Template for Taxonomic Proposal to the ICTV Executive Committee
Removing Species in an existing genus

Code[†] 2007.002P.04 To remove the following as species in the genus:

Begomovirus

belonging to the family° : ***Geminiviridae***

6 species (merging 12 species into 5)
(see list below)

[†] Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order

Order	
Family	***Geminiviridae***
Genus	***Begomovirus***
Type Species	
Species in the Genus	
Tentative Species in the Genus	
Unassigned Species in the family	

New Taxonomic Order

Order	
Family	***Geminiviridae***
Genus	***Begomovirus***
Type Species	
Species in the Genus	
Tentative Species in the Genus	
Unassigned Species in the family	

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

The following criteria should be used as a guideline to establish taxonomic status:

- Number of genomic components. Presence or absence of a DNA B component
- Organization of the genome. Presence or absence of ORF AV2.
- Nucleotide sequence identity. Because of the growing number of recognized species, derivation of the complete nucleotide sequence will be necessary to distinguish species. Nucleotide sequence identity <89% is generally indicative of a distinct species. However, decisions based on nucleotide sequence comparisons, particularly when approaching this value, must take into account the biological properties of the virus. The taxonomic status of a recombinant will depend on relatedness to the parental viruses, the frequency and extent of recombination events, and its biological properties compared with the parental viruses. Information concerning the diversity of related recombinants may be helpful to determine status.
- *Trans*-replication of genomic components. The inability of Rep protein to *trans*-replicate a genomic component suggests a distinct species. However, when considering this criterion, it should be kept in mind that small changes in the Rep binding site of otherwise identical viruses might prevent functional interaction, and recombination involving a small part of the genome may confer replication competence on a distinct species.
- Production of viable pseudorecombinants. Account should be taken of the fitness of the pseudorecombinant in the natural host(s) of the parental viruses. It should be ensured that pseudorecombinant viability is not the result of inter-component recombination.
- Coat protein characteristics. Amino acid sequence identity <90% and substantial serological differences may be indicative of a distinct species in the first instance, but derivation of the complete sequence will be necessary to confirm taxonomic status.

Argument to justify the removal of species in the genus

Homogeneous classification of geminivirus isolates into strains and species

Of 252 isolates, representing 209 species, 102 cluster in more than one strain per species but only 37 of those present some degree of heterogeneity at the species level worth considering (Fig. 1). The other 65 isolates comply with the 89% rule, showing an intra-species pairwise nucleotide identity of 91%. The remaining 37 isolates, currently belonging to 17 species, can be divided into two categories. In the first category, 17 isolates, belonging to 5 species, have intra-species pairwise comparisons that are below the species threshold level. In the second category, 20 isolates, belonging to 14 species, have pairwise comparisons above the species threshold (Fig. 2). This heterogeneity reflects in part the history of geminivirus taxonomy and in part the difficulty in some instances to allocate a virus isolate to the correct species, or the lack of precise guidelines to allocate an isolate to a specific species. The geminiviridae Study-group proposes to correct the heterogeneity of geminivirus isolates at the strain level by including in the same species a number of isolates previously belonging to different species.

In the first category of strains that have intra-species pairwise comparisons below the species level, it is clear that recombination between different isolates led to higher levels of identity between them, constituting a set of viruses that is best kept together as a single species. The example for this situation is the TYLCV cluster, comprising five strains with pairwise percentages from 92 to 85% (Fig 1).

The second category corresponds to viruses belonging to different species for which intermediates have been found or for which, with hindsight, anomalous decisions have been made over the years. A good example is the cluster including TbLCJV-[JR;3] and HYVKgV-[JR;TobKG5]. For these isolates the species threshold was set at 90%. At a 89% threshold these five viruses would be classified as three species. Similarly PYMTV, but not PYMPV, would be clustered with PYMV. Another example, where intermediates have been found, is the AYVCNV/AYVV cluster. It is now clear that this cluster resembles the TYLCV cluster and therefore should be treated similarly. The ToLCIRV/ToLCKV and CLCuMV/CLCuRV clusters are of the same category and should also be reconsidered as a single species (Fig. 2).

If the clusters of the second category are reclassified in single species, the intra-species pairwise percentages for the 21 clusters vary between 92% and 88%, and the inter-species pairwise percentages vary between 62% and 86% (Fig. 2).

Figure 1: Distribution of pairwise sequence comparison (PASC) identity percentages between DNA-A sequences for 672 geminivirus isolates, under the species level; A) for all isolates, B) for members of the strain level, and C) for variants.

