ICTV – Plant Virus Subcommittee

Study Group on Geminiviruses

2002.P108.02: To provide taxonomic status for the following viruses pertaining to the Begomovirus genus, and to provide names for the species

2002.P109.02: To alter the taxonomic status of the following viruses pertaining to the Begomovirus genus, from species to tentative species.
**ICTV – Plant Virus Subcommittee**  
**Study Group on Geminiviruses**

**2002.P108.02:** To provide taxonomic status for the following viruses pertaining to the *Begomovirus* genus, and to provide names for the species

Date: 19th July 2002

From: John Stanley, Chair of the Study Group on Geminiviruses

Subject: Updating the list of species in the genus *Begomovirus*

Proposal: To provide taxonomic status for the following viruses, and to provide names for the species

Purpose: To confer taxonomic status on additional begomoviruses on the basis of revised species demarcation criteria, as specified in taxonomic proposal #1 and described in the annex

In the following list, species names are italicized, and previous names appear in brackets. Viruses described in accompanying taxonomic proposals have not been listed here to avoid redundancy. All viruses have been compared using complete DNA A component sequences and found to be under the proposed threshold of 89% compared to all other viruses known to date. Unpublished sequences are available to the Study Group but not yet in the public domain.

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<tr>
<th>New species</th>
<th>Accession number</th>
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<td>AYVTV-[Tai]</td>
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<td>BYVMV</td>
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*Chilli leaf curl virus*
  Chilli leaf curl virus – [Multan] AF336806 ChiLCuV
  Chilli leaf curl virus – [Multan] [Mul] AF336806 ChiLCuV-[Mul]

*Cotton leaf curl Alabad virus*
  (Cotton leaf curl virus - Pakistan3; CLCuV-Pk3)
    Cotton leaf curl Alabad virus - [802a] AJ002455 CLCuAV-[802a]
    Cotton leaf curl Alabad virus - [804a] AJ002452 CLCuAV-[804a]

*Cotton leaf curl Gezira virus*
  (Okra enation virus ; OkEV)
    Cotton leaf curl Gezira virus AF155064 CLCuGV
    Cotton leaf curl Gezira virus – [Cotton] AF260241 CLCuGV-[Cot]
    Cotton leaf curl Gezira virus – [Okra/Egypt] AY035010 CLCuGV-[Okr/EG]
    Cotton leaf curl Gezira virus – [Okra/Shambat] AF260241 CLCuGV-[Okr/Sha]
    Cotton leaf curl Gezira virus – [Sida] AY036007 CLCuGV-[Sida]

*Cotton leaf curl Kokhran virus*
  (Cotton leaf curl virus - Pakistan2; CLCuV-Pk2)
    (Pakistani cotton leaf curl virus)
      Cotton leaf curl Kokhran virus - [72b] AJ002448 CLCuKV-[72b]
      Cotton leaf curl Kokhran virus - [806b] AJ002449 CLCuKV-[806b]
      Cotton leaf curl Kokhran virus - [Faisalabad1] unpublished CLCuKV-[Fai1]
      (Cotton leaf curl virus - Pakistan2 [Faisalabad1]; CLCuV-PK2[Fai1])

*Cotton leaf curl Multan virus*
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    Cotton leaf curl Multan virus – [Faisalabad1] unpublished CLCuMV-[Fai1]
    (Cotton leaf curl virus - Pakistan1 [Faisalabad1]; CLCuV-PK1[Fai1])
    Cotton leaf curl Multan virus – [Faisalabad2] unpublished CLCuMV-[Fai2]
    (Cotton leaf curl virus - Pakistan1 [Faisalabad2]; CLCuV-PK1[Fai2])
    Cotton leaf curl Multan virus – [Faisalabad3] AJ132430 CLCuMV-[Fai2]
    Cotton leaf curl Multan virus – [Multan] unpublished CLCuMV-[Mul]
    (Cotton leaf curl virus - Pakistan1 [Multan]; CLCuV-PK1[Mul])
    Cotton leaf curl Multan virus – [Okra] AJ002459 CLCuMV-[Ok]
    (Cotton leaf curl virus - Pakistan1 [Okra]; CLCuV-PK1[Ok])

*Cotton leaf curl Rajasthan virus*
  Cotton leaf curl Rajasthan virus AF363011 CLCuRV

