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:	***2016.009a-dP***	(to be completed by ICTV officers)

Short title: Five new species in the family *Closteroviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☐ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

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

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	*Closteroviridae*

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: July 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 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	***2016.009aP***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Closterovirus***
Subfamily:	***Unassigned***
Family:	***Closteroviridae***
Order:	***Unassigned***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Rose leaf rosette-associated virus	RLRaV-CWR.1	Complete genomic RNA (KJ748003)
Tobacco virus 1	TV1-AnHui	Complete genomic RNA (KT203917)

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

Species of the family *Closteroviridae* have filamentous particles (650-2,200nm in length) and monopartite or bipartite single-stranded RNA genomes with size varying from 12,000 to nearly 19,000 nucleotides. Closterovirids are divided into four genera: *Closterovirus* (monopartite genome), *Ampelovirus* (monopartite genome), *Velarivirus* (monopartite genome) and *Crinivirus* (bipartite or tripartite genome). Ampeloviruses are transmitted by pseudococcid mealybugs and soft scale insects, closteroviruses are transmitted by aphids, and criniviruses are transmitted by whiteflies. No vectors are known for velariviruses. Species demarcation criteria used for all genera in the family *Closteroviridae* are particle size, size of the coat protein and coat protein minor, genome structure and organization (number and relative location of the ORFs), vector species and specificity, cytopathological features, host range, as well as differences in amino acid sequence of relevant gene products, i.e. RNA-dependent RNA polymerase, coat protein (CP), heat shock protein 70 homolog (HSP70h), exceeding 25%.

Rose leaf rosette-associated virus (RLRaV)

Deep sequencing of siRNAs from leaves of wild roses (*Rosa multiflora* Thub.) with leaf rosette symptoms led to the reconstruction of the complete genome of rose leaf rosette-associated virus (RLRaV) (He et al., 2015). The 5' and 3' ends of the RLRaV genome were obtained using RACE-PCR. The single-stranded RNA genome of RLRaV isolate CWR.1 consists of 17,653 nt (GenBank accession number KJ748003) and shows a similar organization than members of the genus *Closterovirus* with a 138-nt-long 5' untranslated region (UTR), a 185 nt long 3' UTR, and 13 putative open reading frames (ORF) (He et al. 2015) (Fig. 1). ORF1a (nt 139-8,417) encodes

a replication-associated protein with hallmark domains for two papain-like proteases, a methyltransferase, and a helicase. ORF1b (nt 8,484-9,850) has conserved motifs of an RNA-dependent RNA polymerase (RdRp), which is putatively expressed as a fusion protein with a +1 ribosomal frameshift. Downstream of the polymerase are smallers ORFs coding for p25 (nt 9,894-10,604) with transmembrane domains, and a quintuple gene block coding for p7a (nt 10,622-10,819, a hydrophobic protein), heat shock protein 70 homolog (HSP70h, nt 10,824-12,538), coat protein homolog (CPh, nt 12,614-14,058), minor coat protein (CPm, nt 14,140-14,799) and major coat protein (CP, nt 14,904-15,518), followed by five ORFs coding for p7b (nt 15,521-15,684), p19 (nt 15,715-16,205) with a putative zinc-finger domain, p13 (nt 16,251-16,613), p17 (nt 16,740-17,131) with characteristics of a RNA silencing suppressor and p12 (nt 17,189-17,189). ORFs 9-13 code for proteins of unknown function although similarities with prokaryote proteins are identified (He et al., 2015). Amino acid identity with *Beet yellows virus,* the type member of the genus *Closterovirus*, ranges from 23% in the CP to 54% in the RdRp. Phylogenetic analyses confirm the clustering of RLRaV with members of the genus *Closterovirus* (Fig. 2). Diagnostic primers were designed and RLRaV was found in a few asymptomatic wild roses and in several wild roses showing leaf rosette symptoms (He et al. 2015). No information is available on the vector of RLRaV. In considering the demarcation criteria for species in the family *Closteroviridae*, RLRaV complies with a threshold of 75% amino acid identity for the CP (19.6-51.3%), RdRp (53.8-63.2% identity) and HSP70h (36.7-52.1% identity). Therefore, RLRaV-CWR.1 is proposed as a representative isolate of a new species in the genus *Closterovirus*.

