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:	***2012.018a-pP***	(to be completed by ICTV officers)

Short title: in the family *Geminiviridae*, create two new genera and a new species in the genus *Curtovirus*

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:

J.K. Brown jbrown@ag.arizona.edu (on behalf of the Geminiviridae Study Group)

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

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

Date first submitted to ICTV: June 26, 2012
Date of this revision (if different to above):

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	***2012.018aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Curtovirus***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Spinach severe curly top virus	Spinach severe curly top virus – [US:Arizona:Spinach:2009] **GU734126**

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 meet the >77% proposed genome-wide sequence similarity species demarcation criteria, based on re-evaluated % pairwise identity comparisons (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps, Figure 1) (e.g. previously 89%). Phylogenetically, they all group within the curtovirus genus. Based on maximum likelihood analysis with best fit model: GTR+I+G4 selected by jModeltest; Posada, 2008; Guindon *et al*., 2010; Figure 3). All have a distinctly curtovirus-like genome organization.

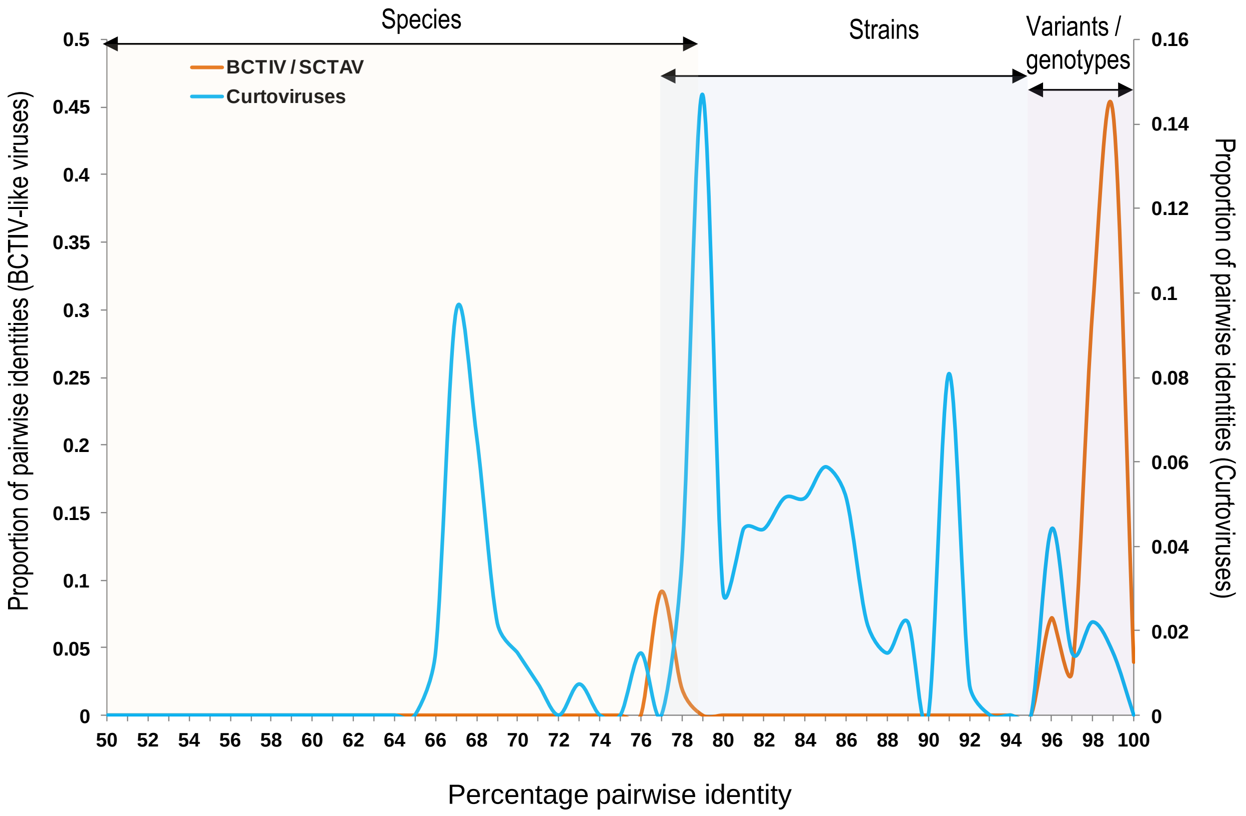

Figure 1. Distribution of curtoviruse and becurtovirus full genome pairwise % nt sequence idenity scores. The 17 curtovirus and 18 becurtovirus sequence pairs were individually aligned to one-another using Muscle (Edgar, 2004) and pairwise Hamming distances (equivalent to p-distances calculated in Mega5.0) were calculated with pairwise deletion of gaps. Similarity scores were calculated as one minus the Hamming distances. Based on the current 17 curtovirus isolates we propose a species demarcation of >77%, and for the BCTIV-like isolates for which there two divergent isolates (17 of the BCTIV isolates share >95% pairwise identities), we propose a cut off of >77%.