*Cucurbit leaf curl virus*
  Cucurbit leaf curl virus AF224760, AF224761 CuLCuV
  Cucurbit leaf curl virus – [Arizona] AF256200, AF327559 CuLCuV-[AZ]

*Dicliptera yellow mottle virus*
  Dicliptera yellow mottle virus AF170101, AF139168 DiYMoV

*East African cassava mosaic Cameroon virus*
  East African cassava mosaic Cameroon virus - Cameroon AF112354, AF112355 EACMCV
  East African cassava mosaic Cameroon virus - Cameroon [Ivory AF259896, AF259897 EACMCV-CM[CI]
  East African cassava mosaic Cameroon virus - Cameroon [Coast] EACMCV
  (East African cassava mosaic virus – Malawi, EACMV-MW)

*East African cassava mosaic Zanzibar virus*
  East African cassava mosaic Zanzibar virus AF422174, AF422175 EACMZV

*Eupatorium yellow vein virus*
  Eupatorium yellow vein virus AB007990 EpYVV
Eupatorium yellow vein virus – [Tobacco] E15418 EpYVV-[Tob]
Eupatorium yellow vein virus – [SOJ3] AJ438939 EpYVV-[SOJ3]
Ipomea yellow vein virus
Ipomaea yellow vein virus
(Sweet potato leaf curl virus – [Ipo])
Macrophtilium yellow mosaic Florida virus
Macrophtilium yellow mosaic Florida virus
Macrophtilium mosaic Puerto Rico virus
Macrophtilium mosaic Puerto Rico virus
Macrophtilium mosaic Puerto Rico virus – [Bean]
Macrophtilium yellow mosaic virus
Macrophtilium yellow mosaic virus – [Cuba]
Malvastrum yellow vein virus
Malvastrum yellow vein virus – [Y47]
Melon chlorotic leaf curl virus
Melong chlorotic leaf curl virus – [Guatemala]
Mungbean yellow mosaic India virus
Mungbean yellow mosaic India virus
Mungbean yellow mosaic India virus – [Bangladesh]
Mungbean yellow mosaic India virus – [Cowpea]
Mungbean yellow mosaic India virus – [Mungbean]
Mungbean yellow mosaic India virus – [Soybean]
Mungbean yellow mosaic India virus – [Soybean TN]
Okra yellow vein mosaic virus
Okra yellow vein mosaic virus - [201]
Pepper leaf curl Bangladesh virus
Pepper leaf curl Bangladesh virus
Potato yellow mosaic Panama virus
Potato yellow mosaic Panama virus
(Potato yellow mosaic virus – Panama)
(Potato leaf curl virus - Panama; ToLCV-PA)
Potato yellow mosaic Trinidad virus
Potato yellow mosaic Trinidad virus – Trinidad & Tobago
Potato yellow mosaic Trinidad virus - [Guadeloupe]
Rhynchosia golden mosaic virus
Rhynchosia golden mosaic virus
Rhynchosia golden mosaic virus – [Chiapas]
Sida golden mosaic Costa Rica virus
Sida golden mosaic Costa Rica virus
Sida golden mosaic Florida virus
Sida golden mosaic Florida virus
Sida golden mosaic Honduras virus
Sida golden mosaic Honduras virus
Sida golden yellow vein virus
Sida golden yellow vein virus
(Sida golden mosaic Florida virus - [A11])
Sida mottle virus
Sida mottle virus – [Brazil]
Sida yellow mosaic virus
Sida yellow mosaic virus
Sida yellow mosaic virus – [Brazil]
Sida yellow vein virus
Sida yellow vein virus
(Sida golden mosaic Honduras virus - yellow vein)
Soybean crinkle leaf virus
Soybean crinkle leaf virus – [Japan]
Squash mild leaf curl virus
- [Imperial Valley] AF421552, AF421553
Squash leaf curl Yunnan virus
- [Y23] AJ420319
Squash yellow mottle virus
- [CR] AY064391, AF440790
Sri Lankan cassava mosaic virus
- [Colombo] AF314738, AF314737
Stachytarpheta leaf curl virus
- [Hn5] unpublished
Sweet potato leaf curl virus
- AF104036
Tobacco curly shoot virus
- [Y1] AF240675
- [Y35] AF420318
- [Y41] AJ457986
Tobacco leaf curl Japan virus
- [Japan; TbLCV-JP] AB028604
- [JP2] AB055008
Tobacco leaf curl Kochi virus
- [KK] AB055009
Tobacco leaf curl Yunnan virus
- AB240674
Tomato chlorotic mottle virus
- [Brazil] AF490004, AF491306
- Crumple AY090557
Tomato golden mottle virus
- [GT94-R2] AF132852
Tomato leaf curl Bangladesh virus
- AF188481
Tomato leaf curl Gujarat virus
- [Vadodara] AF413671
Tomato leaf curl Karnataka virus
- Bangalore 2
- [Bangalore II] U38239
Tomato leaf curl Laos virus
- AF195782
Tomato leaf curl Malaysia virus
- AF327436
Tomato leaf curl Sri Lanka virus
- AF274349
Tomato leaf curl Vietnam virus
- AF264063
Tomato mosaic Havana virus
- [Quivican] Y14874, Y14875
Tomato rugose mosaic virus
- NC002555, NC002556
- [Ube] AF291705, AF291706
Tomato severe rugose virus
- AY029750
Tomato yellow leaf curl Gezira virus
- [1] AY0441137, AY044139
- [2]
ITCV – Plant Virus Subcommittee

