



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:	2015.009a-pP	(to be completed by ICTV officers)
Short title: Four new unassigned genera for plant satellite viruses		
two new species (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>
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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)

Tombusviridae and Virgaviridae SGs

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

Date first submitted to ICTV: June 15, 2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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MODULE 2a: **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	2015.009aP	(assigned by ICTV officers)
To create 3 new species within:		
Genus:	<i>Albetovirus</i> (new)	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.
Subfamily:		
Family:	Unassigned	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Tobacco albetovirus 1</i>	satellite tobacco necrosis virus 1 (STNV-1)	V01468
<i>Tobacco albetovirus 2</i>	satellite tobacco necrosis virus 2 (STNV-2)	M64479
<i>Tobacco albetovirus 3</i>	satellite tobacco necrosis virus C (STNV-C)	AJ000898

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

All three proposed virus species represent satellite viruses that for multiplication depend on members of the genera *Alphanecrovirus* or *Betanecrovirus* of the family *Tombusviridae*. Notably, prior to 2011, the two genera were combined in a single genus *Necrovirus* [10]. The three satellite viruses have similarly-sized (1,221-1,245 nucleotides in length), linear, single-stranded RNA genomes of positive polarity and each encodes only one protein (Module 10; Table 1, Figure 1) [3, 4, 13, 14]. The 5' ends of their genomes are phosphorylated and lack 7-methylguanylate caps or a genome-linked protein, whereas the 3' termini lack polyadenylation sequences [9]. The virions are icosahedral, 17 nm in diameter and are composed of a single capsid protein (CP; Module 10; Table 1). The CPs of viruses in the proposed genus are homologous and share 49-62% pairwise sequence identity (see Module 10; Figure 2). At the sequence level, the CPs are not recognizably similar to proteins encoded by viruses from other taxa, except for the CP of the unclassified satellite maize white line mosaic virus, the CP sequence of which is 29% identical to that of the capsid protein of STNV-1 and is therefore readily identifiable by BLASTp searches (see Module 2b).

The three viruses are serologically different and are activated by different strains of helper tobacco necrosis viruses (TNVs). The replication of STNV-1 and STNV-2 is supported by isolates of the TNV strain A (TNV-A, the sole member of the type species of the genus *Alphanecrovirus*, *Tobacco necrosis virus A*), whereas another group of strain D isolates (TNV-D, the sole member of the type species of the genus *Betanecrovirus*, *Tobacco necrosis virus D*) supports the replication of STNV-C [6].

MODULE 2b: **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	2015.009bP	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Aumaivirus (new)</i>	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.
Subfamily:		
Family:	Unassigned	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Maize aumaivirus 1</i>	satellite maize white line mosaic virus (SMWLMV)	M55012

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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
<p>SMWLMV is dependent on maize white line mosaic virus (MWLMV; species <i>Maize white line mosaic virus</i>, genus <i>Aureusvirus</i>, family <i>Tombusviridae</i>) for multiplication [14]. MWLMV can infect maize in the absence of SMWLMV, whereas SMWLMV particle can infect maize only when co-inoculated with MWLMV.</p> <p>The ssRNA genome of SMWLMV is 1,168 nucleotides in length and encodes one capsid protein, which was shown to be produced in the <i>in vitro</i> translation assay [14]. Like in STNV-like viruses, the SMWLMV virion is 17 nm in diameter, but there is only limited sequence similarity of the capsid protein to the corresponding proteins of STNV-like viruses.</p>

MODULE 2c: **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	2015.009cP	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Papanivirus</i> (new)	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.
Subfamily:		
Family:	Unassigned	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Panicum papanivirus 1</i>	satellite panicum mosaic virus (SPMV)	M17182

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

For multiplication and systemic spread, satellite panicum mosaic virus (SPMV) depends on panicum mosaic virus (PMV), a member of the genus *Panicovirus*, family *Tombusviridae*. Both the virion (16 nm in diameter) and the linear single-stranded RNA genome (826 nt) of SPMV are somewhat smaller than those of STNV-like satellite viruses (Module 10; Table 1). The SPMV genome contains two open reading frames; however, only one of them (for capsid protein) has been shown to be expressed in an *in vitro* translation assay [7]. The SPMV capsid protein is not appreciably similar to those of STNV-like viruses (below 15% identity; Module 10, Figure 2). The 5'-terminus of SPMV genome is phosphorylated and lacks a 7-methylguanylate cap [7].