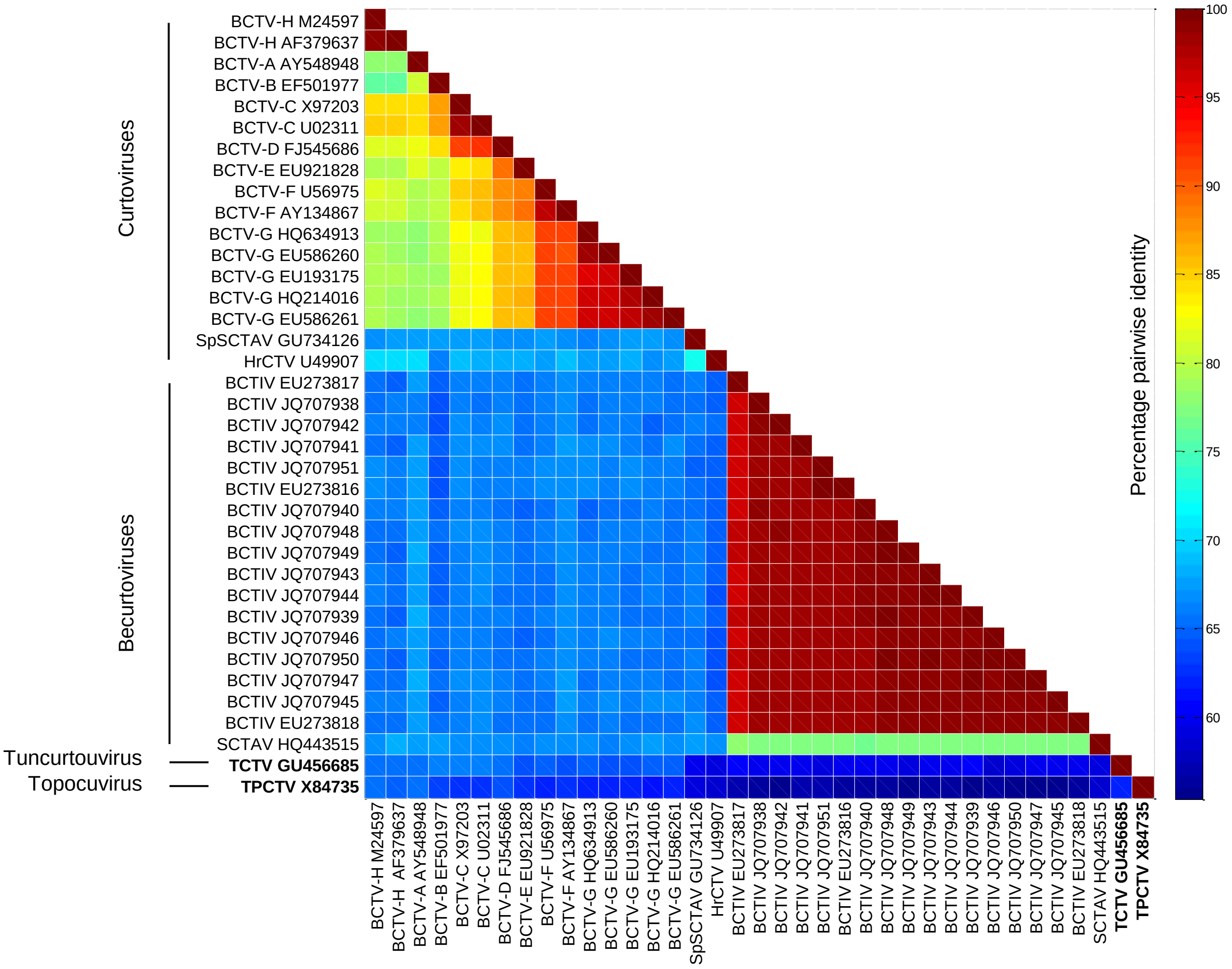

Figure 2. Distribution of curtovirus, becurtovirus, topocuvirus and turncurtovirus full genome pairwise % nt sequence identity scores. The sequence pairs were individually aligned to one-another using Muscle (Edgar, 2004), and pairwise Hamming distances were calculated with pairwise deletion of gaps. Letters (-A, -B, -C, -D, -D, -E, -F and –G) designate strains of BCTV.

