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:	***2016.014a-iP***	(to be completed by ICTV officers)

Short title: Establishment of two new genera and creation of two unassigned species in the family *Geminiviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

Arvind Varsani, Darren Martin, F. Murilo Zerbini, Philippe Roumagnac, Marc Fuchs; on behalf of the *Geminiviridae* SG

Corresponding author with e-mail address:

avarsani@gmail.com

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)	*Geminiviridae* SG

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	***2016.014aP***	(assigned by ICTV officers)

To create four new species within:

Genus:	***Capulavirus* (new)**
Subfamily:	
Family:	***Geminiviridae***
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Alfalfa leaf curl virus	ALCV-[44-1E]	KP732474
Euphorbia caput-medusae latent virus	EcmLV-[Dar10]	HF921459
French bean severe leaf curl virus	FbSLSV-[1]	JX094280
Plantago lanceolata latent virus	PlLV-[ALA13_Pl11]	KT214389

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 11

Please see also the justification for the creation of the new genus *Capulavirus*, in Module 3 below.

- All of the proposed capulavirus species have an inferred genome organization that is distinct from those of the other known geminivirus genera (Figure 1).
- Based on pairwise identity comparisons (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps) all isolates within each of the proposed new capulavirus species share between 63% and 73% genome-wide sequence similarity with all isolates that have been assigned to the other proposed capulavirus species (Figure 2A, Figure 3A).
- Regardless of whether the full genome nucleotide sequence (Figure 4), the inferred replication associated protein (Rep) amino acid sequence (Figure 5), or the inferred coat protein (CP) amino acid sequence (Figure 6) is considered, all of the proposed capulavirus species group with 100% phylogenetic support with other proposed capulaviruses.

Collectively this indicates that all these proposed species should be included within a single genus.

Although there are presently no species demarcation criteria for this genus we have opted to

tentatively use a 78% pairwise identity species demarcation criterion which will align this genus with the *Mastrevirus* and *Curtovirus* genera of the *Geminiviridae*. This cutoff is supported by the distribution of 47 genome-wide pairwise identities of the known capulavirus sequences (Figure 3A). Isolates within the four species that this demarcation criterion yields all cluster with 100% bootstrap support within a phylogenetic tree constructed from the known capulavirus full genome sequences (Figure 3A, Figures 5 to 6). It is also likely that the different proposed species have different natural host and geographical ranges (Table 1), although more extensive sampling will be required to determine whether this is indeed the case.

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	***2016.014bP***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Grablovirus* (new)**
Subfamily:	
Family:	***Geminiviridae***
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Grapevine red blotch virus	GRBV-[RT(456)17NOV10]	JQ901105

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 11

Please see the justification for the creation of the new genus *Grablovirus*, in Module 3 below.

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	***2016.014cP***	(assigned by ICTV officers)

To create two new species within:

Genus:	***Unassigned***
Subfamily:	
Family:	***Geminiviridae***
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Citrus chlorotic dwarf associated virus	CCDaV-[TK4]	JQ920490
Mulberry mosaic dwarf associated virus	MMDaV-[AK1-8]	KP303687

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 11

The two viruses are clearly related to the geminiviruses, based on genome composition, similarities in the origin of replication, and the presence of homologous genes. The deduced amino acid sequences of their replication-associated proteins (Rep) share 30-50% sequence identity with other viruses in the family (Figure 7).

The genome of CCDaV, with 3,640 nt, is significantly larger than those of other geminiviruses. However, its origin of replication has the conserved 5'TAATATTAC3' nonanucleotide present in the *ori* of most geminiviruses.

The size of the genome (2,952 nt) and the conserved origin of replication (5'TAATATTAC3') of Mulberry mosaic dwarf associated virus (MMDaV) are similar to those of members of the *Geminiviridae*, but the genomic organization, number of inferred genes, and the presence of five GAAAAA repeats positioned upstream of the inferred coat protein (CP) gene distinguish it from other geminiviruses (Ma et al., 2015). A virus named Mulberry crinkle leaf virus was reported by Lu et al. (2015) (access number KR131479). The virus has the same genome features and shares 97% sequence identity with MMDaV, and thus is an isolate of the same new species MMDaV.

Regardless of whether the full genome nucleotide sequence (Figure 4), the inferred replication associated protein (Rep) amino acid sequence (Figure 5), or the inferred CP amino acid sequence (Figure 6) is considered, the two proposed species group separately from all other geminiviruses, with strong phylogenetic support.

Traditionally, the type of vector has been used to classify species into genera in the *Geminiviridae*. Because the vectors of CCDaV and MMDaV are currently unknown, we prefer not to assign them to the same (new) genus or to separate (new) genera at this time.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.014dP***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Geminiviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2016.014eP***	(assigned by ICTV officers)

To name the new genus: *Capulavirus*

Assigning the type species and other species to a new genus

Code	***2016.014fP***	(assigned by ICTV officers)

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

Euphorbia caput-medusae latent virus

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:**

Four

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 11

While the viruses within the four proposed species of the new genus clearly cluster phylogenetically within the *Geminiviridae* family and at least one of the members of one of the species (EcmLV; Bernardo et al., 2013) has geminate virions (Bernardo et al., 2016) (i.e. they clearly belong within the *Geminiviridae*), they have a number of distinguishing characteristics:

(1) They share a genome organization that is distinct from those of viruses in the currently recognized *Geminiviridae* genera (Figure 1);

(2) Unique amongst the geminiviruses, one of the proposed species in the family, ALCV, is known to be transmitted by the aphid, *Aphis craccivora* (Bernardo et al., 2016);

(3) The viruses assigned to the *Capulavirus* genus share < 22% CP amino acid sequence identity and <45% Rep amino acid sequence identity with viruses in other known *Geminiviridae* genera (Figure 7);

(4) Isolates tentatively assigned to this proposed genus all cluster with 100% bootstrap support within phylogenetic trees constructed using full genome sequences (Figure 4), inferred Rep amino acid sequences (Figure 5), and inferred CP amino acid sequences (Figure 6).