Tobacco virus 1 (TV1)

Deep sequencing of small RNAs from leaves of tobacco (*Nicotiana tabacum)* cultivar Yunyan 87 with foliar mosaic and yellowing symptoms led to the identification of viral nucleotide sequences with distant similarities to members of the genus *Closterovirus* (Wang et al., 2016). RT-PCR and Sanger sequencing were performed to join the contigs. The 5' and 3' ends of the viral genome were obtained by RACE-PCR and Sanger sequencing. The complete genome of tobacco virus 1 (TV1) consists of 15,395 nt (GenBank accession number KT203917) and shows a similar organization than members of the genus *Closterovirus* with a 193-nt-long 5' untranslated region (UTR), a 356 nt long 3' UTR, and nine putative open reading frames (ORF) (Wang et al., 2016) (Fig. 1). ORF1a (nt 194-7,609) and ORF1b (nt 7,581-8,987) code for replication-associated proteins. ORF1a contains conserved domains of papain-like leader protease, methytransferase and helicase. ORF1b encodes a RNA-dependent RNA polymerase that is expressed via a +1 ribosomal frameshift. The quintuple gene block comprises ORFs 2-6, coding for p7 (a hydrophobic protein with a transmembrane domain, nt 9,010-9,207), p67 (heat shock protein 70 homolog, nt 9,211-11,028), p62 (CP homolog, nt 11,029-12,672), p24 (minor coat protein, nt 12,635-13,285), and p23 (major coat protein, nt 13,336-13,962). ORF7 codes for p19 (a putative systemic transport protein, nt 12,971-14,489) and ORF8 codes for p21 (a putative RNA silencing suppressor, nt 14,486-15,040). Amino acid identity with *Beet yellows virus*, the type member of the genus *Closterovirus*, ranges from 24.5% in the CP to 56.2% in the RdRp. Phylogenetic analyses confirm the clustering of TV1 with members of the genus *Closterovirus* (Fig. 2). No diagnostic primers were designed and no information is available on the vector of TV1. In considering the demarcation criteria for species in the family *Closteroviridae*, TV1 complies with a threshold of 75% amino acid identity for the CP (19.6-48.8%), RdRp (56.2-63.5% identity with the exception of 83.5% with Mint virus 1 – MV-1, AY792620) and HSP70h (34.8-65.7% identity). Therefore, we propose creation of a new species in the genus *Closterovirus* typified by TV1-AnHui.

MODULE 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	***2016.009bP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Crinivirus***
Subfamily:	***Unassigned***
Family:	***Closteroviridae***
Order:	***Unassigned***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Tetterwort vein chlorosis virus	TwVCV-Yesan	Complete RNA1 (KR002686) Complete RNA2 (KR002687)

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

Tetterwort vein chlorosis virus (TwVCV)

Deep sequencing of a total RNA library from tetterwort (*Chelidonium majus*) showing foliar vein chlorosis and distortion symptoms revealed viral sequences that were homologous but distinct from members of the genus *Crinivirus* with a bipartite RNA genome after contig assembly (Zhao et al., 2015). RT-PCR was used to re-amplify the complete viral genome sequences and analyze them by Sanger sequencing. The 3' end of the bipartite genome was determined by RT-PCR and sequencing after the addition of a poly(A) tail to purified total RNA. The bipartite single-stranded RNA genome of tetterwort vein chlorosis virus (TwVCV) isolate Yesan consists of a 8,467-nt-long RNA1 (GenBank accession number KR002686) and a 8,113-nt-long RNA2 (GenBank Accession number KR002687), and shows a similar organization than some members of the genus *Crinivirus* (Fig. 1). TwVCV RNA1 contains four open reading frames (ORFs) designated as ORF1a (nt 67-6,045), ORF1b (nt 6,044-7,561), P6a (ORF2, nt 7,577-7,738), and P19 (ORF3, nt 7,741-8,232). ORF1a codes for a papain like protease, methytransferase, and helicase domains with four transmembrane helices. ORF1b codes for an RNA-dependent RNA polymerase (RdRp) that is expressed through a +1 ribosomal frameshift. P6a contains a transmembrane helix and P19 has no significant sequence homology. TwVCV RNA2 contains nine ORFs coding for p9a (nt 125-358), p5 (nt 526-660), the heat shock protein 70 homolog (HSP70h, nt 1,331-3,004), p6b (nt 3,005-3,169), p60 (nt 3,163-4,716), p9b (nt 4,698-4,944), p23 (major coat protein, nt 5,055-5,780), p54 (minor coat protein, nt 5,780-7,204) and p27 (nt 7,211-7,900). Proteins p9a and p5 (a putative transmembrane protein) are unique to TwVCV and have no equivalent in other criniviruses. The 5' UTR of RNA1 and RNA2 are 66 nt and 124 nt long, respectively, and their 3' UTR are 213