Two other viruses encoding SPMV-like CPs have been reported (Module 10; Table 1, Figure 1). The first one, satellite St. Augustine decline virus (SSADV), is associated with the St. Augustine decline strain of PMV [2]. SSADV is 95% identical to SPMV over the entire genome length (36 nt changes, 5 aa changes) and should be considered as a different variant of SPMV. The second putative satellite virus, satellite grapevine virus (SGVV), has been detected by deep sequencing of total genomic RNA from grapevine [1]; however, neither the viral particles nor the associated helper virus have been characterized.

MODULE 2d: **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	2015.009dP	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Virtovirus</i> (new)	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.
Subfamily:		
Family:	Unassigned	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Tobacco virtovirus 1</i>	satellite tobacco mosaic virus (STMV)	M25782

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

Satellite tobacco mosaic virus (STMV) has been isolated from tree tobacco (*Nicotiana glauca*) and can use different members of the genus *Tobamovirus*, family *Virgaviridae* for replication [5]. STMV is the only satellite virus that uses rod-shaped viruses as helpers. The STMV genome is a linear ssRNA molecule of 1,059 nt that contains two genes, both of which are functional in the *in vitro* translation assay [8]. The first ORF encodes a protein of 58 aa which shows no similarity to proteins in the public databases and appears to be dispensable for STMV multiplication [11]. The second ORF encodes for the STMV CP; the protein also has no identifiable homologs in the sequence databases.

MODULE 3a: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2015.009eP	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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 family is specified, enter “unassigned” in the family box
Family:	Unassigned	
Order:		

naming a new genus

Code	2015.009fP	(assigned by ICTV officers)
To name the new genus: <i>Albetovirus</i>		

Assigning the type species and other species to a new genus

Code	2015.009gP	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Tobacco albetovirus 1</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
3		

Reasons to justify the creation of a new genus:

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

Satellite viruses in this genus depend on members of the genera *Alphanecrovirus* or *Betanecrovirus* (family *Tombusviridae*) for replication. All three satellite viruses contain similarly-sized genomes, in the range of 1,221-1,245 nucleotides (Module 10; Table 1, Figure 1), and encode homologous capsid proteins. The latter proteins display 49-62% pairwise sequence identity (Module 10; Figure 2) but are not closely related to corresponding proteins of other viruses. Consistently, the diameter of icosahedral capsids is similar (17 nm) for all three viruses. Based on these shared features, we conclude that STNV-1, STNV-2, and STNV-C have evolved from a common ancestor and are best assigned within the same genus.

Origin of the new genus name:

Al- for alphanecrovirus (helper virus), *be-* for betanecrovirus (helper virus), *to-* for tobacco.

Reasons to justify the choice of type species:

The representative of this species has been extensively studied and its genome sequence as well as virion structure is available.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

We recommend using pairwise sequence identity between the capsid proteins as the main species demarcation criterion. The three founding members of the proposed genus *Albetovirus* (STNV-1, STNV-2 and STNV-C) encode capsid proteins that are 49-62% identical to each other. Accordingly, new species within the proposed genus will include viruses encoding capsid proteins with 45-90% sequence identity to those of the existing members. Viruses with >90% protein sequence identity will be considered as strains within the corresponding existing species.

MODULE 3b: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2015.009hP	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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 family is specified, enter “ unassigned ” in the family box
Family:	Unassigned	
Order:		

naming a new genus

Code	2015.009iP	(assigned by ICTV officers)
To name the new genus: <i>Aumaivirus</i>		

Assigning the type species and other species to a new genus

Code	2015.009jP	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Maize aumaivirus 1</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
1		

Reasons to justify the creation of a new genus:

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

Although it is generally considered that SMWLMV is unrelated to other satellite viruses [12, 14], BLASTp searches seeded with the SMWLMV CP sequence result in a significant match to the corresponding protein of STNV-1 (32% identity over 177 aa; E=1e-14). Consistently, CD-search analysis shows that SMWLMV CP contains the TNV_CP domain (PF03898; E= 4.5e-96), strongly suggesting that SMWLMV and members of the proposed genus *Albetovirus* have diverged from a common ancestor. However, the low sequence similarity between their capsid proteins calls for the creation of a separate genus for classification of SMWLMV. Furthermore, unlike STNV-like viruses, which use members of the genera *Alphanecrovirus* or *Betanecrovirus* as helpers, SMWLMV for replication relies on viruses of the genus *Aureusvirus* (family *Tombusviridae*).

Origin of the new genus name:

Au- for aureusvirus (helper virus), *mai-* for maize.