Origin of the new genus name:

Based on the name of the type species *Euphorbia caput-medusae latent virus*

Reasons to justify the choice of type species:

Euphorbia caput-medusae latent virus is the best characterized species and is the only one for which geminate particles have been observed.

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.

An analysis of the distribution of pairwise identities of known capulavirus genomes (n=47) indicates that pairwise identity-based species demarcation criteria that would minimize conflicts (i.e. possible assignments of individual isolates to two or more species) could be 72-84%, or 87-94% (Figure 3A). Whereas a species demarcation threshold within the 87-94% range would yield 5 species, that within the 72-84% range would yield four species. In the case of a threshold within the 87-94% range, the ALCV sequences, which have all been isolated from alfalfa plants, would be split into two species. Given that there seems to be no good biological reason to split the ALCVs into two species, we have opted to tentatively place the species demarcation threshold in the 72%-84% range. In order to place the capulavirus species demarcation threshold in line with that of the *Mastrevirus* genus (the recognized geminivirus genus that the capulaviruses are most closely related to; Figure 4) we have opted to tentatively select 78% as the pairwise identity above which two sequences should be considered isolates of the same species.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.014gP***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Geminiviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2016.014hP***	(assigned by ICTV officers)

To name the new genus: *Grablovirus*

Assigning the type species and other species to a new genus

Code	***2016.014iP***	(assigned by ICTV officers)

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

Grapevine red blotch virus	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:**

One

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 11

- The type (and, currently, the only) species in the genus, Grapevine red blotch virus (GRBV), has an inferred genome organization that is distinct (greater length and unique gene arrangement) from those of viruses in all other known geminivirus genera (Figure 1). Nevertheless, it has a genome of circular, ssDNA, and geminate particles have been observed in purified preparations from symptomatic grapevines (M.R. Sudarshana, *personal communication*; Sudarshana et al., 2015).
- All GRBV isolates (n=27) share >91% genome-wide sequence identity among each other (Figure 2B), and <50% similarity in their Rep sequences with all other geminiviruses (Figure 7).
- Regardless of whether the full genome nucleotide sequence (Figure 4) or the inferred replication associated protein (Rep) amino acid sequence (Figure 5) is considered, GRBV isolates group, with strong phylogenetic support, separately from all other geminiviruses.
- GBRV seems to be transmitted by the three cornered alfalfa treehopper, *Spissistilus festinus* Say (Hemiptera: Membracidae) (M.R. Sudarshana, *personal communication*). Within the *Geminiviridae*, only *Tomato pseudo curly top virus*, the single species in the genus *Topocuvirus*, is known to be transmitted by a treehopper.

Origin of the new genus name:

Based on the name of the type species, Grapevine red blotch virus

Reasons to justify the choice of type species:

Currently the only species in the 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.

Currently, GRBV is the only species in the new genus. All GRBV isolates share >91% identity (Figure 2B; Figure 3B). Based on the species demarcation criteria used for most genera in the *Geminiviridae*, isolates sharing <80% genome wide pairwise identity will be classified as distinct *Grablovirus* species. This is a tentative species demarcation criteria that will need to be refined as more sequences are assigned to the genus.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Capulaviruses:

Bernardo, P., Golden, M., Akram, M., Naimuddin, Nadarajan, N., Fernandez, E., Granier, M., Rebelo, A.G., Peterschmitt, M., Martin, D.P., Roumagnac, P. (2013). Identification and characterisation of a highly divergent geminivirus: evolutionary and taxonomic implications. Virus Research 177:35-45.

Bernardo, P., Muhire, B., Francois, S., Deshoux, M., Hartnady, P., Farkas, K., Kraberger, S., Filloux, D., Fernandez, E., Galzi, S., Ferdinand, R., Granier, M., Marais, A., Monge Blasco, P., Candresse, T., Escriu, F., Varsani, A., Harkins, G.W., Martin, D.P., Roumagnac, P. (2016). Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. Virology 493:142-153.

Muhire, B.M., Varsani, A., Martin, D.P. (2014). SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9:e108277.

Grabloviruses:

Krenz, B., Thompson, J.R., Fuchs, M., Perry, K.L. (2012). Complete genome sequence of a new circular DNA virus from grapevine. Journal of Virology 86:7715.

Sudarshana, M.R., Perry, K., Fuchs, M.F. (2015). Grapevine red blotch-associated virus, an emerging threat to the grapevine industry. Phytopathology 105:1026-1032.

Unassigned:

Loconsole, G., Saldarelli, P., Doddapaneni, H., Savino, V., Martelli, G.P., Saponari, M. (2012). Identification of a single-stranded DNA virus associated with citrus chlorotic dwarf disease, a new member in the family *Geminiviridae*. Virology 432:162-172.

Lu, Q.Y., Wu, Z.J., Xia, Z.S., Xie, L.H. (2015) Complete genome sequence of a novel monopartite geminivirus identified in mulberry (*Morus alba* L.). Archives of Virology 160:2135-2138.