nt and 235 nt long, respectively. Amino acid identity with *Lettuce infectious yellows virus*, the type member of the genus *Crinivirus*, ranged from 26.1% in the CP to 53.35% in the RdRp. Phylogenetic analyses confirm the clustering of TwVCV with members of the genus *Crinivirus* (Fig. 2). No diagnostic primers were designed and no information is available on the vector of TVCV. In considering the demarcation criteria for species in the family *Closteroviridae*, TVCV complies with a threshold of 75% amino acid identity for the CP (16.5-64.7%), RdRp (8.4-74.3% identity with the exception of 76.6% with Bean yellow disorder virus – BYDV, EU191904) and HSP70h (23.3-71.4% identity with the exception of 79.0% with Lettuce chlorosis virus - LCV, FJ380118). Therefore, TwVCV-Yesan is proposed as a member of a new species in the genus *Crinivirus*.

MODULE 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	***2016.009cP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Velarivirus***
Subfamily:	***Unassigned***
Family:	***Closteroviridae***
Order:	***Unassigned***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Areca palm velarivirus 1	ArPV1-HN	Complete genomic RNA (KR349464)

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

Areca palm velarivirus 1 (ArPV1)

Deep sequencing of a small RNA library from areca palm (*Areca catechu* L.) showing foliar yellowing symptoms revealed 21 contigs of viral sequences that were homologous but distinct from members of the genus *Velarivirus* (Yu et al., 2015). RT-PCR and Sanger sequencing were performed to join the contigs. The 5' and 3' ends of the viral genome were obtained by RACE-PCR and Sanger sequencing. The complete genome of areca palm velarivirus 1 (ArPV1) consists of 16,080 nt with 11 open readings frames (ORFs) and a 11-nt-long 5' UTR and a 37-nt-long 3' UTR (Fig 1). ORF1a (nt 145-6,294) encodes a 234-kDa protein with papain-like protease, a methyltransferase and helicase domains. ORF1b encodes a putative RNA-dependent RNA polymerase (RdRp, nt 6,293-7,819) that is expressed by a +1 ribosomal frameshift. The quintuple gene block consists of ORF2 (nt 7,812-7,922) that encodes a hydrophobic, membrane protein (p4), ORF3 (nt 7,978-9,618) that encodes a heat shock 70 protein homolog (p61), ORF5 (nt 10,087-11,628) that encodes a protein with a conserved viral-HSP90 domain (p60), ORF6 (nt 11,641-12,537) that encodes the major coat protein (p33), and ORF7 (nt 23,540-14,420) that encodes the minor coat protein (p72). ORF4 (nt 9,560-10,096) overlaps ORF3 and ORF5 within the quintuple gene block and encodes a protein (p21) with no similarity with other proteins in GenBank. ORF8 (nt 14,396-15,043), ORF9 (nt 15,040-15,489) and ORF10 (nt 15,534-16,043) encode putative proteins p26, p18 and p19, respectively, with no similarity to other viral proteins. ORF10 is unique to ArPV1. The amino acid identity with *Grapevine leafroll-associated virus 7*, the type member of the genus *Velarivirus*, ranged from 26.4% in the CP to 57% in the RdRp. Phylogenetic analyses confirm the clustering of ArPV1 with members of the genus *Velarivirus* (Fig. 2). No diagnostic primers were designed. In considering the demarcation criteria for species in the family

Closteroviridae, ArPV1 complies with a threshold of 75% amino acid identity for the CP (23.6-26.4%), RdRp (51.5-57.0% identity) and HSP70h (41.0-44.5% identity). Therefore, ArPV1-HN is proposed as a new member of the genus *Velarivirus*.