Study Group on Geminiviruses

2002.P109.02: To alter the taxonomic status of the following viruses pertaining to the Begomovirus genus, from species to tentative species.

Date: 20th July 2002

From: John Stanley, Chair of the Study Group on Geminiviruses

Subject: Updating the list of species in the genus Begomovirus

Proposal: To alter the taxonomic status of the following viruses from species to tentative species

Purpose: To downgrade viruses that have insufficient biological and/or molecular information to support their taxonomic status as species, based on the revised species demarcation criteria, as specified in taxonomic proposal #1 and described in the annex

Tentative Species

<table>
<thead>
<tr>
<th>Acronym</th>
<th>Tentative Species</th>
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<td>Acalypha yellow mosaic virus</td>
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<td>AGMV</td>
<td>Asystasia golden mosaic virus</td>
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<td>CYVMV</td>
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<td>HLCV</td>
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<td>MGMV</td>
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Annex to taxonomic proposals #1-7

ICTV – Plant Virus Subcommittee
Study Group on Geminiviruses

Revision of taxonomic criteria for species demarcation

Introduction

Members of the family Geminiviridae characteristically have circular single-stranded DNA genomes packaged within twinned (so-called geminate) particles. Geminiviruses are currently divided into four genera on the basis of their genome organization and biological properties (Briddon et al. 1996; Rybicki et al., 2000). Those that have a monopartite genome and are transmitted by leafhopper vectors, primarily to monocotyledonous plants, are included in the genus Mastrevirus, of which Maize streak virus is the type species. Viruses that have monopartite genomes distinct from those of the mastreviruses and are transmitted by leafhopper vectors to dicotyledonous plants are included in the genus Curtovirus, with Beet curly top virus as the type species. The genus Topocuvirus, recently recognized by the ICTV, has only one member (also the type species), Tomato pseudo-curly top virus, which has a monopartite genome and is transmitted by a treehopper vector to dicotyledonous plants. The genus Begomovirus includes viruses that are transmitted by whitefly vectors to dicotyledonous plants, with Bean golden yellow mosaic virus as the type species. Most begomoviruses have bipartite genomes (DNA A and DNA B components), although there are some exceptions for which no DNA B component has been found.

Geminiviruses cause significant yield losses to many crop plants throughout the world. Because of their economic importance and the relative ease with which their DNA genomes can be cloned, many geminiviruses have now being isolated and characterized. Guidelines for naming geminiviruses have recently been proposed (Fauquet et al., 2000) and accepted by the Study Group and the geminivirologist community as a whole, providing a means for distinguishing viruses that are sufficiently different to warrant the label of species. However, guidelines for determining the taxonomic status of a virus, as outlined in the Seventh ICTV Report, are no longer precise enough to be decimate some viruses, and consequently require urgent revision. The problem is compounded by the recent discovery of a high frequency of recombination between species of geminiviruses (Padidam et al., 1999). Several case studies illustrating the problems of taxonomy (Fauquet et al., 2002) have served to emphasize the need to have a set of guidelines, which may be to some extent arbitrary, to provide the geminivirologist community with uniform and durable species demarcation criteria. Some of these examples were discussed at the last International Geminivirus Workshop, held at Norwich in July 2001, and a consensus has been reached on species demarcation guidelines required. We present here a system for demarcating geminivirus species and provide the list of geminivirus species identified according to these guidelines.