Ma, Y., Navarro, B., Zhang, Z., Lu, M., Zhou, X., Chi, S., Di Serio, F., Li, S. (2015). Identification and molecular characterization of a novel monopartite geminivirus associated with mulberry mosaic dwarf disease. Journal of General Virology 96:2421-2434.

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.

In recent years, a number of highly divergent ssDNA plant viruses have been described, and their molecular characterization has indicated that they are related to viruses in the family *Geminiviridae*. The discovery of these viruses has been greatly facilitated by the development of detection methods which are unbiased in terms of previous sequence knowledge, namely, rolling-circle amplification (RCA) and next generation sequencing (NGS). For some of these viruses, a large number of full genome sequences are currently available and this has allowed us to determine with great confidence that these viruses should, indeed, be classified as members of two new genera in the family *Geminiviridae*. Additional viruses are being proposed as unassigned species in the family.

A group of four closely related viruses are being proposed to comprise the new genus *Capulavirus*. For one of these viruses (EcmLV), geminate particles have been observed in purified preparations by TEM, and for another (ALCV), aphid transmission has been demonstrated. These features warrant their classification in a new genus within the family, since all geminiviruses (and only the geminiviruses) have geminate particles, and vector transmission has been used as a criterion for genus differentiation in the family. Also, these capulaviruses have a unique genome arrangement compared to other known geminiviruses.

Another new genus, named *Grablovirus*, is being proposed with a single species, *Grapevine red blotch virus* (GRBL). GRBL also has a unique genome arrangement, and seems to have a treehopper vector. Geminate particles have been visualized in purified preparations from infected grapevine, indicate that it is a *bona fide* geminivirus.

Table 1. Details of the isolates of the four new species being proposed in the new genus *Capulavirus* whose full genomes have been sequenced and were used in the analyses for taxonomic classification.

Species	Accession #	Acronym	Isolate	Country	Host
Alfalfa leaf curl virus	KP732474	ALCV	44-1E	France	*Medicago sativa*
	KT214350	ALCV	TDV14_44-16	France	*Medicago sativa*
	KT214351	ALCV	PB14_LUZ166	France	*Medicago sativa*
	KT214352	ALCV	ASS14_Assas2	France	*Medicago sativa*
	KT214353	ALCV	BON14_LUZ075	France	*Medicago sativa*
	KT214354	ALCV	SSL14_Toul1	France	*Medicago sativa*
	KT214355	ALCV	ALB14_LUZ147	France	*Medicago sativa*
	KT214356	ALCV	ALB14_LUZ163	France	*Medicago sativa*
	KT214357	ALCV	SSL14_Toul7	France	*Medicago sativa*
	KT214358	ALCV	TDV12_48-2A	France	*Medicago sativa*
	KT214359	ALCV	PB14_LUZ184	France	*Medicago sativa*
	KT214360	ALCV	ASS14_Assas1	France	*Medicago sativa*
	KT214361	ALCV	VAU14_LUZ136	France	*Medicago sativa*
	KT214362	ALCV	GAG14_LUZ193	France	*Medicago sativa*
	KT214363	ALCV	PB14_LUZ182	France	*Medicago sativa*
	KT214364	ALCV	ALB14_LUZ148	France	*Medicago sativa*
	KT214365	ALCV	PB14_LUZ-GS4	France	*Medicago sativa*
	KT214366	ALCV	ALB14_LUZ164	France	*Medicago sativa*
	KT214367	ALCV	PB14_LUZ171	France	*Medicago sativa*
	KT214368	ALCV	PB14_LUZ188	France	*Medicago sativa*
	KT214369	ALCV	PB14_LUZ-GS6	France	*Medicago sativa*
	KT214370	ALCV	BON14_LUZ076	France	*Medicago sativa*
	KT214371	ALCV	PB14_LUZ165	France	*Medicago sativa*
	KT214372	ALCV	PB14_LUZ178	France	*Medicago sativa*
	KT214373	ALCV	VAU14_LUZ142	France	*Medicago sativa*
	KT214374	ALCV	PB14_GS8	France	*Medicago sativa*
	KT214375	ALCV	PB14_LUZ179	France	*Medicago sativa*
Euphorbia caput-medusae latent virus	HF921459	EcmLV	Dar10	South Africa	*Euphorbia caput-medusae*
	HF921460	EcmLV	Dar11	South Africa	*Euphorbia caput-medusae*
	HF921477	EcmLV	Lap11	South Africa	*Euphorbia caput-medusae*
	KT214376	EcmLV	DAR12_CM243	South Africa	*Euphorbia caput-medusae*
	KT214377	EcmLV	DAR12_CM26	South Africa	*Euphorbia caput-medusae*
	KT214378	EcmLV	DAR12_CM176	South Africa	*Euphorbia caput-medusae*
	KT214379	EcmLV	DAR12_CM27	South Africa	*Euphorbia caput-medusae*
	KT214380	EcmLV	DAR12_CM192	South Africa	*Euphorbia caput-medusae*
	KT214381	EcmLV	DAR12_CM186	South Africa	*Euphorbia caput-medusae*
	KT214382	EcmLV	DAR12_CM240	South Africa	*Euphorbia caput-medusae*
	KT214383	EcmLV	DAR12_CM162	South Africa	*Euphorbia caput-medusae*
	KT214384	EcmLV	PAT12_CM96	South Africa	*Euphorbia caput-medusae*
	KT214385	EcmLV	PAT12_CM99	South Africa	*Euphorbia caput-medusae*
	KT214386	EcmLV	PAT12_CM101	South Africa	*Euphorbia caput-medusae*
	KT214387	EcmLV	DAR12_CM217	South Africa	*Euphorbia caput-medusae*
	KT214388	EcmLV	DAR12_CM251	South Africa	*Euphorbia caput-medusae*
French bean severe leaf curl virus	JX094280	FbSLSV	FbSLSV-1	India	*Phaseolus vulgaris*
	JX094281	FbSLSV	FbSLCV-2	India	*Phaseolus vulgaris*
Plantago lanceolata latent virus	KT214389	PlLV	ALA13_Pl11	Finland	*Plantago lanceolata*
	KT214390	PlLV	ALA13_Pl5	Finland	*Plantago lanceolata*