MODULE 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	***2016.009dP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Unassigned***
Subfamily:	***Unassigned***
Family:	***Closteroviridae***
Order:	***Unassigned***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Persimmon virus B	PeBV1-variant 1	Complete genomic RNA (AB923924)

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

Persimmon virus B (PeVB)

Deep sequencing of a double stranded RNAs from leaf petiole and midvein of declining American persimmon (*Diospyros virginiana* L.) top-grafted onto a Japanese persimmon (*Diospyros kaki* Thunb.) revealed contigs of viral sequences that are homologous but distant from members of the family *Closteroviridae*. RT-PCR was used to fill sequence gaps and the 5' and 3' termini were obtained with RACE-PCR after a poly(A) tail was added to total RNA followed by Sanger sequencing. The complete genome sequence of persimmon virus B (PeVB) variant 1 consists of 18,569 nt (GenBank accession number AB923924) with 11 open reading frames with a genomic structure similar to closterovirids (Ito et al., 2015) (Fig. 1). The 5' and 3' UTRs are 183 nt and 282 nt long, respectively. ORF1a (nt 184-9,633) encodes a protein containing a putative protease, a methytransferase, and a helicase. ORF1 (nt 9,632-11,179) encodes a putative RNA-dependent RNA polymerase (p60). ORF2 (nt 11,254-11,475) encodes a hydrophobic protein (p9) with a transmembrane motif. ORF3 (nt 11,830-13,587) encodes the heat shock 70 protein homolog (p65). ORF4 (nt 13,478-14,989) encodes p59 and ORF5 (nt 14,877-15,644) encodes p29. PeVB seems to lack a minor coat protein. ORF6 (nt 15,651-16460) encodes a coat protein (p30). ORF7 (nt 16,463-16,672), ORF8 (nt 16,669-17,142), ORF9 (nt 17,132-17,635), ORF10 (nt 17,623-18,048) and ORF11 (nt 18,051-18,287) encode putative proteins p8, p18, p19, p16 and p9, respectively. These proteins lack significant similarities with viral sequences available in databases. A putative protein (p9) is predicted to be expressed by a +1 reading frame within p29 (Ito et al., 2015). Diagnostic primers were designed for the detection of PeVB in three Japanese persimmon trees proximal to the tested tree. No information is available on the vector of PeVB. Phylogenetic analyses confirm the clustering of PeVB with members of the family *Closteroviridae* (Fig. 2). In addition to PeVB,

sequence analyses revealed the presence of three other PeVB variants in the same infected American persimmon sample. These three variants are designated as PeVB variant 2 with a complete genome of 18,030 nt (GenBank accession number AB923925), PeVB variant 3 with a partial genome of 4,899 nt (GenBank accession number AB923926) and PeVB variant 4 with a partial genome of 9,019 nt (GenBank accession number AB923927) (Ito et al., 2015), acknowledging that PeVB is variant 1. PeBV variants 1 and 2 share high amino sequence identifies in the RdRP (72%), HSP70h (82%) and CP (87%). As expected, PeVB variant 2 clusters with PeBV variant 1 within the family *Closteroviridae*. In considering the demarcation criteria for species in the family *Closteroviridae*, PeVB shows less than 75% amino acid identity for the CP (9.0-16.9%), RdRp (8.0-38.2% identity) and HSP70h (20.0-34.0% identity). Therefore, PeVB-variant 1 is proposed as a member of a new unassigned species in the family *Closteroviridae*.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- He, Y., Yang, Z., Hong, N., Wang, G., Ning, G., and Zu W. 2015. Deep sequencing reveals a novel closterovirus associated with wild rose leaf rosette disease. Molecular Plant Pathology 16:449-458.
- Ito, T., Sato, A., and Suzaki, K. 2015. An assemblage of divergent variants of a novel putative closterovirus from American persimmon. Virus Genes 51:105-111.
- Martelli, G.P., Agranowski, A.A., Bar-Joseph, M., Boscia, D., Candresse, T., Couts, R.H.A., Dolja, V.V., Hu, J.S., Jelkmann, W., Karasev, A.V., Martin R.R., Minafra, A., Namba, S., Vetten H.J. (2012). Family *Closteroviridae*. In: King A., Adams, M.J., Carstens, E.B., Lefkowitz, E. (Eds.). Virus Taxonomy: Ninth report of the International Committee on Taxonomy of Viruses. Elsevier-Academic Press, San Diego, pp. 987-1001.
- Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. & Higgins, D. G. (1997). The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25, 4876-4882.
- Wang, F., Qi, S., Gao Z., Akinyemi, I.A., Zu, D. and Zhou, B. 2016. Complete genome sequence of tobacco virus 1, a closterovirus from *Nicotiana tabacum*. Arch Virol. 161:1087-1090.
- Zhao, F., Yoo, R.H., Lim, S., Igori, D., Lee, S-H., and Moon, J.S. 2015. Nucleotide sequence and genome organization of a new proposed crinivirus, tetterwort vein chlorosis virus. Arch. Virol. 160:2899-2902.