]

Maximum likelihood phylogenetic tree (GTR+I+G4)

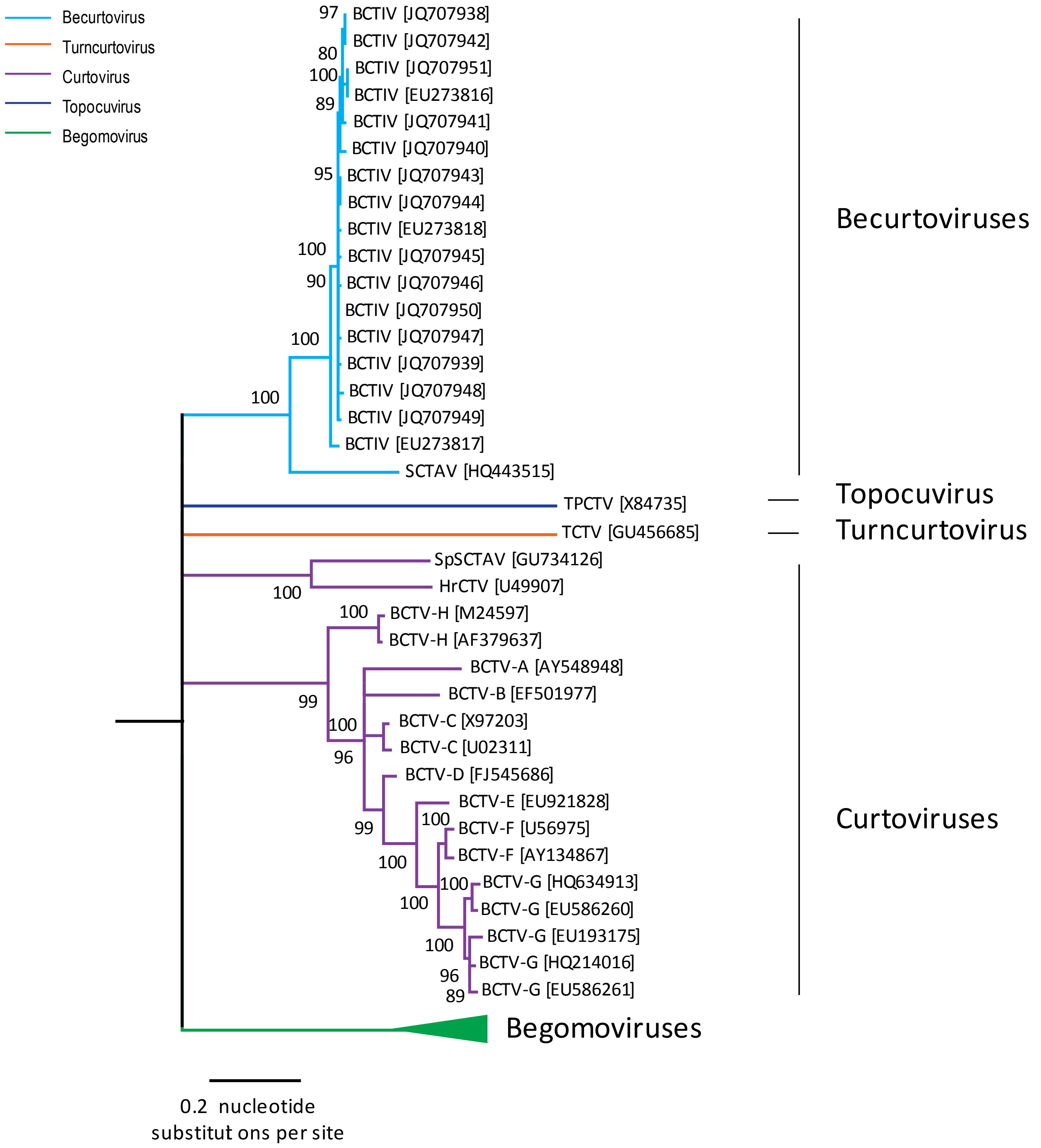

Figure 3. Maximum likelihood phylogenetic tree (with nucleotide substitution model GTR+I+G4; Posada, 2008; Guindon et al., 2010) depicting the likely evolutionary relationships of curtovirus species, and their comparison with the most closely related genera in the geminivirus family. Letters (-A, -B, -C, -D, -D, -E, -F and –G) designate strains of BCTV. The Maximum likelihood phylogenies are inferred using full genomes.

Table 1. Details of curtovirus isolates (A-H denote subclades or strains) and species, and the GenBank accession number, respectively.