Table 2. Details of the isolates of Grapevine red blotch virus (GRBV), the proposed new species in the new genus *Grablovirus* whose full genomes have been sequenced and were used in the analyses for taxonomic classification.

Species	Accession	Acronym	Isolate	Country	Host
Grapevine red blotch virus	KF147916	GRBV	NY175	USA	*Vitis vinifera*
	KU564249	GRBV	NY701	USA: CA	*Vitis vinifera* cv. Cabernet sauvignon
	JQ901105	GRBV	JRT[456]17NOV10	USA: NY	Vitis vinifera
	KC896623	GRBV	CF214-1	USA	Vitis vinifera
	KC896625	GRBV	Z1A-1	USA	Vitis vinifera
	KF137562	GRBV	OR1a	USA: OR	*Vitis vinifera* cv. Pinot noir
	KF147917	GRBV	NY135	USA	*Vitis vinifera*
	KF147918	GRBV	NY137	USA	*Vitis vinifera*
	KF751708	GRBV	NY147	USA: NY	*Vitis vinifera* cv. Pinot Noir
	KP221559	GRBV	1	USA	*Vitis vinifera* cv. Early Burgundy
	KU564247	GRBV	NY699	USA: CA	*Vitis californica* x *Vitis vinifera* hybrid
	KU564248	GRBV	NY700	USA: CA	*Vitis californica* x *Vitis vinifera* hybrid
	KU564250	GRBV	NY702	USA: CA	*Vitis vinifera* cv. Merlot
	KU564251	GRBV	NY703	USA: CA	*Vitis vinifera* cv. Cabernet franc
	KU564252	GRBV	NY704	USA: CA	*Vitis vinifera* cv. Cabernet franc
	KU564253	GRBV	NY705	USA: CA	*Vitis vinifera* cv. Cabernet franc
	KU564254	GRBV	NY913	USA: CA	Vitis californica x *Vitis vinifera* hybrid
	KU564255	GRBV	NY921	USA: CA	*Vitis vinifera* cv. Cabernet franc
	KU564256	GRBV	NY926	USA: CA	*Vitis vinifera* cv. Cabernet franc
	JX559642	GRBV	3138-03	Canada	*Vitis vinifera*
	KC896624	GRBV	CS337-1	USA	*Vitis vinifera*
	KF147915	GRBV	NY271	USA	*Vitis vinifera*
	KU821056	GRBV	SW6	South Korea	*Vitis vinifera*
	KC427993	GRBV	GiGV-WA-RS	USA	*Vitis vinifera*
	KC427994	GRBV	GiGV-WA-DS	USA	*Vitis vinifera*
	KC427995	GRBV	GiGV-WA-MR	USA	*Vitis vinifera* cv. Merlot
	KC427996	GRBV	GiGV-WA-CF	USA	*Vitis vinifera* cv. Cabernet Franc

Figure 1. Genome organisation of viruses in the various genera in the family *Geminiviridae*.