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 but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

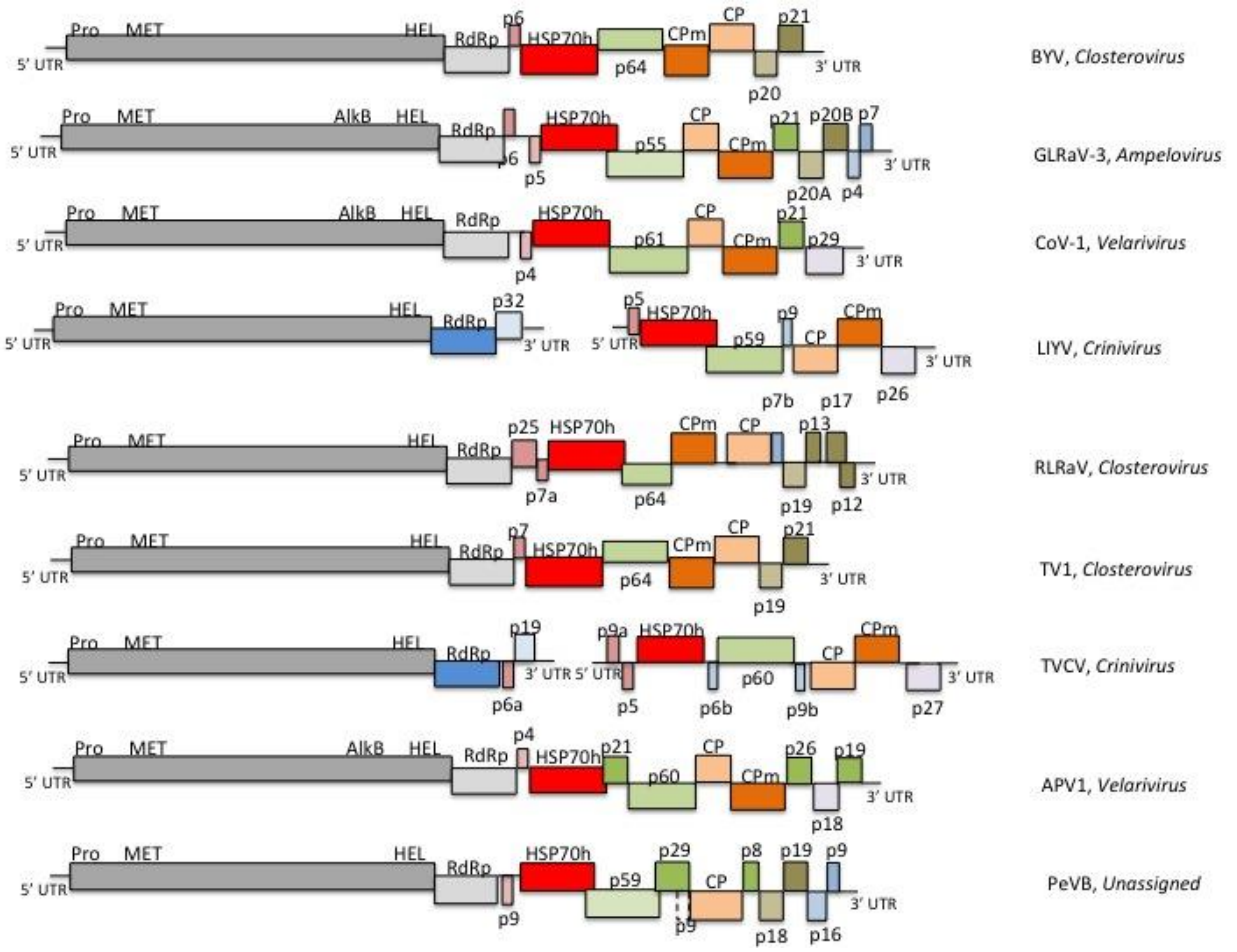

Fig. 1. Schematic representation of the genome organization for the type species or a representative species of four genera (beet yellows virus from the genus *Closterovirus*, grapevine leafroll-associated virus 3 from the genus *Ampelovirus*, cordyline virus 1 from the genus *Velarivirus*, and lettuce infectious yellows virus from the genus *Crinivirus*) within the family *Closteroviridae* and for rose leaf rosette-associated virus (RLRaV), a proposed new closterovirus, tobacco virus 1 (TV1), a proposed new closterovirus, areca palm velarivirus (ArPV1), a proposed new velarivirus, tetterwort vein chlorosis virus (TwVCV), a proposed new crinivirus, and persimmon virus B (PeVB), a proposed new unassigned member of the family *Closteroviridae*. Blocks represent predicted open reading frames (ORFs). The replicase proteins are shown in grey with the papain-like protease (Pro), methyltransferase (Met), alkB domain (AlkB) helicase (HEL), and RNA-dependent RNA polymerase (RdRp). Small transmembrane proteins (p4, p5 and/or p6) are shown in pink, the heat shock protein 70 homolog (HSP70h) in red, the coat protein (CP) in salmon, and the minor coat protein (CPm) in orange.