Old name	Genbank accesson #	New species names	New acronym and strain
Spinach severe curly top virus	GU734126	Spinach severe curly top virus	SpSCTAV
Horse radish curly top virus	U49907	Horse radish curly top virus	HrCTV
Spinach curly top virus	AY548948	Beet curly top virus - (strain A)	BCTV-A
Pepper curly top virus	EF501977	Beet curly top virus (strain B)	BCTV-B
Beet severe curly top virus	X97203	Beet curly top virus (strain C)	BCTV-C
Beet severe curly top virus	U02311	Beet curly top virus (strain C)	BCTV-C
Beet severe curly top virus	FJ545686	Beet curly top virus –(strain D)	BCTV-D
Pepper yellow dwarf virus	EU921828	Beet curly top virus –(strain E)	BCTV-E
Beet mild curly top virus	U56975	Beet curly top virus – (strain F)	BCTV-F
Beet mild curly top virus	AY134867	Beet curly top virus – (strain F)	BCTV-F
Beet mild curly top virus	HQ634913	Beet curly top virus – (strain G)	BCTV-G
Beet mild curly top virus	EU586260	Beet curly top virus – (strain G)	BCTV-G
Beet mild curly top virus	EU193175	Beet curly top virus – (strain G)	BCTV-G
Beet mild curly top virus	HQ214016	Beet curly top virus – (strain G)	BCTV-G
Beet mild curly top virus	EU586261	Beet curly top virus – (strain G)	BCTV-G
Beet curly top virus	M24597	Beet curly top virus – (strain H)	BCTV-H
Beet curly top virus	AF379637	Beet curly top virus – (strain H)	BCTV-H

Table 2. BCTV isolate names (A-H denote subclades or strains) and the GenBank accession numbers, respectively.

Isolate name	Isolate name (short)	Genbank accession
Spinach severe curly top virus [US:Arizona:Spinach:2009]	SpSCTV [US:AZ:Sp09-10:2009]	GU734126
Horseradish curly top virus [US:Salinas:1988]	HrCTV-[US:Sal:88]	U49907
Beet curly top virus - A [US:Spinach 3:1996]	BCTV-A [US:Sp3:96]	AY548948
Beet curly top virus - B [US:New Mexico:2005]	BCTV-B [US:NM:05]	EF501977
Beet curly top virus - C [Iran:1986]	BCTV-C [IR:86]	X97203
Beet curly top virus - C [US:Cfh]	BCTV-C [US:Cfh]	U02311
Beet curly top virus - D [US:NM:Pepper:2001]	BCTV-D [US:NM:Pep:01]	FJ545686
Beet curly top virus - E [US:New Mexico:2007]	BCTV-E [US:NM:07]	EU921828
Beet curly top virus - F [US:Worland]	BCTV- F [US:Wor]	U56975
Beet curly top virus - F [US:Worland 4]	BCTV-F [US:Wor4]	AY134867
Beet curly top virus - F [Mexico:8-10: 2010]	BCTV-F [MX:8-10:10]	HQ634913
Beet curly top virus - G [Mexico:SLP1:2007]	BCTV-G [MX:SLP1:07]	EU586260
Beet curly top virus - G [Mexico:2006]	BCTV-G [MX:06]	EU193175
Beet curly top virus - G [Mexico:MX-P24:2007]	BCTV-G [MX:MX-P24:07]	HQ214016
Beet curly top virus - G [Mexico:SLP2:2007]	BCTV-G [MX:SLP2:07]	EU586261
Beet curly top virus - H [US:California:1985]	BCTV-H [US:Cal:85]	M24597
Beet curly top virus –H [US:Logan:1976]	BCTV-H[US:Log:76]	AF379637

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	***2012.018bP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Becurtovirus (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Spinach curly top Arizona virus	**HQ443515**

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

See justification in Module 3 below on the creation of genus *Becurtovirus*

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	***2012.018cP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Turncurtovirus (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Turnip curly top virus	**GU456685**

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

See justification in Module 3 below on the creation of genus *Turncurtovirus*

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	***2012.018dP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Eragrovirus (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Eragrostis curvula streak virus	FJ665631

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

See justification in Module 3 below on the creation of genus *Eragrovirus*

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2012.018eP***	(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	***2012.018fP***	(assigned by ICTV officers)

To name the new genus: *Becurtovirus*

Assigning the type species and other species to a new genus

Code	***2012.018gP***	(assigned by ICTV officers)