Reasons to justify the choice of type species:

SMWLMV is the sole representative of the proposed genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Not applicable; only one species has been assigned to this genus.

MODULE 3c: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2015.009kP	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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 family is specified, enter “ unassigned ” in the family box
Family:	Unassigned	
Order:		

naming a new genus

Code	2015.009lP	(assigned by ICTV officers)
To name the new genus: <i>Papanivirus</i>		

Assigning the type species and other species to a new genus

Code	2015.009mP	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Panicum papanivirus 1</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
1		

Reasons to justify the creation of a new genus:

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

SPMV does not display considerable genome or capsid protein sequence similarity to other known viruses. Unlike other plant satellite viruses, SPMV uses viruses of the genus *Panicovirus* (family *Tombusviridae*) as its helpers. Therefore, classification of this virus calls for the creation of a new genus.

Origin of the new genus name:

Pa- for panicovirus (helper virus), *pani-* for panicum.

Reasons to justify the choice of type species:

This representative has been extensively studied and its genome sequence as well as virion structure is available.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Not applicable; only one species has been assigned to this genus.

MODULE 3d: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2015.009nP	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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 family is specified, enter “ unassigned ” in the family box
Family:	Unassigned	
Order:		

naming a new genus

Code	2015.009oP	(assigned by ICTV officers)
To name the new genus: <i>Virtovirus</i>		

Assigning the type species and other species to a new genus

Code	2015.009pP	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Tobacco virtovirus 1</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
1		

Reasons to justify the creation of a new genus:

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

STMV does not display considerable genome or capsid protein sequence similarity to other known viruses. Unlike other plant satellite viruses, STMV uses viruses of the family *Virgaviridae* as its helpers. Therefore, classification of this virus calls for the creation of a new genus.

Origin of the new genus name:

Vir- for *virgavirus* (helper virus), *to-* for *tobacco*.

Reasons to justify the choice of type species:

This representative has been extensively studied and its genome sequence as well as virion structure is available.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Not applicable; only one species has been assigned to this genus.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Al Rwahnih M, Daubert S, Sudarshana MR, Rowhani A (2013) Gene from a novel plant virus satellite from grapevine identifies a viral satellite lineage. *Virus Genes* 47:114-118
2. Berger PH, Shiel PJ, Gunasinghe U (1994) The nucleotide sequence of satellite St. Augustine decline virus. *Mol Plant Microbe Interact* 7:313-316
3. Bringloe DH, Gulyaev AP, Pelpel M, Pleij CW, Coutts RH (1998) The nucleotide sequence of satellite tobacco necrosis virus strain C and helper-assisted replication of wild-type and mutant clones of the virus. *J Gen Virol* 79 (Pt 6):1539-1546
4. Danthinne X, Seurinck J, Van Montagu M, Pleij CW, van Emmelo J (1991) Structural similarities between the RNAs of two satellites of tobacco necrosis virus. *Virology* 185:605-614
5. Dodds JA (1998) Satellite tobacco mosaic virus. *Annual review of phytopathology* 36:295-310
6. Kassanis B, Phillips MP (1970) Serological relationship of strains of tobacco necrosis virus and their ability to activate strains of satellite virus. *J Gen Virol* 9:119-126
7. Masuta C, Zuidema D, Hunter BG, Heaton LA, Sopher DS, Jackson AO (1987) Analysis of the genome of satellite panicum mosaic virus. *Virology* 159:329-338
8. Mirkov TE, Mathews DM, Du Plessis DH, Dodds JA (1989) Nucleotide sequence and translation of satellite tobacco mosaic virus RNA. *Virology* 170:139-146
9. Murrant AF, Mayo MA (1982) Satellites of plant viruses. *Annu Rev Phytopathol* 20:49-70
10. Rochon D (2011) Divide the genus *Necrovirus* into 2 new genera, *Alphanecrovirus* and *Betanecrovirus*. http://ictvonline.org/proposals/2011.009a-mP.A.v3.split_Necrovirus.pdf
11. Routh G, Dodds JA, Fitzmaurice L, Mirkov TE (1995) Characterization of deletion and frameshift mutants of satellite tobacco mosaic virus. *Virology* 212:121-127
12. Xu P, Roossinck MJ (2011) Plant virus satellites. *Encyclopedia of Life Sciences (ELS)*. John Wiley & Sons, Ltd, Chichester
13. Ysebaert M, van Emmelo J, Fiers W (1980) Total nucleotide sequence of a nearly full-size DNA copy of satellite tobacco necrosis virus RNA. *J Mol Biol* 143:273-287
14. Zhang L, Zitter TA, Palukaitis P (1991) Helper virus-dependent replication, nucleotide sequence and genome organization of the satellite virus of maize white line mosaic virus. *Virology* 180:467-473

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.