Taxonomic considerations

In 1990, the ICTV agreed to add species to the categories of genus, subfamily, family, and order in the universal classification of viruses, and endorsed the following definition of virus species: "A virus species is a polythetic class of viruses that constitutes a replicating lineage and
occupies a particular ecological niche" (van Regenmortel, 1990). Inherent in the definition of virus species is the requirement that more than one discriminating character should be considered for distinguishing species, and this has been established for geminiviruses (Rybicki et al., 2000). However this definition does not precisely define the species demarcation criteria for particular families or genera. There is no official definition for a strain, but it is usually considered that strains are viruses belonging to the same species that have distinct but stable and heritable biological, serological, and/or molecular traits. Strain identification could include, but is not restricted to, a particular symptom descriptor, a different host, a different vector or a significant genetic difference such as a deletion, repetition, or recombination. An isolate can be used to refer to any virus isolated that can later be classified as a member of either a strain or species when sufficient information becomes available.

The current list of demarcation species criteria for begomoviruses may be summarized as follows:

- Different numbers of genome components
- Different organization of genes in the genome
- No transcomplementation of gene products
- No pseudorecombination between components
- Nucleotide sequence identity (<75% for mastreviruses, <80% for curtoviruses and <90% for begomoviruses)
- Virions react differently with key antibodies
- <90% coat protein sequence identity
- Different vector species
- Different host range/pathogenicity

As the number of characterized begomoviruses increases, it is becoming increasingly clear that most of these established criteria are useful only as a rough guide with which to identify new species due to the growing number of exceptions to these rules. A few examples are as follows:

**Different number of genome components.** Begomoviruses have either one or two components, although some bipartite viruses (Rochester et al., 1990; Saunders et al., 2002), have the capacity to infect a plant with only one component, so this criterion may not provide a clear distinction. The fact that some begomoviruses are unable to produce the disease phenotype unless accompanied by a satellite DNA component (Saunders et al., 2000) further complicates the application of this criterion.

**Different organization of genes in the genome.** Geminiviruses within a particular genus are extremely conserved in their genome composition, both in terms of length and organization. The exception is the different arrangement of genes between begomoviruses from the New World and Old World. This criterion, therefore, has only limited use for virus species determination within this genus.

**No trans-complementation of products.** It is known that viral proteins of one species, for example begomovirus AC2, AC3 and movement proteins (Frischmuth et al., 1993; Saunders and Stanley, 1995), can functionally trans-complement defects in another. Rep protein interaction with the origin of replication, that is generally considered to be highly species-specific, can alter in response to small changes to the sequence (Fontes et al., 1994), and the propensity of
begomoviruses to capture components by origin exchange (Saunders et al., 2002) may also confuse the issue.

_No pseudo-recombination between components_. This was proposed a few years ago as an important criterion with which to distinguish species. However, there are now examples of pseudo-recombination between components of distinct species (Gilbertson et al., 1993; Saunders et al., 2002), reflecting the ability of Rep and movement proteins to _trans_-complement functions between species.

_Nucleotide sequence identity_. The gap between species and strains is becoming blurred with the increasing number of geminivirus sequences that are becoming available (www.danforthcenter.org/iltab/geminiviridae), made worse by frequent recombination events that are known to occur between species.

_Virions react differently with key antibodies_. Although this is true, this criterion is decreasing in importance as the number of exceptions is growing.

_<90% coat protein sequence identity_. As is the case for overall nucleotide sequence identity, this criterion is becoming less accurate with time as more sequences become available, and may be misleading if recombination has caused coat protein sequences to be exchanged between species (Padidam et al., 1999).

_Different vector species_; although this criterion is applicable for leafhopper-transmitted geminiviruses, it is of no use for whitefly-transmitted viruses as they are all transmitted by the same whitefly species, _Bemisia tabaci_. Although different whitefly populations exist in nature, it has been shown that they readily adapt to transmission of a variety of begomoviruses (Bedford et al., 1994).