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

Beet curly top Iran 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: 2**

Beet curly top Iran virus

Beet curly top Iran virus	BCTIV [IR:Kerman:07]	EU273818
Beet curly top Iran virus	BCTIV [IR:Shiraz:07]	EU273817
Beet curly top Iran virus	BCTIV [IR:Yazd:07]	EU273816
Beet curly top Iran virus	BCTIV [IR:Neg:B34P:Sug:08]	JQ707950
Beet curly top Iran virus-	BCTIV [IR:Neg:B32P:Sug:08]	JQ707948
Beet curly top Iran virus-	BCTIV [IR:Dash:B29P:Sug:08]	JQ707946
Beet curly top Iran virus-	BCTIV [IR:Neg:B25P:Sug:08]	JQ707944
Beet curly top Iran virus-	BCTIV [IR:Kam:B23K:Sug:08]	JQ707942
Beet curly top Iran virus-	BCTIV [IR:Neg:B19K:Sug:04]	JQ707940
Beet curly top Iran virus-	BCTIV [IR:Yaz:B15P:Sug:06]	JQ707938
Beet curly top Iran virus-	BCTIV [IR:Yaz:B35K:Sug:06]	JQ707951
Beet curly top Iran virus-	BCTIV [IR:Neg:B33P:Sug:08]	JQ707949
Beet curly top Iran virus-	BCTIV [IR:Neg:B31K:Sug:08]	JQ707947
Beet curly top Iran virus-	BCTIV [IR:Neg:B26P:Sug:08]	JQ707945
Beet curly top Iran virus-	BCTIV [IR:Kam:B24K:Sug:08]	JQ707943
Beet curly top Iran virus-	BCTIV [IR:Kav:B22K:Sug:08]	JQ707941
Beet curly top Iran virus-	BCTIV [IR:Shi:B18K:Sug:06]	JQ707939

Spinach curly top Arizona virus

Spinach curly top Arizona virus	SpSCTV [US:AZ:Spinach:2009]	HQ443515

Reasons to justify the creation of a new genus:

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

- The virion strand origin of replication sequence is TAAGATTCC
- Although the biological properties of BCTIV are most similar to those of curtoviruses, the virus is distinct from curtoviruses in its phylogenetic relationship (Figure3) and genome organisation (Figure 4). For example, the replication-associated (initiation) protein is more closely related to mastreviruses than curtoviruses whereas the coat protein is more curotvirus-like (at 77-83% amino acid identity; Figure 5).
- Based on the distribution of the pairwise identities of the 18 becurtoviruses (Figure 1) a >77% cut off is established for species demarcation. BCTIV shares ~ 77% pairwise identity with Spinach curly top Arizona virus (SCTAV) and therefore the two are distinct species.
- BCTIV is transmitted by the leafhopper vector *Circulifer haematoceps* (Mulsant et Rey) (Cicadellidae), a close relative of the beet leafhopper (BCTV vector), extant in the Mediterranean and Near East.

Origin of the new genus name:

<u>Be</u>et <u>cu</u>rtly <u>to</u>p Iran <u>virus</u>

Reasons to justify the choice of type species:

BCTIV and SCTAV share 77% pairwise identity, and therefore are distinct species.

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.

Analysis of the % nt pairwise identity genome sequence comparisons (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps, Figure 1) revealed a gap located at approximately 77-80%. Based on this isolates that share <80% genome wide pairwise nt identity are considered distinct species in the genus, *Becurtovirus*.