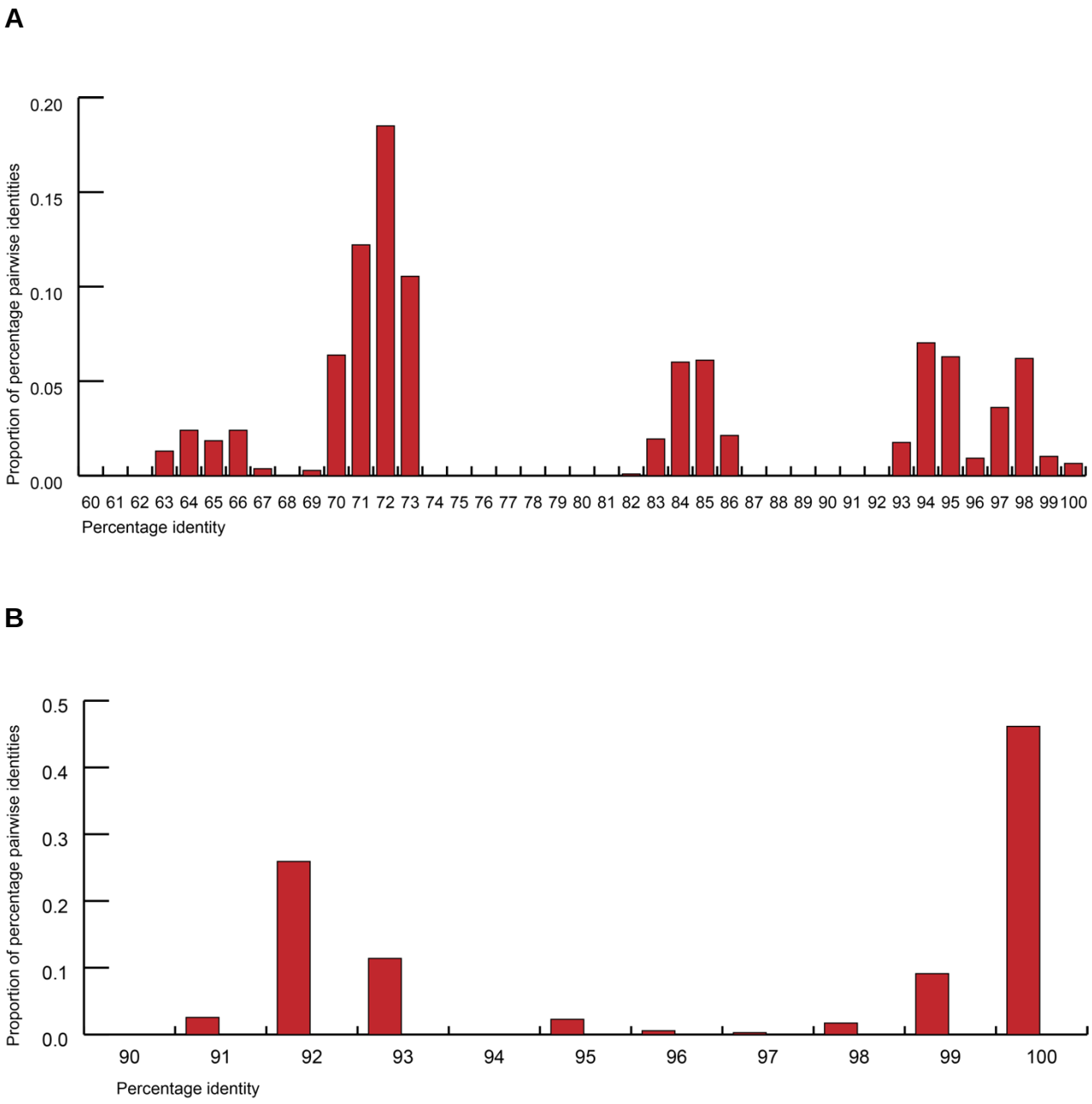

Figure 2. Distribution of genome-wide pairwise identities (47 genomes) of capulaviruses (A) and grabloviruses (B) calculated using SDT v1.2 (Muhire et al., 2014).