_Different hosts and symptom phenotype_. This is a very useful criterion but it may be difficult to provide a comprehensive assessment. There are examples where different strains of the same species can infect very different hosts. For example, strains of _Potato yellow mosaic virus_ (PYMV) infect potatoes in Venezuela and a range of solanaceous crops in Trinidad where the primary host seems to be tomato. Some strains of _Pepper Huasteco yellow vein virus_ (PHYVV) are so well adapted to tomato that they cannot infect peppers, the host from which the virus was first isolated. On the contrary more than fifteen species of geminiviruses have been isolated from tomatoes and there are probably many more waiting to be found (Polston and Anderson, 1997). This does not take into account the many viruses isolated from a range of natural hosts that are perfectly capable of infecting tomato. In addition, the range of symptoms induced by different strains of the same species may vary, and so will not provide a reliable species distinguishing feature.

In summary, because of the large number of begomoviruses that have been isolated, these criteria are becoming less reliable for distinguishing species and strains. The molecular criteria probably have the most practical value. For example, if we consider begomoviruses that have two components and are transmitted by whiteflies to tomato, there is essentially only a single criterion, nucleotide sequence identity, that can be used to distinguish them. This is equally true for many other begomoviruses that have recently been isolated from cotton, pepper and cassava.

**The importance of genome sequence comparisons for begomovirus taxonomy**

The viral genome encodes proteins that are necessary for virus particle structure, replication, movement, transmission, tissue tropism and host range and, hence, it is arguable that the sequence contains a wealth of information necessary for virus classification. It is possible to
establish and exploit correlations between biological properties and sequences, and a correlation between sequence identity and taxonomic relatedness has been established (Padidam et al., 1995) and is being strengthened with the increasing number of sequences that are becoming available (www.danforthcenter.org/iltab/geminiviridae). However, the gap between species and strain, particularly for the begomoviruses, is becoming less distinct with time due to the number of sequences available and the frequent recombination events that have been identified (Padidam et al., 1999). For this reason, it is necessary to establish a clear set of guidelines that will allow geminivirologists to propose taxonomic status for new viruses in a more uniform manner.

Guidelines with which to demarcate begomovirus species

It is proposed to retain biological criteria as possible indicators of taxonomic status although limitations to their predictive value will be made clear. Nucleotide sequence comparison will play a much greater role in determining taxonomic status. Because DNA B components can be exchanged between some begomoviruses, it is proposed that only DNA A components are considered in the first instance. That some viruses have only a DNA A component strengthens this argument. The high recombination frequency that is known to occur between different begomovirus species invalidates the use of small genomic fragments for comparison. Hence, it is proposed that only full-length genome sequences are considered for comparative analyses. Extensive analysis of more than 200 full-length DNA A component sequences indicates that a figure of 89% nucleotide sequence identity provides a realistic cut-off value with which to demarcate species (Fauquet, 2002). However the high frequency of inter-species recombination is complicating the partition between strains and taxa. Currently there is no genetic basis that may be used to assess the contribution of recombination to species demarcation, therefore overall identity will be used in the first instance. Above 89% identity, virus isolates may be considered to belong to the same species and should have the same name, irrespective of the host from which they were derived. Biological differences may justify strain designation, and the name would then be supplemented with the relevant information. This rule is based on the analysis of begomoviruses, but will also be applied to curtoviruses and topocuviruses, which have basically similar genome organization. Mastreviruses show several fundamental differences in their genome organization and host range characteristics, for which reason the previously established cut-off figure of 75% for species demarcation will remain at this time.

Updating the list of geminivirus species and tentative species

Taking in account the revised guidelines (taxonomic proposal #1), the entire list of begomovirus DNA A components for which full-length nucleotide sequences are available has been revisited. Viruses that have a pair-wise identity value above or below 89% when compared with previously established species have been classified accordingly (taxonomic proposal #5). Viruses for which there is insufficient information to allow designation as species have been downgraded to the level of tentative species (taxonomic proposal #6). A revised list of all begomovirus species and tentative species, based on the list of approved viruses appearing in the Seventh Report and updated according to these proposals and the suggested name changes (taxonomic proposals #7 and #8), is provided below. The lists of curtovirus, topocuvirus and mastrevirus species are unaffected by the proposed changes in taxonomic proposals #2-4.