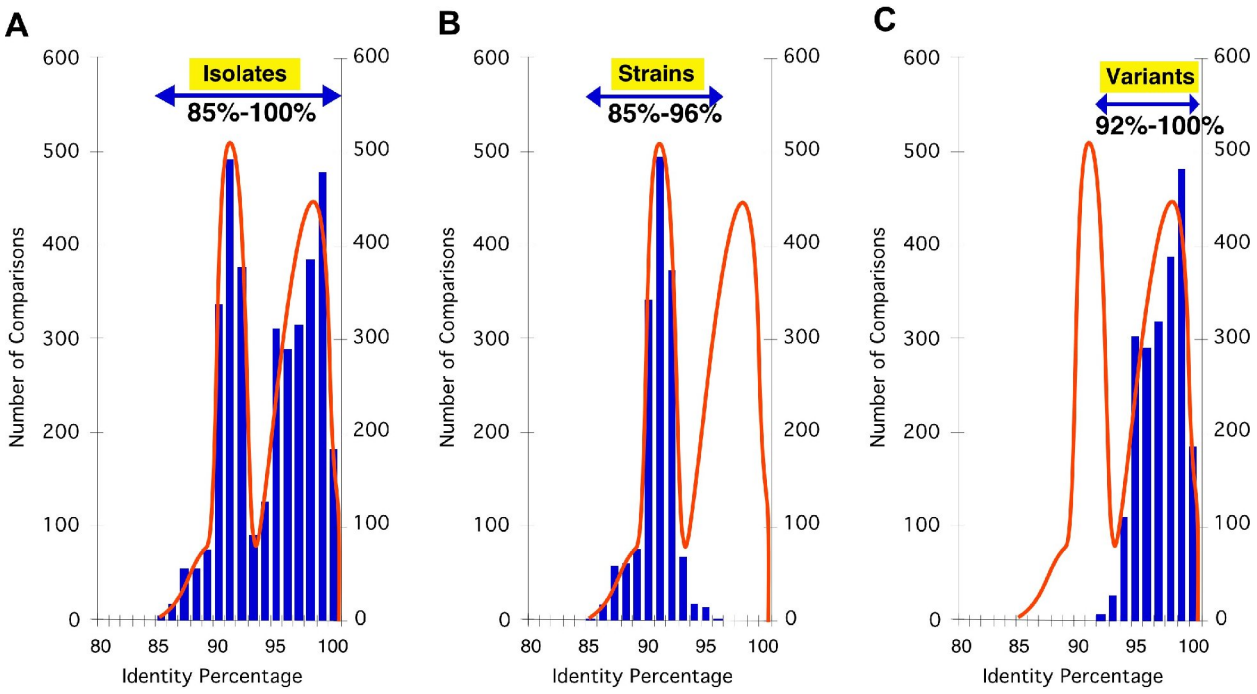
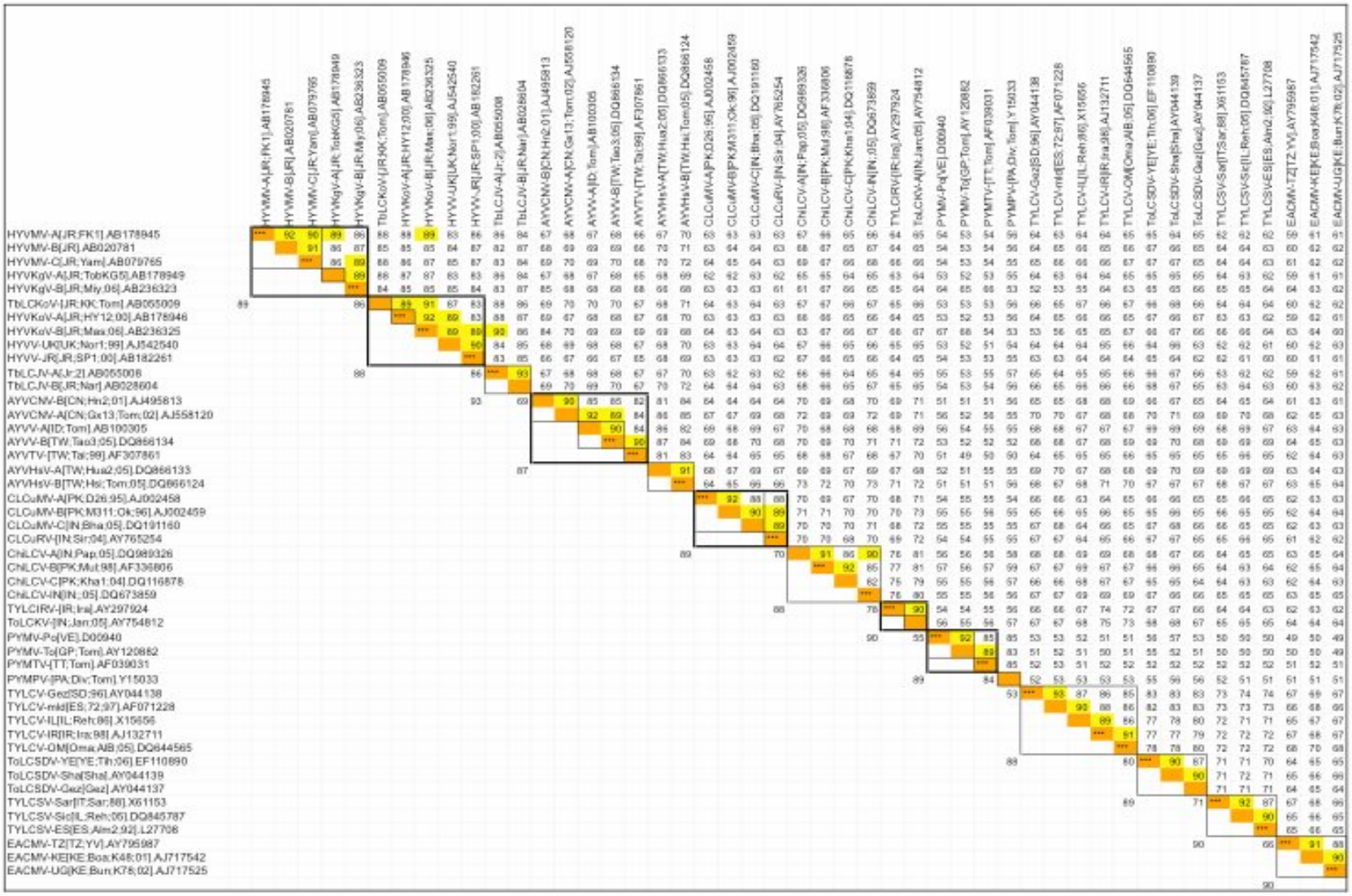