Table 1. General properties of plant satellite viruses.

Satellite virus	Genome type	Helper virus	Accession #	Genome, nt	Capsid Ø, nm	Comments
<i>Albetovirus</i>						
satellite tobacco necrosis virus (STNV-1)	ssRNA(+)	tobacco necrosis virus strain A (<i>Tombusviridae</i>)	V01468	1,239	17	STNV suppresses the replication of its helper virus and ameliorate the TNV-induced symptoms in different hosts.
satellite tobacco necrosis virus 2 (STNV-2)	ssRNA(+)	tobacco necrosis virus strain A (<i>Tombusviridae</i>)	M64479	1,245	17	STNV and STNV-2 coat protein genes share 55% nucleotide sequence identity, whereas the UTRs are more similar.
satellite tobacco necrosis virus strain C (STNV-C)	ssRNA(+)	tobacco necrosis virus strain D (<i>Tombusviridae</i>)	AJ000898	1,221	17	STNV and STNV-C coat proteins share 62% sequence identity, whereas the 3'UTRs are 40% identical.
<i>Aumaivirus</i>						
satellite maize white line mosaic virus (SMWLMV)	ssRNA(+)	maize white line mosaic virus (<i>Tombusviridae</i>)	M55012	1,168	17	CP is 32% identical to that of STNV.
<i>Papanivirus</i>						
satellite panicum mosaic virus (SPMV)	ssRNA(+)	panicum mosaic virus (<i>Tombusviridae</i>)	M17182	826	16	Besides virion formation, CP of SPMV has several other biological functions, including systemic accumulation, maintenance and movement of the SPMV RNA.
satellite St. Augustine decline virus (SSADV)	ssRNA(+)	St. Augustine decline virus strain of PMV (<i>Tombusviridae</i>)	L10083	824	ND	SSADV is a strain of SPMV (36 nt substitutions; 5 aa changes).
satellite grapevine virus (SGVV)	RNA	grapevine virus F (<i>Betaflexiviridae</i>) ?	KC149510	1,060	ND	SGVV and GVF share stem-loop structures at the 5' ends of the genomes.
<i>Virtovirus</i>						
satellite tobacco mosaic virus (STMV)	ssRNA(+)	tobacco mosaic virus (<i>Virgaviridae</i>)	M25782	1,059	17	The 3'UTR is similar to that of tobamoviruses, with a clear sequence similarity between STMV and TMV.

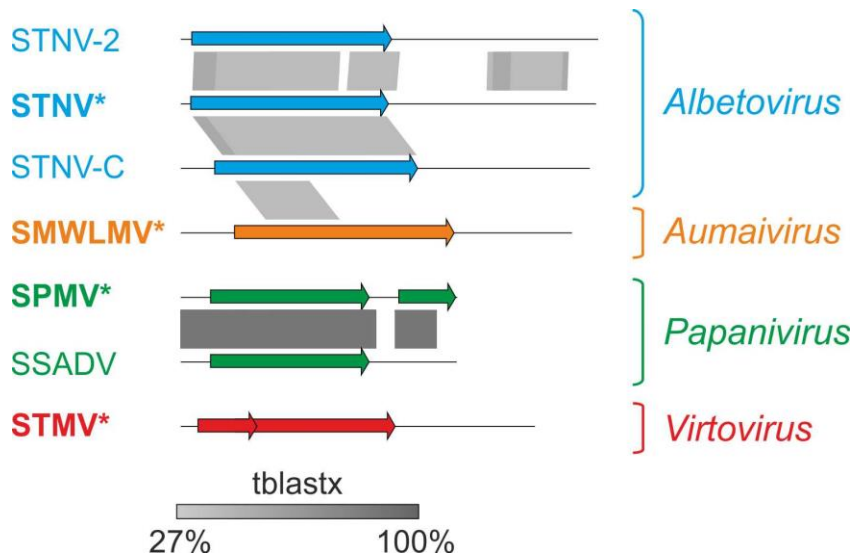


Figure 1. Genome maps of plant satellite viruses. The maps are coloured according to the proposed classification of the plant satellite viruses: *Albetovirus*, cyan; *Aumaivirus*, orange; *Papanivirus*, green; *Virtovirus*, red. The viruses of the proposed type species of the four tentative genera are designated with asterisks. The relationship between depicted viral genomes is indicated with grey shading.