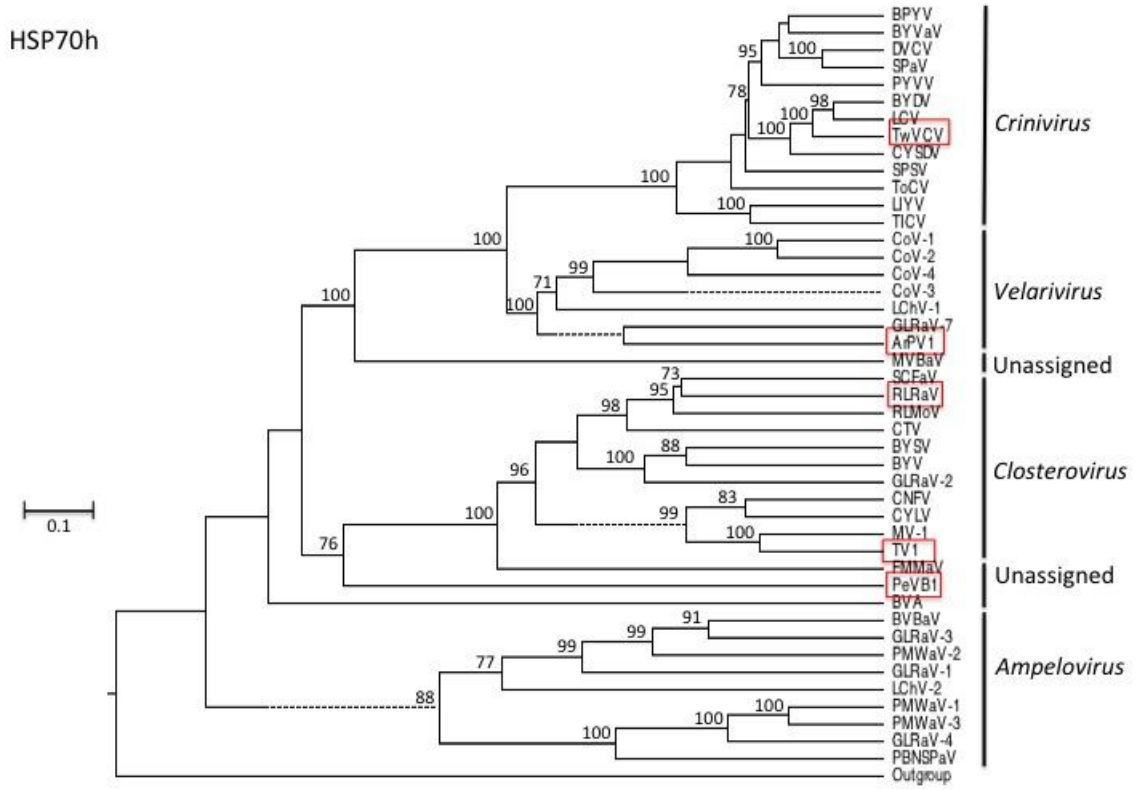

Fig. 2. Phylogenetic tree showing the relationships between the species and genera of the family *Closteroviridae* based on the complete amino acid sequence of the heat shock protein 70 homolog. The neighbour-joining tree was produced and bootstraped using CLUSTAL W (Thompson et al., 1997). Distances are proportional to branch lengths. Bootstrap values (1,000 replicates) above 75% are indicated at main branch nodes. The heat shock protein 70 from *Arabidopsis thaliana* (AEE75218) was used as outgroup. An identical tree topology was obtained with the Maximum Likelihood method applying best substitution model. Newly proposed species in the genera *Closterovirus, Crivivirus* and *Velarivirus*, and the newly proposed unassigned species in the family *Closteroviridae* are boxed in solid red line. The GenBank accession numbers used for each virus are as follows: areca palm velarivirus 1 (ArPV1, KR349464), bean yellow disorder virus (BYDV, EU191904), beet pseudoyellows virus (BPYV, AY330918), beet yellow stunt virus (BYSV, U51931), beet yellows virus (BYV, AF056575), blackberry vein banding-associated virus (BVBaV, KC904540), blueberry virus A (BVA, AB733585), carnation necrotic fleck virus (CVFV, GU234166), carrot yellow leaf virus (CYLV, FJ869862), citrus tristeza virus (CTV, U16304), cordyline virus 1 (CoV-1, HM588723), cordyline virus 2 (CoV-2, JQ599282), cordyline virus 3 (CoV-3, JQ599283), cordyline virus 4 (CoV-4, JQ599284), cucurbit yellow stunting