References


Revised list of begomovirus species and tentative species

In the following list, species names are italicized and previous names appear in brackets. All viruses have been compared using their complete DNA A component sequences and found to be under the proposed threshold of 89%. Unpublished sequences are available to the Study Group but not yet in the public domain.

Species colour key:
**Blue:** unchanged from the Seventh Report
**Turquoise:** name change of species appearing in the Seventh Report
**Green:** new species (taxonomic proposal #5)
**Pink:** downgraded from species to tentative species (taxonomic proposal #6)
**Light green:** name changes (taxonomic proposals #7 and #8)
**Red:** new tentative species

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AF241479 BYVMV-[Mad]

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Cabbage leaf curl virus
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Chayote mosaic virus
Chayote mosaic virus
AJ223191 ChaMV

Chilli leaf curl virus
Chilli leaf curl virus – [Multan]
AF336806 ChiLCuV-[Mul]

Chino del tomate virus
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Chino del tomate virus
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Chino del tomate virus – [B52]
AF226666 CdTV-[B52]
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AF226665 CdTV-[H6]
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AF226664 CdTV-[H8]
Chino del tomate virus – [IC]
AF101476, AF101478 CdTV-[H8]

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Cotton leaf curl virus
unpublished CLCrV
(Cotton leaf curl virus – Pakistan3; CLCuV-Pk3)
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Cotton leaf curl Gezira virus – [Okra/Gezira]
AY036006 CLCuGV-[Okr/Gez]
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AF260241 CLCuGV-[Okr/Sh]
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AY036007 CLCuGV-[Sida]

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unpublished CLCuKV-[Fai1]

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  (Cotton leaf curl virus - Pakistan1 [Faisalabad2]; CLCuV-
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Cotton leaf curl Multan virus – [Multan] unpublished CLCuMV-[Mul]
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  (Cotton leaf curl virus - Pakistan1 [Okra]; CLCuV-PK1[Ok])

Cotton leaf curl Rajasthan virus
  Cotton leaf curl Rajasthan virus AF363011 CLCuRV

Cowpea golden mosaic virus
  Cowpea golden mosaic virus- [Nigeria] AF029217 CPGMV-
[NG]

Cucurbit leaf curl virus
  Cucurbit leaf curl virus AF224760, AF224761 CuLCuV
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Dicliptera yellow mottle virus
  Dicliptera yellow mottle virus AF170101, AF139168 DiYMoV

East African cassava mosaic Cameroon virus
  East African cassava mosaic Cameroon virus - Cameroon AF112354, AF112355 EACMCV-CM
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   Coast] AF259896, AF259897 EACMCV-CM[CI]

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Honeysuckle yellow vein mosaic virus
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Indian cassava mosaic virus
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    MYMV-TH
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    MYMV-Vig[Mah]

Okra yellow vein mosaic virus
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    OYVMV-[201]

Papaya leaf curl virus
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Pepper golden mosaic virus
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Pepper leaf curl Bangladesh virus
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    PepLCBV

Pepper leaf curl virus
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    AF134484
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    PepLCV-[MY]

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Potato yellow mosaic Trinidad virus
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Sida golden yellow vein virus
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Sida golden mosaic virus
  Sida golden mosaic virus AF049336, AF039841 SiGMV

Sida mottle virus
  Sida mottle virus – [Brazil] AY090555 SiMoV-[BZ]

Sida yellow mosaic virus
  Sida yellow mosaic virus – [Brazil] AY090558 SiYMV-[BZ]

Sida yellow vein virus
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  Soybean crinkle leaf virus – [Japan] AB050781 SbCLV-[JP]

Squash leaf curl China virus
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ToSLCV-

**Tomato yellow leaf curl Gezira virus**
Tomato yellow leaf curl Gezira virus – [1]
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Tomato yellow leaf curl Sardinia virus
X61153
TYLCSV

(Tomato yellow leaf curl virus - Sardinia; TYLCV-Sar)
Tomato yellow leaf curl Sardinia virus – Sicily
Z28390
TYLCSV-Sic

(Tomato yellow leaf curl virus - Sardinia [Sicily]; TYLCV-Sar[Sic])
Tomato yellow leaf curl virus – Sicily, TYLCV-SY

(Tomato yellow leaf curl virus - Sardinia [Spain1]; TYLCV-Sar[ES1])