STNV-1	100%						
STNV-2	49.48%	100%					
STNV-C	62.75%	52.02%	100%				
SMWLMV	29.08%	29.29%	28.35%	100%			
SPMV	8.91%	10.82%	13.37%	12.1%	100%		
SSADV	7.64%	10.19%	13.37%	11.46%	96.81%	100%	
STMV	8.8%	5.66%	8.8%	7.54%	10.82%	10.82%	100%
	STNV-1	STNV-2	STNV-C	SMWLMV	SPMV	SSADV	STMV

Figure 2. Pairwise identity between capsid proteins of plant satellite viruses calculated using SIAS (<http://imed.med.ucm.es/Tools/sias.html>). Identity values among the capsid proteins of STNV-like viruses, SMWLMV, SPMV-like viruses, and STMV are highlighted in cyan, orange, green and red, respectively.

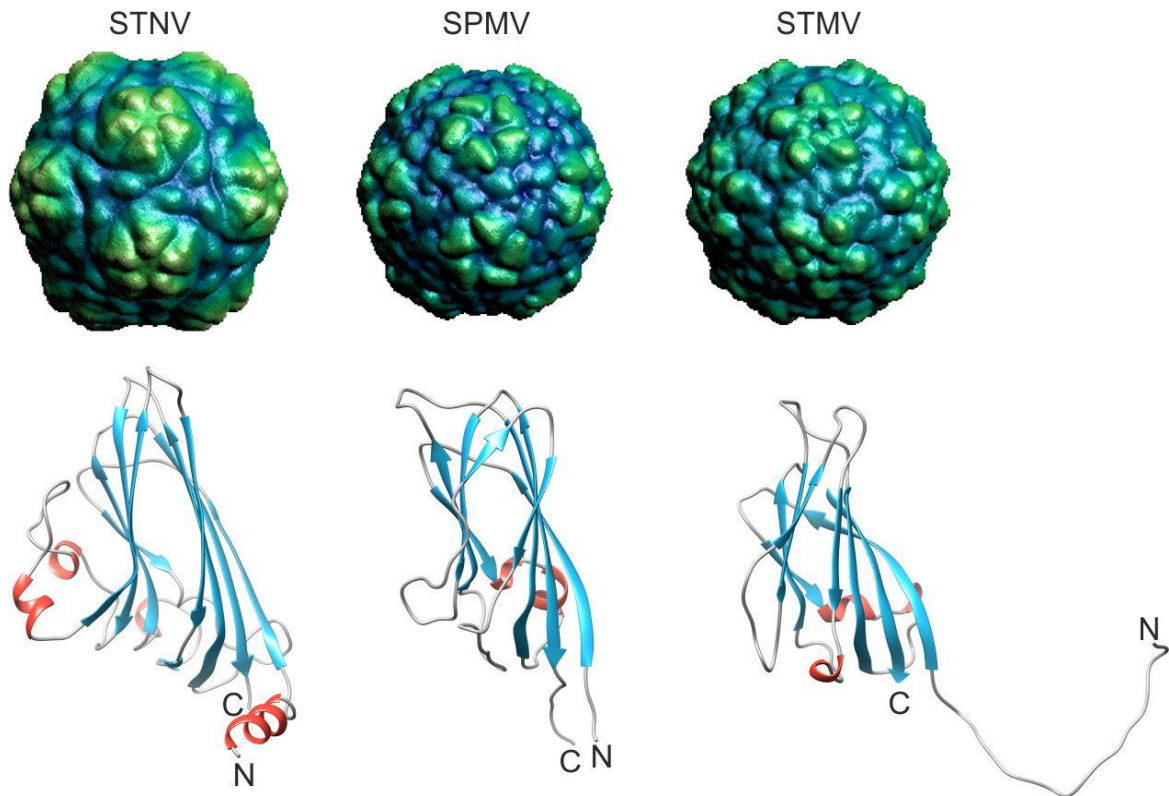


Figure 3. Structural similarity between the virions (top) and jelly-roll capsid proteins (bottom) of satellite tobacco necrosis virus (STNV; PDB ID: 2BUK), satellite panicum mosaic virus (SPMV; PDB ID: 1STM), and satellite tobacco mosaic virus (STMV; PDB ID: 4OQ8). All three virions have a $T=1$ icosahedral symmetry. Images of the depicted virions were downloaded from the VIPER database (viperd.b.scripps.edu/).