disorder virus (CYSDV,AY242077), diodia vein chlorosis virus (DVCV, GQ225585), fig leaf mottle-associated virus 2 (FLMaV-2, FJ73383), fig mild mottle-associated virus (FMMaV, FJ611959), grapevine leafroll-associated virus 1 (GLRaV-1, JQ023131), grapevine leafroll-associated virus 2 (GLRaV-2, JX513891), grapevine leafroll-associated virus 3 (GLRaV-3, EU259806), grapevine leafroll-associated virus 4 (GLRaV-4, FJ467503), grapevine leafroll-associated virus 7 (GLRaV-7, HE588185), lettuce chlorosis virus (LCV, FJ380118), lettuce infectious yellows virus (LIYV, U15440), little cherry virus 1 (LChV-1, EU715989), little cherry virus 2 (LChV-2, AF531505), mint vein banding-associated virus (MVBaV, KJ572575), mint virus 1 (MV-1, AY792620), persimmon virus B (PeBV, AB923924), pineapple mealybug wilt-associated 1

(PMWaV-1, AF414119), pineapple mealybug wilt-associated 2 (PMWaV-2, AF283103), pineapple mealybug wilt-associated 3 (PMWaV-3, DQ399259), plum bark necrosis stem pitting-associated virus (PMNSPaV, EF546442), raspberry leaf mottle virus (RLMoV, DQ357218), rose leaf rosette-associated virus (RLRaV, KJ7488003), strawberry chlorotic fleck-associated virus (SCFaV, DQ860839), potato yellow vein virus (PYVV, AJ557128), strawberry pallidosis-associated virus (SPaV, AY488137), sweet potato chlorotic stunt virus (SPCSV, AJ428554), tetterwort vein chlorosis virus (TwVSV, KR002687), tobacco virus 1 (TV1, KT203917), tomato chlorosis virus (ToCV, AY903447), and tomato infectious chlorosis virus (TICV, FJ815440).