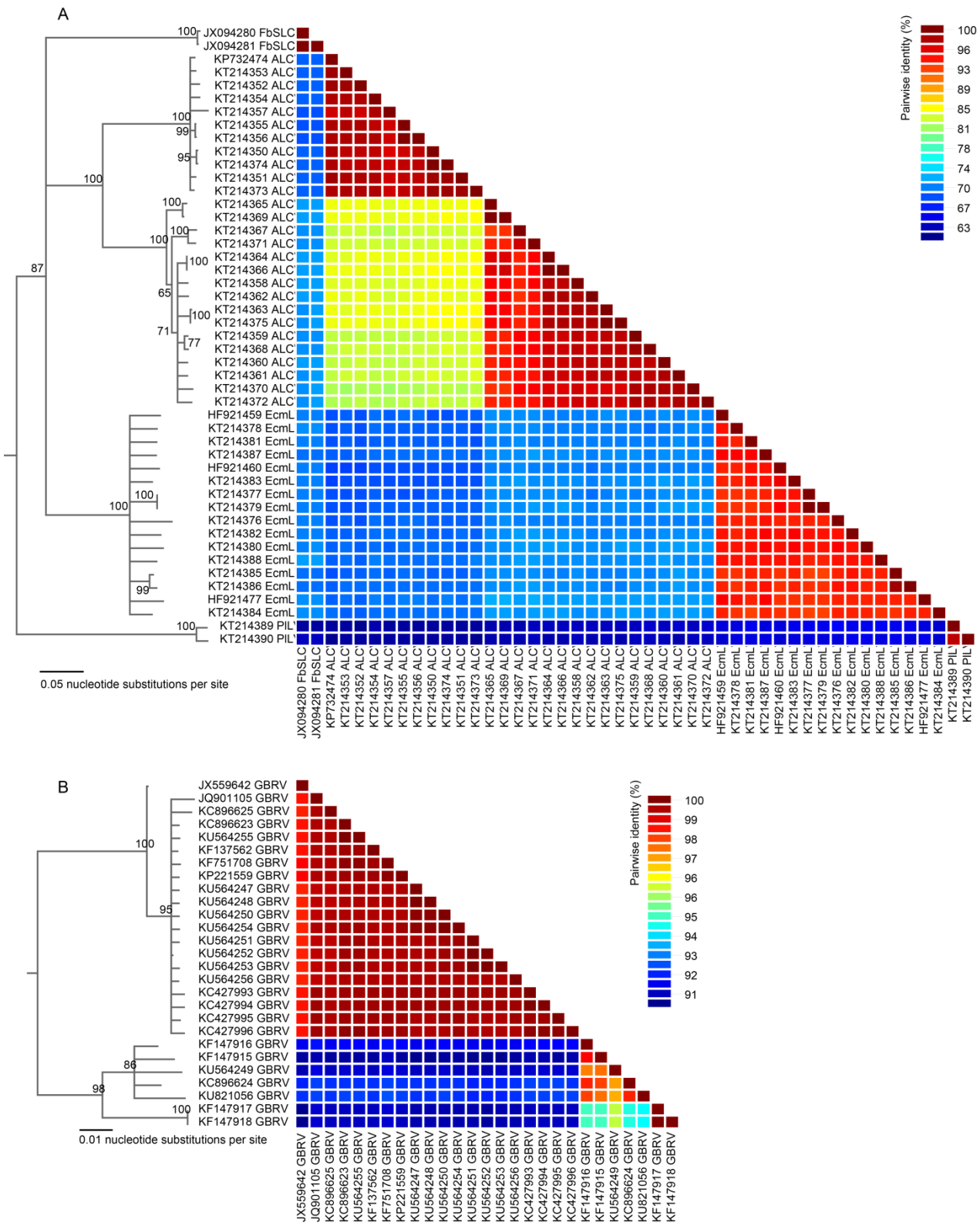

Figure 3. Genome-wide pairwise identities determined using SDT v1.2 (Muhire et al., 2014) and neighbor-joining phylogenetic tree of capulavirus (A) and grablovirus (B) isolates. The trees are rooted with mastrevirus genome sequences.

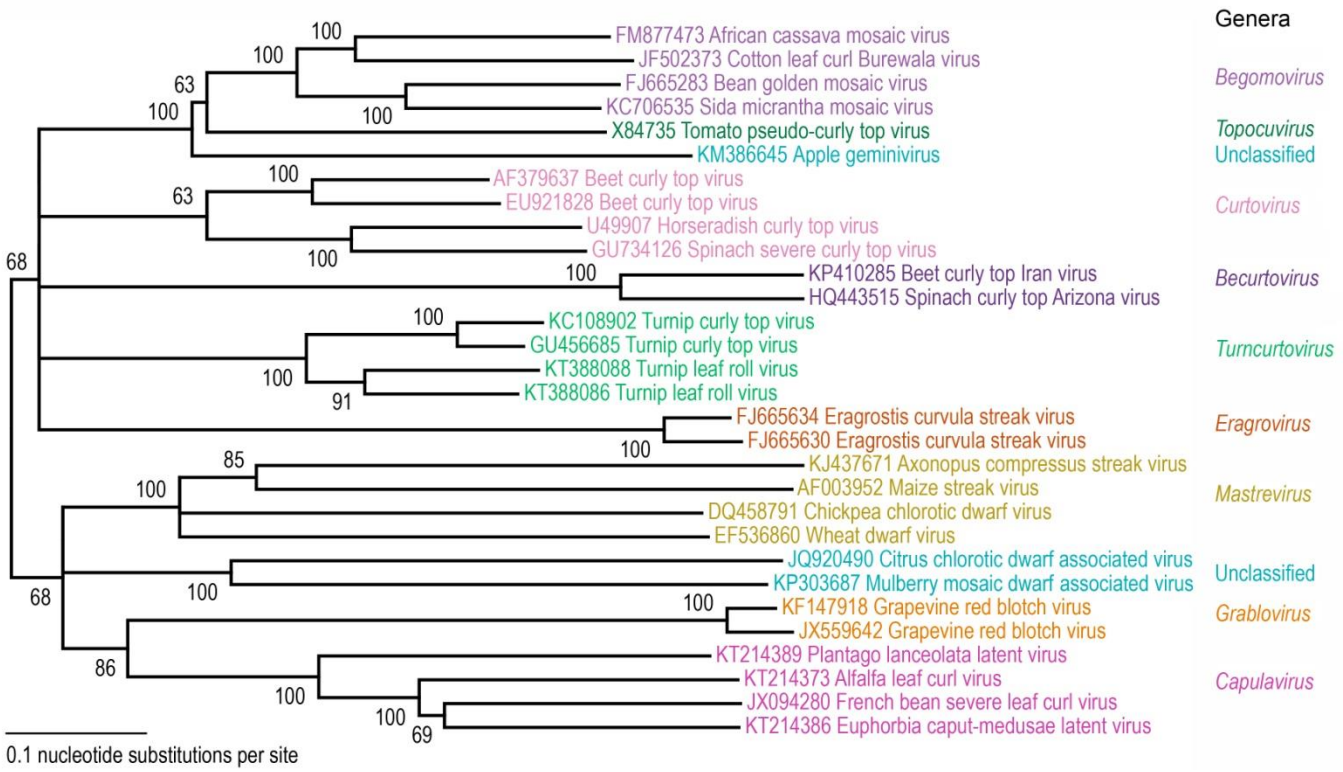

Figure 4. Unrooted phylogenetic tree (neighbour-joining method) inferred from aligned genome sequences of representative isolates from various genera in the *Geminiviridae* family. Numbers at the nodes indicate bootstrap values (2,000 replications).