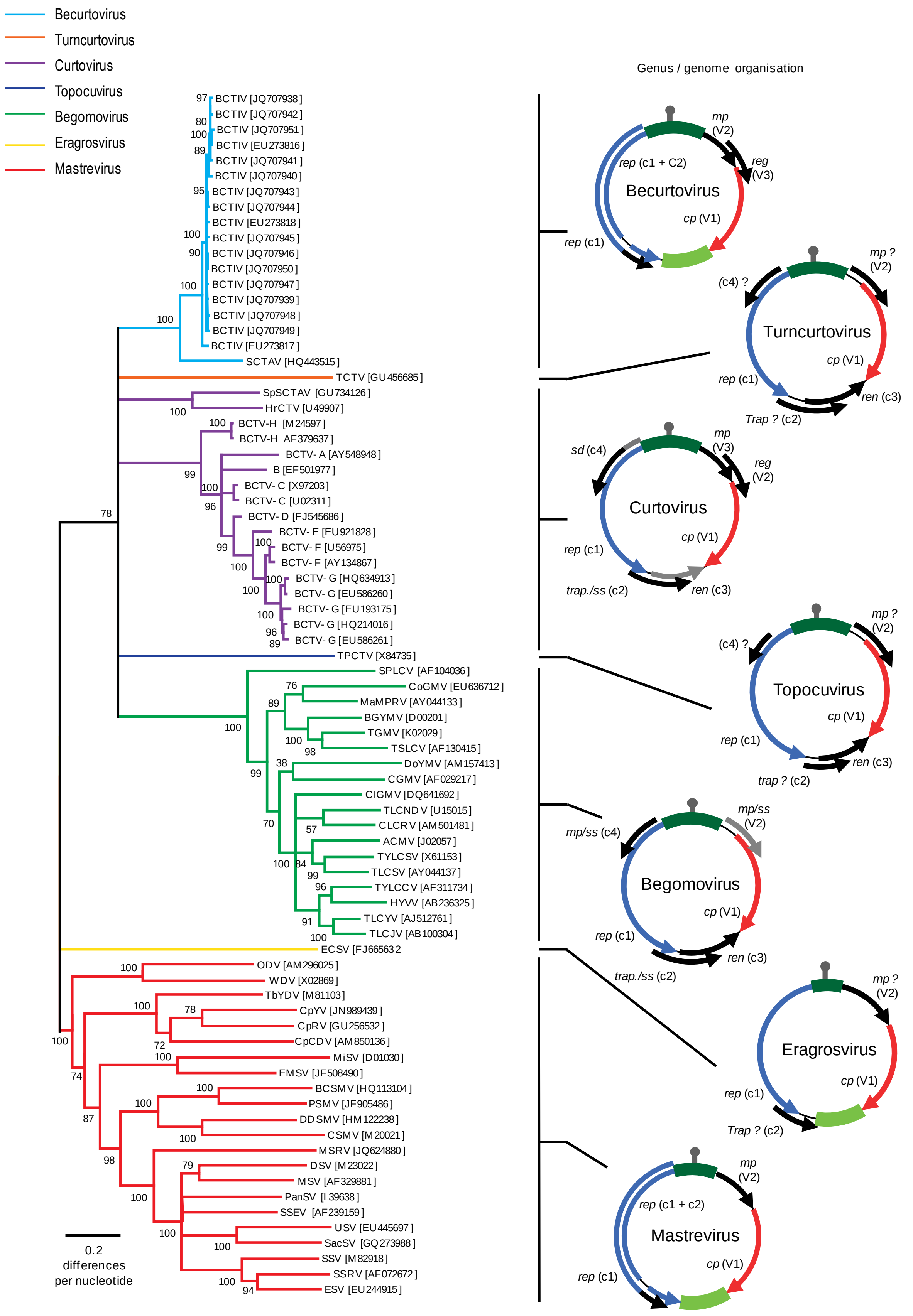

Figure 4. Maximum likelihood tree (based on alignment of complete genome sequences) of becurto-, turncurto-, eragros-, curto-, topocu- viruses and other representative geminiviruses, constructed using PhyML with GTR+I+G4. The genome organization for each genus is shown.

