



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:	2009.014c-fP	(to be completed by ICTV officers)			
Short title: create 1 species in the genus Curtovirus and 3 species in the genus Mastrevirus, family Geminiviridae (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>	

Author(s) with e-mail address(es) of the proposer:

Judith Brown on behalf of the Geminiviridae Study Group. E-mail: jbrown@Ag.arizona.edu

Has this proposal been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	Yes
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ICTV-EC or Study Group comments and response of the proposer:

The EC considered that parts a,b of the original proposal (for species in the genus *Begomovirus*) required further work by the SG. The document has therefore been divided to allow the remaining sections to be advanced more quickly.

Date first submitted to ICTV: May 3, 2009
Date of this revision (if different to above): June 12, 2009

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	2009.014cP	(assigned by ICTV officers)
To create 1 new species with the name(s):		
<i>Beet curly top Iran virus</i>		

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	2009.014dP	(assigned by ICTV officers)
To assign the species listed in section 2(a) as follows:		
Genus:	<i>Curtovirus</i>	Fill in all that apply. <ul style="list-style-type: none"> • 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:	<i>Geminiviridae</i>	
Order:		

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Criteria established by the Study Group for the creation of new species in the genus are that:

- (a) There should be at least one complete monopartite genome sequence of the proposed new species.
- (b) There should be less than about 89% nucleotide sequence identity between isolates of the proposed new species and those of existing species in the genus.

The complete genome (BCTIRV-[IR;Arm;07], EU273818) is not very closely related to any of the existing sequences in the genus (40.3% nt identity to Spinach curly top virus (SpCTV-[US;Sp3;96], AY548948). However, the coat protein is ~80% identical to *Beet severe leaf curl virus*, suggesting a common ancestor. This geminivirus has some unique characteristics (nonanucleotide) and may share some features with other genera; it may ultimately represent a separate genus (Yazdi et al., 2008). For now we recommend placement in the genus *Curtovirus* until further studies can be carried out.

See also the phylogenetic tree (figure) and Table 1 (pairwise % nt identity matrix) in the Appendix (module 9).

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	2009.014eP	(assigned by ICTV officers)
To create 3 new species with the name(s):		
<i>Eragrostis streak virus</i>		
<i>Setaria streak virus</i>		
<i>Urochloa streak virus</i>		

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	2009.014fP	(assigned by ICTV officers)
To assign the species listed in section 2(a) as follows:		
Genus:	<i>Mastrevirus</i>	Fill in all that apply. <ul style="list-style-type: none"> • 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:	<i>Geminiviridae</i>	
Order:		

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Criteria established by the Study Group for the creation of new species in the genus are that:

- (a) There should be at least one new monopartite genome sequence.
- (b) There should be less than about 75% nucleotide sequence identity between isolates of the proposed new species and those of existing species in the genus.

NOTE: The SG is discussing altering the working cutoff to 89% as for the other genera but no consensus has been reached.

Accession details and the most closely related members of other species in the genus are:

Virus	Nearest neighbour	% nt identity
ESV-[ZM;Gur186;07].EU244915	SSREV-[RE;574].AF072672	70.6
SetSV-A[MZ;g201;07].EU628623	DSV-VU].M23022	49.5
UroSV-[NG;g74.07].EU445692	MSV-A[KE;Ama;98].AF329878	51.8

See also the phylogenetic tree (figure) and Table 2 (pairwise % nt identity matrix) in the Appendix (module 9).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Yazdi, H.R., Heydarnejad, J., and Massumi, H. 2008. Genome characterization and genetic diversity of beet curly top Iran virus: a geminivirus with a novel nonanucleotide. <i>Virus Genes</i> 36: 539-545.
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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.

Figure 1. Section of phylogenetic tree of the complete genomes (or A-components) of isolates of all recognized and proposed species in the family Geminiviridae. The subjects of this proposal are marked with *.

