV	100%								
DdV1	50%	100%							
DdV2	56%	63%	100%						
FsV1	35%	35%	35%	100%					
GaRV-MS1	56%	52%	54%	38%	100%				
OPV1	51%	51%	51%	34%	50%	100%			
PsV-F	18%	**16.3%**	20%	18%	17%	19%	100%		
PsV-S	**63.6%**	53%	55%	36%	56%	51%	19%	100%	
BfPV1	57%	62%	62%	35%	56%	53%	18%	54%	100%

Table 18. Pairwise identity scores within genus *Gammapartitivirus* (new): RdRp+CP

Viruses	AoV	DdV1	DdV2	FsV1	GaRV-MS1	OPV1	PsV-F	PsV-S	BfPV1
AoV	100%								
DdV1	57%	100%							
DdV2	60%	**76.7%**	100%						
FsV1	48%	46%	47%	100%					
GaRV-MS1	62%	60%	60%	50%	100%				
OPV1	58%	62%	62%	45%	58%	100%			
PsV-F	23%	24%	24%	24%	24%	**22.3%**	100%		
PsV-S	68%	62%	62%	48%	65%	60%	24%	100%	
BfPV1	62%	73%	73%	47%	64%	64%	23%	63%	100%

Table 19. Pairwise identity scores within genus *Deltapartitivirus* (new): RdRp

Viruses	BCV2	BCV3	FiCV	PepCV1	PepCV2	FcCV	RsCV2	RsCV3	RoCV1	PerCV
BCV2	100%									
BCV3	54%	100%								
FiCV	34%	39%	100%							
PepCV1	55%	53%	35%	100%						
PepCV2	59%	58%	36%	56%	100%					
FcCV	33%	33%	36%	**32.9%**	36%	100%				
RsCV2	35%	35%	38%	33%	34%	60%	100%			
RsCV3	56%	55%	35%	64%	57%	37%	37%	100%		
RoCV1	34%	33%	36%	33%	35%	**87.7%**	60%	37%	100%	
PerCV	61%	57%	35%	59%	65%	35%	36%	61%	35%	100%

Table 20. Pairwise identity scores within genus *Deltapartitivirus* (new): CP

Viruses	BCV2	FiCV	PepCV1	PepCV2	FcCV	RsCV2	RsCV3	RoCV1	PerCV
BCV2	100%								
FiCV	15%	100%							
PepCV1	31%	15%	100%						
PepCV2	28%	10%	32%	100%					
FcCV	15%	12%	16%	13%	100%				
RsCV2	11%	13%	12%	15%	22%	100%			
RsCV3	25%	15%	32%	28%	18%	13%	100%		
RoCV1	**3.4%**	11%	14%	15%	**69.5%**	24%	17%	100%	
PerCV	37%	19%	32%	37%	17%	17%	31%	17%	100%

Table 21. Pairwise identity scores within genus *Deltapartitivirus* (new): RdRp+CP

Viruses	BCV2	FiCV	PepCV1	PepCV2	FcCV	RsCV2	RsCV3	RoCV1	PerCV
BCV2	100%								
FiCV	26%	100%							
PepCV1	44%	26%	100%						
PepCV2	44%	26%	45%	100%					
FcCV	25%	26%	26%	26%	100%				
RsCV2	25%	27%	**23.3%**	26%	43%	100%			
RsCV3	41%	26%	50%	44%	28%	27%	100%		
RoCV1	23%	25%	25%	26%	**80.0%**	44%	28%	100%	
PerCV	49%	28%	46%	51%	27%	27%	47%	27%	100%

Table 22. Ranges of pairwise identity scores between members within proposed genera of fungal and plant viruses in family *Partitiviridae*

Genus*	RdRp	CP	RdRp+CP
Alphapartitivirus	84.6–26.1%	62.2–17.9%	74.9–23.3%
Betapartitivirus	90.1–29.0%	78.4–16.8%	83.9–23.6%
Gammapartitivirus	87.6–24.6%	63.6–16.3%	76.7–22.3%
Deltapartitivirus	87.7–32.9%	69.5–3.4%	80.0–23.3%

Table 23. Maximum pairwise identity scores between members of proposed genera of fungal and plant viruses in family *Partitiviridae*: RdRp

Genus	*Alphapartitivirus*	*Betapartitivirus*	*Gammapartitivirus*	*Deltapartitivirus*
Alphapartitivirus	(84.6–26.1%)*			
Betapartitivirus	26.4%	(90.1–29.0%)*		
Gammapartitivirus	23.3%	20.9%	(87.6–24.6%)*	
Deltapartitivirus	21.7%	18.6%	23.2%	(87.7–32.9%)*

*Within-genus ranges from Table 22

Table 24. Maximum pairwise identity scores between members of proposed genera of fungal and plant viruses in family *Partitiviridae*: CP

Genus	*Alphapartitivirus*	*Betapartitivirus*	*Gammapartitivirus*	*Deltapartitivirus*
Alphapartitivirus	(62.2–17.9%)*			
Betapartitivirus	19.8%	(78.4–16.8%)*		
Gammapartitivirus	20.0%	16.0%	(63.6–16.3%)*	
Deltapartitivirus	17.9%	16.9%	18.5%	(69.5–3.4%)*

*Within-genus ranges from Table 22

Table 25. Maximum pairwise identity scores between members of proposed genera of fungal and plant viruses in family *Partitiviridae*: RdRp+CP

Genus	*Alphapartitivirus*	*Betapartitivirus*	*Gammapartitivirus*	*Deltapartitivirus*
Alphapartitivirus	(74.9–23.3%)*			
Betapartitivirus	22.5%	(83.9–23.6%)*		
Gammapartitivirus	21.9%	18.6%	(76.7–22.3%)*	
Deltapartitivirus	19.5%	17.6%	20.1%	(80.0–23.3%)*

*Within-genus ranges from Table 22

Table 26. Approved and probable species moved to genus "Unassigned" due to lack of reported sequences

Species	Species status	Current genus	New genus
Alfalfa cryptic virus 1	approved	*Alphacryptovirus*	Unassigned
Carnation cryptic virus 1	approved	*Alphacryptovirus*	Unassigned
Carrot temperate virus 1	approved	*Alphacryptovirus*	Unassigned
Carrot temperate virus 4	approved	*Alphacryptovirus*	Unassigned
Hop trefoil cryptic virus 1	approved	*Alphacryptovirus*	Unassigned
Hop trefoil cryptic virus 3	approved	*Alphacryptovirus*	Unassigned
Radish yellow edge virus	approved	*Alphacryptovirus*	Unassigned
Ryegrass cryptic virus	approved	*Alphacryptovirus*	Unassigned
Spinach temperate virus	approved	*Alphacryptovirus*	Unassigned
White clover cryptic virus 3	approved	*Alphacryptovirus*	Unassigned
Carrot temperate virus 2	approved	*Betacryptovirus*	Unassigned
Agaricus bisporus virus 4	approved	*Partitivirus*	Unassigned
Gaeumannomyces graminis virus 019/6-A	approved	*Partitivirus*	Unassigned
Gaeumannomyces graminis virus T1-A	approved	*Partitivirus*	Unassigned
Cucumber cryptic virus	probable	*Alphacryptovirus*	Unassigned
Alfalfa cryptic virus 2	probable	*Betacryptovirus*	Unassigned