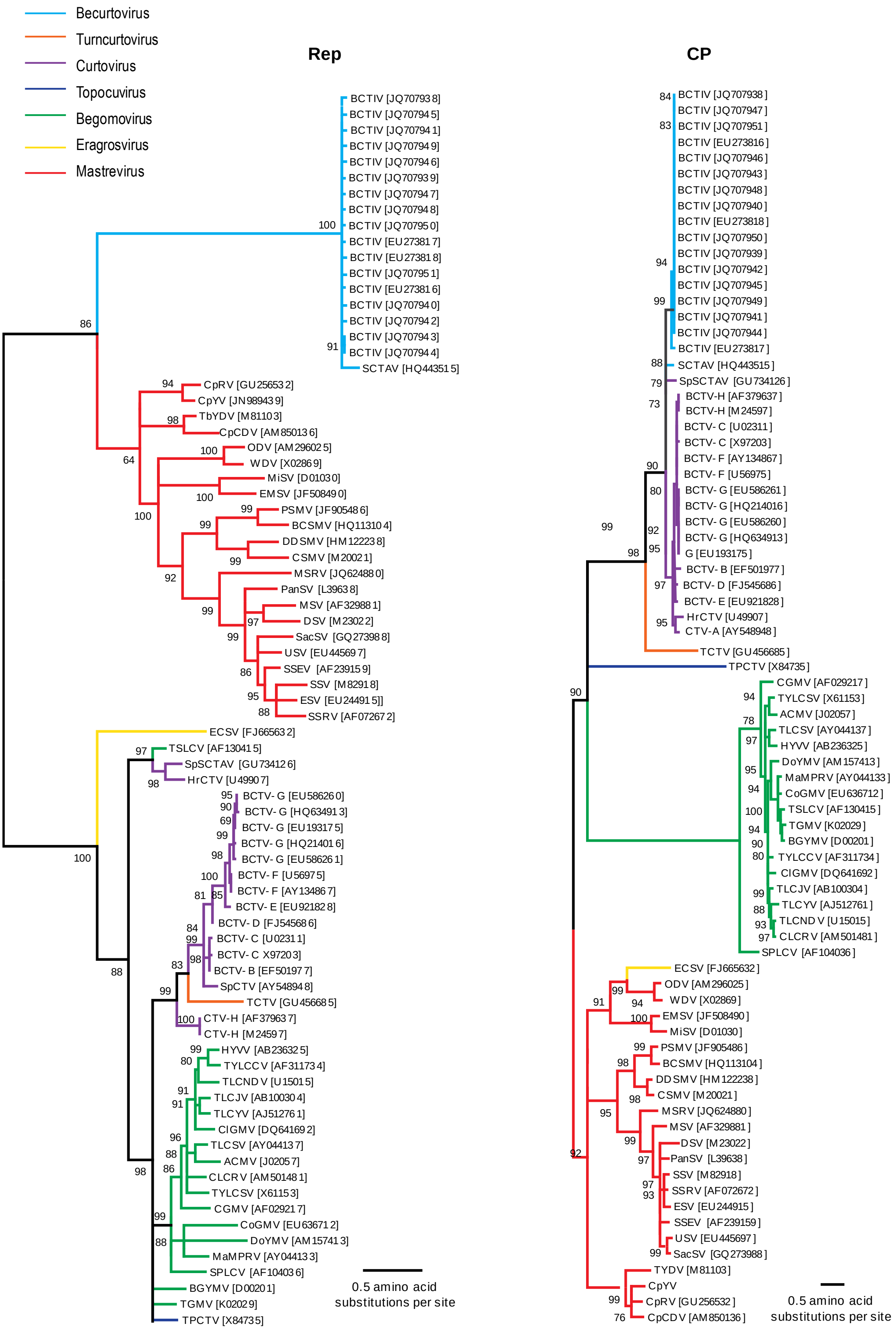

Figure 5: Maximum likelihood relationships based upon alignment of the predicted amino acid sequences of the replication-associated (initiator) protein (Rep) and coat protein (CP) of becurto-, turncurto-, eragros-, curto-, topocu- viruses and representative geminiviruses, constructed with PhyML using the LG model with chi-squared aLRT branch support.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2012.018hP***	(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	***2012.018iP***	(assigned by ICTV officers)

To name the new genus: *Turncurtovirus*

Assigning the type species and other species to a new genus

Code	***2012.018jP***	(assigned by ICTV officers)

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

Turnip curly top 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: 1**

Turnip curly top virus

Turnip curly top virus	TCTV [IR:Zaf:B11:06]	GU456685
Turnip curly top virus	TCTV [IR:Hom2:8k:09]	GU456687
Turnip curly top virus	TCTV [IR:Hom3:7k:09]	GU456689
Turnip curly top virus	TCTV [IR:Hom3:4k:09]	GU456688
Turnip curly top virus	TCTV [IR:Hom:T57K:Tur:10]	JQ742019
Turnip curly top virus	TCTV [IR:Hom1:2k:09;]	GU456686

Reasons to justify the creation of a new genus:

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

- TCTV is as divergent from *members of the genus, Curtovirus* as is TPCTV, the latter being the only known member of the distinct genus *Topocurvirus* (Figure 3).
- TCTV has a genome arrangement in the complementary-sense similar to that of curtoviruses (consisting of four overlapping genes) but only two open reading frames in the virion-sense (the curtoviruses encode three) (Figure 4). The complementary-sense genes are homologous to those of curtoviruses but show little sequence identity to their curtovirus homologs, with the exception of the product of the C4 open reading frame (ORF) which shows ~70.6% amino acid sequence identity to the C4 of the North American curtoviruses.
- The virion-sense predicted product of the V2 ORF of TCTV shows no significant similarity with any proteins in public databases, whereas the product of the V1 ORF (encoding the coat protein of geminiviruses) shows low levels of sequence identity to curtovirus CPs.

Reasons to justify the creation of a new genus:

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

Notes:
No information is currently available on the viral host range except that it infects turnip plants. The insect vector remains to be identified.

Origin of the new genus name:

Turnip curly top virus

Reasons to justify the choice of type species:

Currently, there is one species placed in this 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 this genus contains only one species and all isolates share >90% identity. Projecting from the *Mastrevirus* and *Curtovirus* proposed species demarcations, new isolates that share <*80%* genome wide pairwise nt identity will be classified as *Turncurtovirus* species.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2012.018kP***	(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	***2012.018lP***	(assigned by ICTV officers)

To name the new genus: *Eragrovirus*

Assigning the type species and other species to a new genus

Code	***2012.018mP***	(assigned by ICTV officers)

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

Eragrostis curvula streak 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: 1**

Eragrostis curvula streak virus

Eragrostis curvula streak virus	ECSV-[ZA:Esc1:g382:08]	FJ665631
Eragrostis curvula streak virus	ECSV-[ZA:Gre3:g257:07]	FJ665632
Eragrostis curvula streak virus	ECSV-[ZA:Gre4:Ky3:08]	FJ665630
Eragrostis curvula streak virus	ECSV-[ZA:Gre5:Ky6:08]	FJ665634
Eragrostis curvula streak virus	ECSV-[ZA:Gre1:g261:07]	FJ665633
Eragrostis curvula streak virus	ECSV-[ZA:Gre2:g256:07]	FJ665629