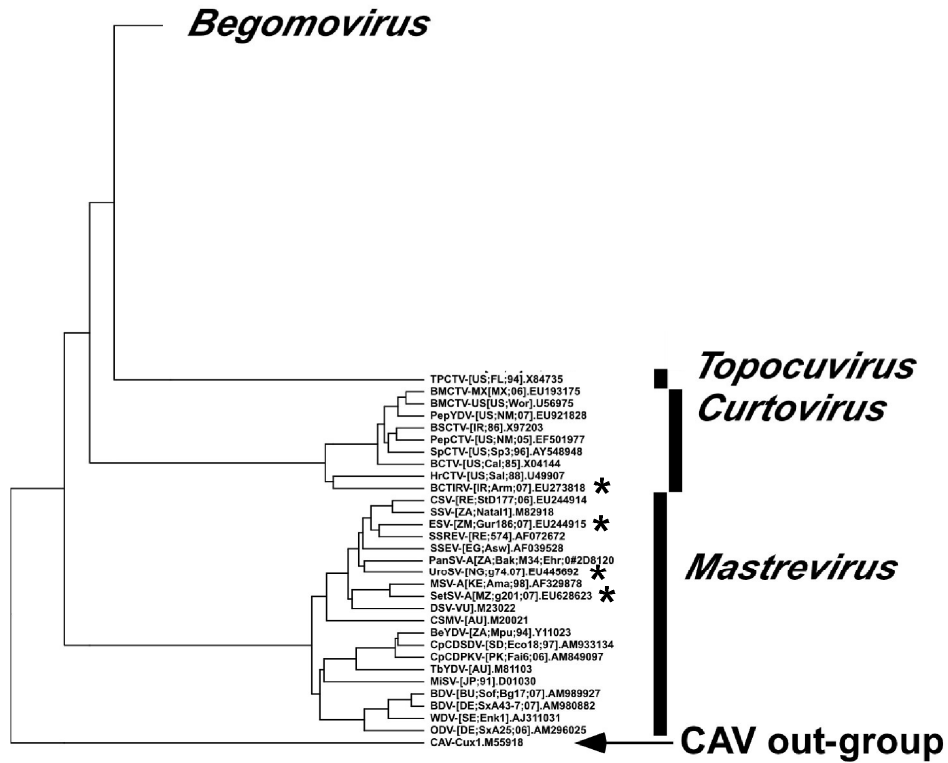


Table 1. Pairwise nucleotide identity matrix for comparisons between complete genomes of isolates of species in the genus *Curtovirus*. The proposed new species is highlighted.

Virus and isolate details	BMCTV-MX[MX;06].EU193175	PepYDV-[US;NM;07].EU921828	BSCTV-[IR;86].X97203	PepCTV-[US;NM;05].EF501977	SpCTV-[US;Sp3;96].AY548948	BCTV-[US;Cal;85].X04144	HrCTV-[US;Sal;88].U49907	BCTIRV-[IR;Arm;07].EU273818
BMCTV-MX[MX;06].EU193175	***	81.6	73.7	70.5	69.6	70.8	46.2	40.1
PepYDV-[US;NM;07].EU921828		***	75.0	72.5	74.5	70.6	50.5	38.8
BSCTV-[IR;86].X97203			***	82.2	80.3	77.0	47.5	39.9
PepCTV-[US;NM;05].EF501977				***	74.3	65.8	48.3	38.8
SpCTV-[US;Sp3;96].AY548948					***	69.5	51.8	40.3
BCTV-[US;Cal;85].X04144						***	52.1	39.9
HrCTV-[US;Sal;88].U49907							***	39.0
BCTIRV-[IR;Arm;07].EU273818								***

Table 2. Pairwise nucleotide identity matrix for comparisons between complete genomes of isolates of species in the genus *Mastrevirus*. The three proposed new species are highlighted.

virus	ESV	SSREV	SSEV	PanSV	UroSV	MSV	SetSV	DSV	CSMV	BeYDV	CpCSDSV	CpCDPKV	TbYDV	MiSV	BDV	WDV	ODV
SSV	69.0	65.6	58.7	52.5	53.5	47.3	49.3	49.2	31.3	32.3	32.3	32.5	31.8	27.2	28.4	29.9	31.1
ESV	***	70.6	61.7	54.3	56.9	47.5	50.6	50.5	30.9	34.4	32.2	31.7	33.3	29.0	30.2	31.0	29.8
SSREV		***	59.4	55.4	55.3	46.8	49.1	51.1	31.4	33.7	31.7	33.1	30.5	27.7	27.9	28.7	29.7
SSEV			***	57.1	59.4	49.5	53.3	52.5	34.2	31.3	31.6	31.4	31.4	31.0	30.9	30.2	31.4
PanSV				***	57.8	53.0	51.4	49.2	33.2	32.5	32.6	31.8	31.4	27.1	31.8	30.5	31.3
UroSV					***	51.8	50.5	48.6	32.6	32.4	33.1	31.6	30.9	30.2	30.9	29.8	29.6
MSV						***	77.7	51.5	33.8	31.7	31.7	31.0	29.4	28.2	25.0	27.6	29.6
SetSV							***	49.5	36.2	31.7	31.6	31.9	31.2	28.3	30.2	27.5	29.6
DSV								***	30.9	34.1	32.7	32.0	31.2	28.3	30.0	25.5	31.6
CSMV									***	31.5	31.1	33.4	33.8	32.0	29.4	28.5	29.7
BeYDV										***	83.4	80.8	55.4	30.4	32.8	30.9	31.9
CpCSDSV											***	82.3	55.0	32.1	32.2	30.5	32.2
CpCDPKV												***	54.8	32.3	33.6	31.3	31.8
TbYDV													***	33.4	34.2	33.8	31.9
MiSV														***	31.5	31.1	30.4
BDV															***	80.0	59.9
WDV																***	60.9

Isolates used are: SSV=[ZA;Natal1].M82918, ESV=[ZM;Gur186;07].EU244915, SSREV=[RE;574].AF072672, SSEV=[EG;Asw].AF039528, PanSV=A[ZA;Bak;M34;Ehr;0#2D8120, UroSV=[NG;g74.07].EU445692, MSV=A[KE;Ama;98].AF329878, SetSV=A[MZ;g201;07].EU628623, DSV=VU].M23022, CSMV=[AU].M20021, BeYDV=[ZA;Mpu;94].Y11023, CpCSDSV=[SD;Eco18;97].AM933134, CpCDPKV=[PK;Fai6;06].AM849097, TbYDV=[AU].M81103, MiSV=[JP;91].D01030, BDV=[BU;Sof;Bg17;07].AM989927, WDV=[SE;Enk1].AJ311031, ODV=[DE;SxA25;06].AM296025