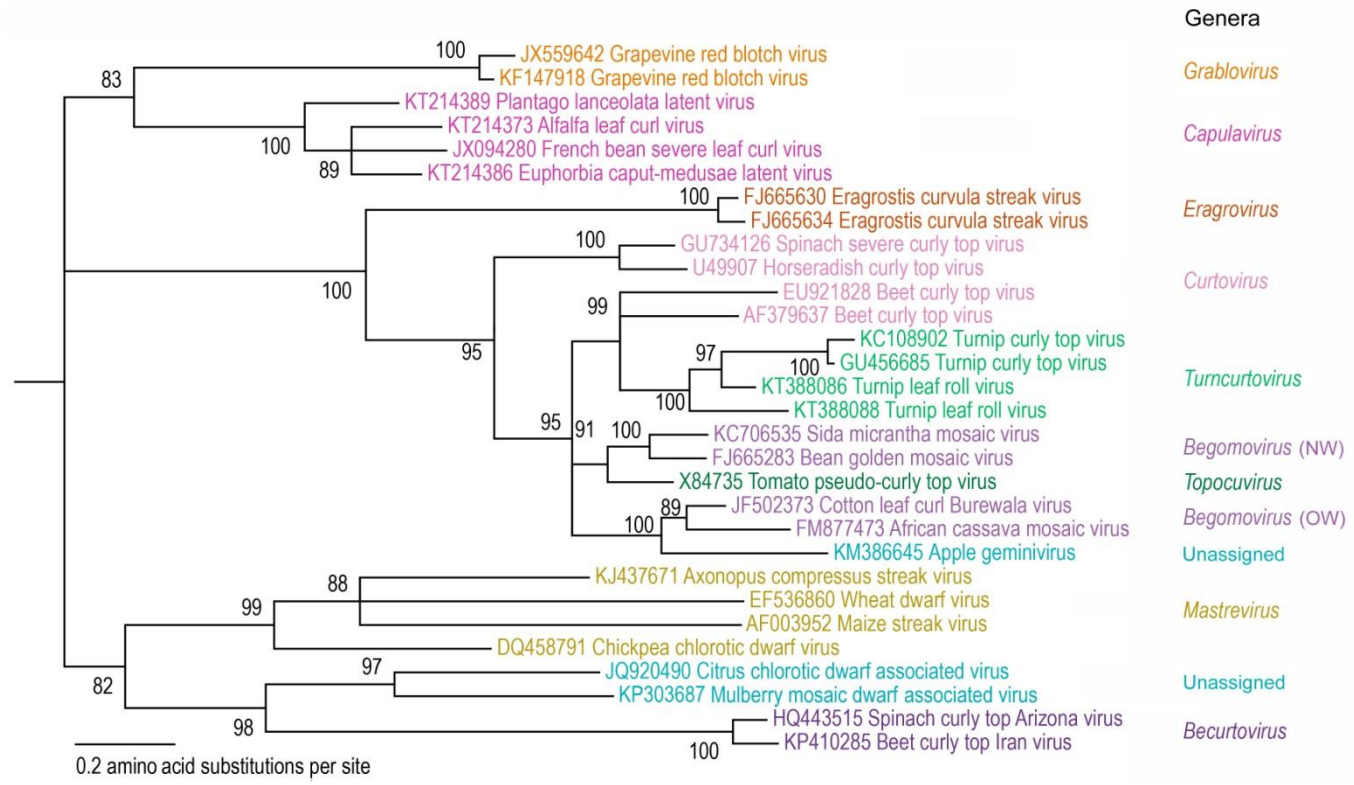

Figure 5. Maximum-likelihood phylogenetic tree (LG+G+I) inferred from aligned Rep sequences of representative isolates from various genera in the *Geminiviridae* family with aLRT branch support. The Rep ML phylogenetic tree is rooted with the Rep sequences of members of the *Genomoviridae* family. Branches with less than 80% bootstrap support (1,000 replications) have been collapsed.