Reasons to justify the creation of a new genus:

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

- ECSV has an unspliced Rep, and a unique genome organization (Figure 4).
- ECSV has a unique TAAGATTCC virion strand origin of replication (similar to BCTIV)
- Most transcription and replication origins are structurally more similar to those found in begomoviruses and curtoviruses, than to those of BCTIV and the genus mastrevirus.
- Superficially, exemplars resemble a chimera representing different geminivirus genera. The ECSV genome is not an obvious recombinant. Collectively, data suggest that the features it shares in common with other extant geminiviruses are those that were probably present within the last common ancestor of all of them.
- The C2 ORF is a positional analog of begomovirus, topocuvirus, and curtovirus TrAP/TrAP-like genes (Figure 4).

Reasons to justify the creation of a new genus:

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

- The CP of ECSV is most similar to those of the Eurasian mastreviruses -WDV and ODV
- The ECSV Rep appears most closely related to the Rep of begomoviruses, curtoviruses, and topocuviruses; the rep-associated (initiator) protein gene of these three genera share a far more recent common ancestor than do their coat protein genes.
- ECSV represents a new genus-level geminivirus group displaying a mixture of characteristics normally associated with specific geminivirus genera.
- As the most divergent geminivirus species yet identified, the genome features that ECSV shares with other geminiviruses provides some indication of what the last common ancestor of the geminiviruses may have looked like.

Notes:

No information is currently available regarding the host range of ECSV, other than that it infects *Eragrostis curvula.* The insect vector remains to be identified.

Origin of the new genus name:

Eragrostis curvula streak virus

Reasons to justify the choice of type species:

Currently, ECSV is the only species in this 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, ECSV is the only known species and all isolates share >90% identity. Projecting from mastrevirus and curtovirus proposed species demarcation the isolates sharing <80% genome wide pairwise identity are classified as *Eragrovirus* species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

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

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

Code	***2012.018nP***	(assigned by ICTV officers)

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

Spinach curly top virus
Pepper curly top virus
Beet severe curly top virus
Beet mild curly top virus

The present taxonomic position of these taxon/taxa:

Genus:	***Curtovirus***	Fill in all that apply.
Subfamily:		
Family:	***Geminiviridae***	
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:
Spinach curly top virus, *Pepper curly top virus*, *Beet severe curly top virus*, , *Beet mild curly top virus* isolates share are >80% similar to *Beet curly top virus* isolates. Based on this new working cutoff they are all considered strains or isolates of *Beet curly top virus* (BCTV). Letters are used to designate isolates or strains that group as members of the same subclade (e.g. BCTV-A, BCTV-B etc).

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

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

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

Code	***2012.018oP***	(assigned by ICTV officers)

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

Beet curly top Iran virus

The present taxonomic position of these taxon/taxa:

Genus:	***Curtovirus***	Fill in all that apply.
Subfamily:		
Family:	***Geminiviridae***	
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:
See justification in Module 3 (above) on the creation of the genus *Becurtovirus*

Part (b) re-assign to a higher taxon

Code	***2012.018pP***	(assigned by ICTV officers)

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

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

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See justification in Module 3 (above) on the creation of the genus *Becurtovirus*

MODULE 9: **APPENDICES**: none
All supporting materials are included in this proposal.

References:

Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research. 32: 1792-97.

Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W., Gascuel O. 2010. New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Systematic Biology, 59:307-21, 2010.

Posada D. 2008. jModelTest: Phylogenetic Model Averaging. Molecular Biology and Evolution. 25: 1253-1256.

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.

Comparison of the old and proposed new taxonomy: summary of the proposed changes

OLD TAXONOMY
Curtovirus
Beet curly top Iran virus (will be moved to new genus *Becurtovirus*)
Beet curly top virus
Beet mild curly top virus (will become an isolate of *Beet curly top virus* and species will be removed)
Beet severe curly top virus (will become an isolate of *Beet curly top virus* and species will be removed)
Horseradish curly top virus
Pepper curly top virus (will become an isolate of *Beet curly top virus* and species will be removed)
Spinach curly top virus (will become an isolate of *Beet curly top virus* and species will be removed)
Topocuvirus
Tomato pseudo-curly top virus

PROPOSED NEW TAXONOMY
Curtovirus
Beet curly top virus
Horseradish curly top virus
Spinach severe curly top virus (new species)
Topocuvirus
Tomato pseudo-curly top virus
Becurtovirus (new genus)
Beet curly top Iran virus (moved from genus *Curtovirus)*
Spinach curly top Arizona virus (new species)
Turncurtovirus (new genus)
Turnip curly top virus (new species)
Eragrovirus (new genus)
Eragrostis curvula streak virus (new species)