Figure 2: Matrix of distances (% identity) of pairwise sequence comparison (PASC) identity percentages between DNA-A sequences of 47 geminivirus isolates belonging to 21 virus species. The grey and light grey cells identify variant, strain and species relationships, respectively. The thick cell borders represent proposed new species. At the lower left end side of the species boxes is indicated the intra-species pairwise percentage identity, while the inter-species pairwise percentage identity is indicated between two species boxes.

Strain demarcation.xls



List of removed species in the genus

Removed:	**Now a strain of:**
Ageratum yellow vein China virus	*Ageratum yellow vein virus*
Ageratum yellow vein Taiwan virus	*Ageratum yellow vein virus*
Cotton leaf curl Rajasthan virus	*Cotton leaf curl Multan virus*
Potato yellow mosaic Trinidad virus	*Potato yellow mosaic virus*
Tobacco leaf curl Kochi virus	*Honeysuckle yellow vein virus*
Tomato leaf curl Iran virus	*Tomato leaf curl Karnataka virus*

List of revised species in the genus

Ageratum yellow vein virus	
AYVV-A[ID;Tom].AB100305	AYVV-A[ID;Tom].AB100305
AYVV-B[TW;Tao3;05].DQ866134	AYVV-B[TW;Tao3;05].DQ866134
AYVTV-[TW;Tai;99].AF307861	AYVV-C[TW;Tai;99].AF307861
AYVCNV-A[CN;Gx68;03].AJ849916	AYVV-D[CN;Gx68;03].AJ849916
AYVCNV-B[CN;Hn2.19;01].AJ564744	AYVV-E[CN;Hn2.19;01].AJ564744
Cotton leaf curl Multan virus	
CLCuMV-A[PK;Y62;95].AJ002447	CLCuMV-A[PK;Y62;95].AJ002447
CLCuMV-B[PK;Mul].AJ496461	CLCuMV-B[PK;Mul].AJ496461
CLCuMV-C[IN;Bha;05].DQ191160	CLCuMV-C[IN;Bha;05].DQ191160
CLCuRV-[IN;Abo;03].AY795606	CLCuMV-D[IN;Abo;03].AY795606
Honeysuckle yellow vein virus	
HYVV-UK[UK;Nor1;99].AJ542540	HYVV-A[UK;Nor1;99].AJ542540
HYVKoV-[JR;HY12;00].AB178946	HYVV-C[JR;HY12;00].AB178946
TbLCKoV-[JR;KK;Tom].AB055009	HYVV-D[JR;KK;Tom].AB055009
Potato yellow mosaic virus	
PYMV-Po[VE].D00940	PYMV-Po[VE].D00940
PYMV-To[GP;Tom].AY120882	PYMV-To[GP;Tom].AY120882
PYMTV-[TT;Tom].AF039031	PYMV-TT[TT;Tom].AF039031
Tomato leaf curl Karnataka virus	
ToLCKV-A[IN;Jan;05].AY754812	ToLCKV-A[IN;Jan;05].AY754812
ToLCKV-B[IN;Ban;93].U38239	ToLCKV-B[IN;Ban;93].U38239
ToLCIRV-[IR;Ira].AY297924	ToLCKV-C[IR;Ira].AY297924