(Tomato yellow leaf curl virus - Spain, TYLCV-Sp)

(Tomato yellow leaf curl virus - Sardinia [Spain2]; TYLCV-Sar[ES2])

(Tomato yellow leaf curl virus - Almeria, TYLCV-Almeria)

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TYLCTHV-[1]

(Tomato yellow leaf curl Thailand virus - [1]; TYLCV-TH-[1])

(Tomato yellow leaf curl Thailand virus - [2]; TYLCV-TH-[2])

(Tomato yellow leaf curl Thailand virus - [Myanmar]
AF206674
TYLCTHV-[MM]

(Tomato yellow leaf curl Thailand virus - [Y72]
unpublished
TYLCTHV-[Y72]

**Tomato yellow leaf curl virus**

(Tomato yellow leaf curl virus - Israel; TYLCV-IL)

(Tomato yellow leaf curl virus – Mild
X76319
TYLCV-Mld

(Tomato yellow leaf curl virus - Israel [Mild]; TYLCV-IL[Mld])

**Tomato mottle Taino virus**
Tomato mottle Taino virus
AF012300, AF012301
ToMoTV

**Tomato mottle virus**
Tomato mottle virus - [Florida]
L14460, L14461
ToMoV-[FL]

**Tomato rugose mosaic virus**
Tomato rugose mosaic virus
NC002555, NC002556
ToRMV

**Tomato rugose mosaic virus –[Ube]**
AF291705, AF291706
ToRMV-[Ube]

**Tomato severe leaf curl virus**
Tomato severe leaf curl virus - [Guatemala96 – 1]
AF130415
ToSLCV-

**Tomato yellow leaf curl Gezira virus**
Tomato yellow leaf curl Gezira virus – [1]
AY044137
TYLCSV-[1]

**Tomato yellow leaf curl Sardinia virus**
(Tomato yellow leaf curl virus - Sardinia; TYLCV-Sar)
Tomato yellow leaf curl Sardinia virus
X61153
TYLCSV

(Tomato yellow leaf curl virus - Sardinia; TYLCV-Sar)
Tomato yellow leaf curl Sardinia virus – Sicily
Z28390
TYLCSV-Sic

(Tomato yellow leaf curl virus - Sardinia [Sicily]; TYLCV-Sar[Sic])
Tomato yellow leaf curl virus – Sicily, TYLCV-SY

(Tomato yellow leaf curl virus - Sardinia [Spain1]; TYLCV-Sar[ES1])

(Tomato yellow leaf curl virus - Spain, TYLCV-Sp)

(Tomato yellow leaf curl virus - Sardinia [Spain2]; TYLCV-Sar[ES2])

(Tomato yellow leaf curl virus - Almeria, TYLCV-Almeria)
Tomato yellow leaf curl virus - [Aichi]  AB014347  TYLCV-[Aic]
(Tomato yellow leaf curl virus - Israel [Aichi]; TYLCV-IL[Ai])

Tomato yellow leaf curl virus - [Cuba]  AJ223505  TYLCV-[CU]
(Tomato yellow leaf curl virus - Israel [Cuba]; TYLCV-IL[Cu])

Tomato yellow leaf curl virus - [Dominican Republic]  AF024715  TYLCV-[DO]
(Tomato yellow leaf curl virus - Israel [DO]; TYLCV-IL[DO])

Tomato yellow leaf curl virus – Iran  AJ132711  TYLCV-IR
(Tomato yellow leaf curl virus - Israel [Iran]; TYLCV-IL[IR])

Tomato yellow leaf curl virus - [Portugal]  AF105975  TYLCV-[PT]
(Tomato yellow leaf curl virus - Israel [Portugal]; TYLCV-IL[PT])

Tomato yellow leaf curl virus - [Saudi Arabia]  TYLCV-[SA]
(Tomato yellow leaf curl virus - Israel [Saudi Arabia1]; TYLCV-IL[SA1])
(Tomato yellow leaf curl virus - Northern Saudi Arabia; TYLCV-NSA)

Tomato yellow leaf curl virus - [Shizuokaua]  AB014346  TYLCV-[Shi]
(Tomato yellow leaf curl virus - Israel [Shizuokua]; TYLCV-IL[Shi])