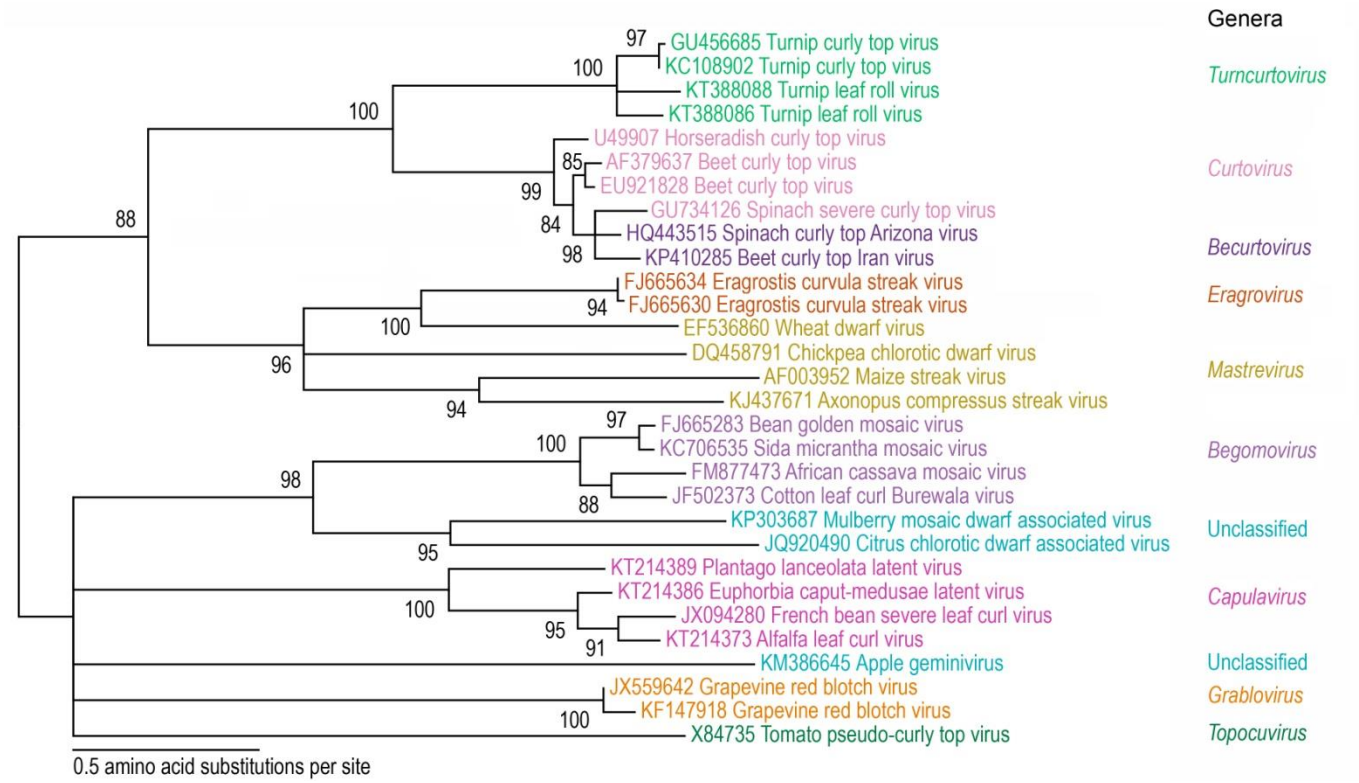

Figure 6. Maximum-likelihood phylogenetic tree (WAG+G+I) inferred from aligned CP sequences of representative isolates from various genera in the *Geminiviridae* family with aLRT branch support. The CP ML phylogenetic tree is mid-point rooted. Branches with less than 80% bootstrap support (1,000 replications) have been collapsed.

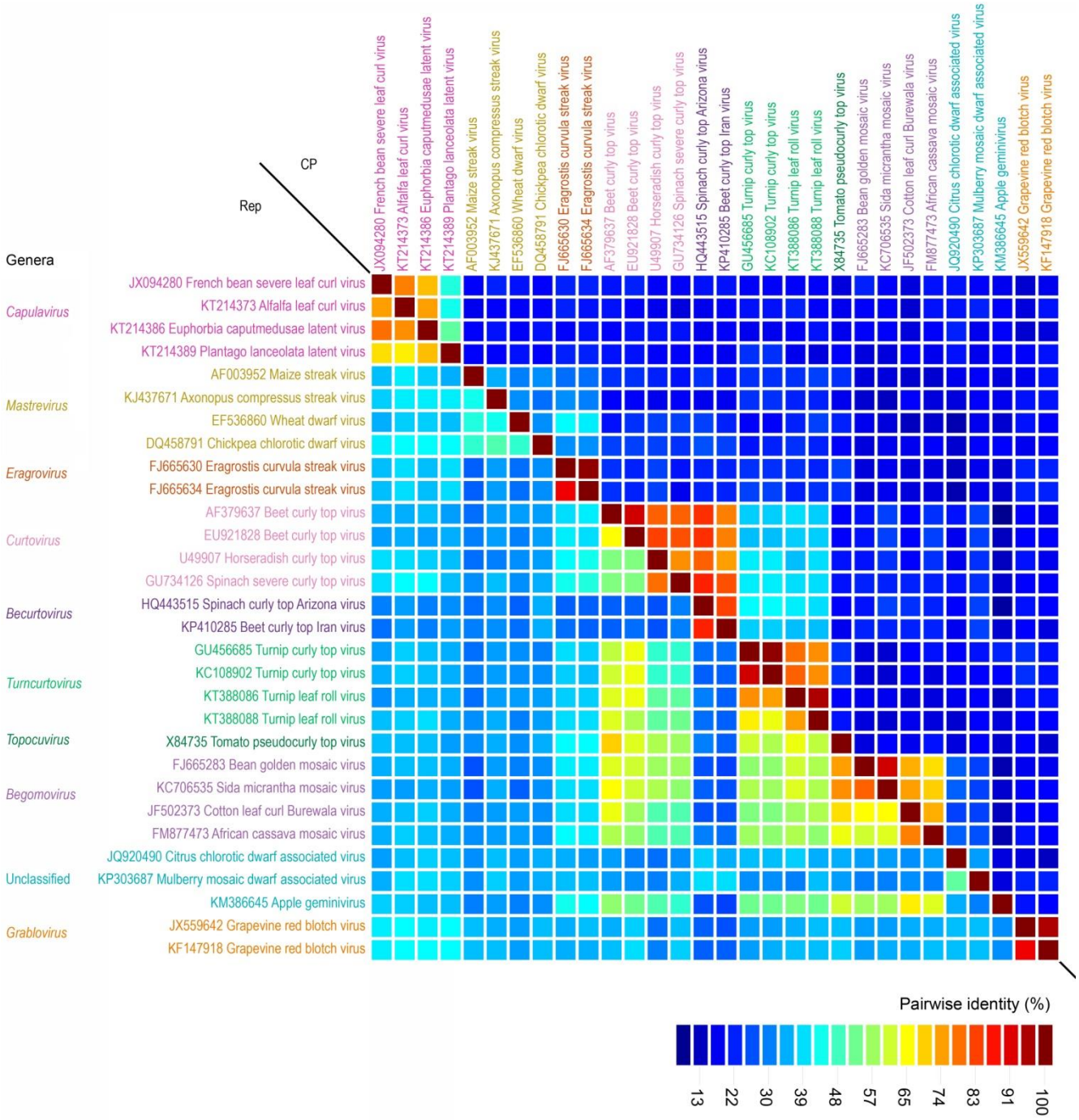

Figure 7. Pairwise identities of the Rep and CP sequences of representative isolates from various genera in the *Geminiviridae* family determined using SDT v1.2 (Muhire et al., 2014).