Tomato yellow leaf curl virus - [Spain7297]  AF071228  TYLCV-[ES7297]
(Tomato yellow leaf curl virus - Israel [Spain7297]; TYLCV-IL[ES7297])

Tomato yellow leaf curl virus – Sudan  AY044138  TYLCV-SD

Watermelon chlorotic stunt virus
Watermelon chlorotic stunt virus  AJ012081, AJ012082  WmCSV
Watermelon chlorotic stunt virus – [IR]  AJ245652, AJ245653  WmCSV-[IR]
Watermelon chlorotic stunt virus – [SD]  AJ245650, AJ245651  WmCSV-[SD]

Tentative Species

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<th>Acalypha yellow mosaic virus</th>
<th>AYMV</th>
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<td>Cotton yellow mosaic virus</td>
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<td>(Okra leaf curl virus - India; OLCV-IN)</td>
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<td>Okra leaf curl virus</td>
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**Pseudanthernum yellow vein virus**
**PYVV**

**Sida golden mosaic Jamaica virus**
**SiGMJV**
- Sida golden mosaic Jamaica virus
- Sida golden mosaic Jamaica virus - [ 3 ]
- Sida golden mosaic Jamaica virus - [ Macroptilium 19 ]

**Solanum apical leaf curl virus**
**SALCV**

**Solanum yellow leaf curl virus**
**SYLCV**

**Squash yellow mottle virus**
**SYMoV**

**Tobacco apical stunt virus**
**TbASV**

**Tomato leaf curl India virus**
**ToLCIV**
- (Tomato leaf curl virus - India; ToLCV-IN)

**Tomato curly stunt virus**
**ToCSV**

**Tomato dwarf leaf curl virus**
**ToDLCV**

**Tobacco leaf curl China virus**
**TbLCCNV**
- (Tobacco leaf curl virus - China; TbLCV-CN)

**Tomato leaf curl India virus**
**ToLCIV**

**Tomato leaf curl Indonesia virus**
**ToLCIDV**

**Tomato leaf curl Nicaragua virus**
**ToLCNV**

**Tomato leaf curl Philippines virus**
**ToLCPV**

**Tomato leaf curl Senegal virus**
**ToLCSV**
- (Tomato leaf curl virus - Senegal; ToLCV-SN)

**Tomato leaf curl Sinaloa virus**
**ToLCSinV**
- (Tomato leaf curl virus - Sinaloa; ToLCV-Sin)
  - (Sinaloa tomato leaf curl virus, STLCV)

**Tomato leaf curl Tanzania virus**
**ToLCTZV**
- (Tomato leaf curl virus - Tanzania; ToLCV-TZ)

**Tomato mild mottle virus**
**ToMMoV**

**Tomato mosaic Barbados virus**
**ToMBV**

**Tomato Uberlandia virus**
**ToUV**

**Tomato yellow dwarf virus**
**ToYDV**

**Tomato yellow leaf curl Nigeria virus**
**TYLNCV**
- (Tomato yellow leaf curl virus - Nigeria; TYLCV-NG)

**Tomato yellow leaf curl Kuwait virus**
**TYLCKWV**

**Tomato yellow leaf curl Saudi Arabia virus**
**TYLCSAV**
- (Tomato yellow leaf curl virus - Saudi Arabia; TYLCV-SA)
  - (Tomato yellow leaf curl virus - Southern Saudi Arabia; TYLCV-SSA)

**Tomato yellow leaf curl Tanzania virus**
**TYLCTZV**
- (Tomato yellow leaf curl virus - Tanzania; TYLCV-TZ)

**Tomato yellow leaf curl Yemen virus**
**TYLCYV**
- (Tomato yellow leaf curl virus - Yemen ; TYLCV-YE)

**Tomato yellow mosaic virus**
**ToYMV**
- Tomato yellow mosaic virus - Brazil [ 1 ]
  - Tomato yellow mosaic virus - Brazil [ 2 ]

**Tomato yellow mottle virus**
**ToYMoV**

**Tomato yellow vein streak virus**
**ToYVSV**
- (Tomato yellow vein streak virus - Brazil; ToYVSV-BR)

**Watermelon curly mottle virus**
**WmCMV**

**Wissadula golden mosaic virus**
**WGMV**

**Zinnia leaf curl virus**
**ZiLCV**