

Revision of *Begomovirus* taxonomy based on pairwise sequence comparisons

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Abstract Viruses of the genus *Begomovirus* (family *Geminiviridae*) are emergent pathogens of crops throughout the tropical and subtropical regions of the world. By virtue of having a small DNA genome that is easily cloned, and due to the recent innovations in cloning and low-cost sequencing, there has been a dramatic increase in the number of available begomovirus genome sequences. Even so, most of the available sequences have been obtained from cultivated plants and are likely a small and phylogenetically unrepresentative sample of begomovirus diversity, a factor constraining taxonomic decisions such as the establishment of operationally useful species demarcation criteria. In addition, problems in assigning new viruses to established species have highlighted

shortcomings in the previously recommended mechanism of species demarcation. Based on the analysis of 3,123 full-length begomovirus genome (or DNA-A component) sequences available in public databases as of December 2012, a set of revised guidelines for the classification and nomenclature of begomoviruses are proposed. The guidelines primarily consider a) genus-level biological characteristics and b) results obtained using a standardized classification tool, Sequence Demarcation Tool, which performs pairwise sequence alignments and identity calculations. These guidelines are consistent with the recently published recommendations for the genera *Mastrevirus* and *Curtovirus* of the family *Geminiviridae*. Genome-wide pairwise identities of 91 % and 94 % are proposed as the demarcation threshold for begomoviruses belonging to different species and strains, respectively. Procedures and

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guidelines are outlined for resolving conflicts that may arise when assigning species and strains to categories wherever the pairwise identity falls on or very near the demarcation threshold value.

Keywords *Geminiviridae* · Nomenclature · Sequence Demarcation Tool · Single-stranded DNA virus · Species demarcation · Taxonomy · Whitefly-transmitted viruses

Introduction

The genus *Begomovirus* (family *Geminiviridae*) is the largest genus of plant viruses with respect to the number of species that it includes. In fact, with 288 species currently recognized by the International Committee on Taxonomy of Viruses (ICTV) (<http://www.ictvonline.org/virusTaxonomy.asp>), it is the largest genus of all viral taxonomy. Begomoviruses infect a wide range of dicotyledonous plants, mostly in tropical and subtropical regions of the world. Their circular, single-stranded DNA genomes can be either monopartite or bipartite (with genomic components known as DNA-A and DNA-B), with the two components of bipartite genomes sharing a common region of approximately 200 nucleotides that includes the origin of replication [1]. In the Old World (OW; Africa, Asia, Australasia and Europe), most begomoviruses are monopartite, with a few having a bipartite genome. Begomoviruses native to the New World (NW; the Americas) are almost exclusively bipartite, with only a single monopartite virus having been identified so far [2, 3]. However, a number of monopartite begomoviruses occur in the NW as a result of their recent introduction from the OW [4, 5].

Geminiviruses have characteristically twinned or “geminate” particle morphology. The capsid consists of two joined, incomplete $T = 1$ icosahedral heads, with 110 molecules of the capsid protein organized as 22 pentameric capsomers [6]. Geminate particles contain a single molecule of circular ssDNA that ranges from 2.5 to 3.0 kilobases (kb) [1]. Therefore, for viruses having a bipartite genome, two particles, each containing a different genomic component (DNA-A and DNA-B), are required to establish infection.

Due to their economic importance as plant pathogens and their small genomes, begomoviruses were among the first

plant viruses whose complete genomes were cloned and sequenced [7, 8]. By January 2014, more than 3500 full-length begomovirus sequences had been deposited in public databases. Even during the early days of full-genome sequencing, the increasingly large numbers of begomovirus sequences being determined worldwide made it clear that these viruses are abundant and widespread, and that they display a significant degree of genetic diversity [9]. Also, it created the opportunity for the development of a sequence-based taxonomy that relied primarily on pairwise sequence comparisons [10]. Such a system has been in place for the *Geminiviridae* since the mid-1990s, and it has been remarkably stable. It was also widely embraced by the begomovirus community, mostly due to its simplicity and ease of use. Similar classification systems have been adopted by a number of ICTV study groups, including those concerned with the *Anelloviridae* and the *Circoviridae*.

As useful as it has been to establish and streamline taxonomic communications, begomovirus taxonomy is not without controversy. Several criticisms have been voiced in the literature (one recent example being ref. [11]) and by the ICTV Executive Committee (EC), which rejected the *Geminiviridae* Study Group’s taxonomic proposals for creating new begomovirus species in 2010 and 2011. The main points of contention can be summarized as follows: (i) the creation of “too many” species in the genus; (ii) the recognition of new species based solely on sequence comparisons of members, without taking into consideration the biological properties of the viruses; and (iii) the establishment of species demarcation criteria that were “too relaxed” compared to those for other genera in the family, thus leading to point i. Moreover, and as pointed out by the *Geminiviridae* Study Group (SG) itself in the recent *Mastrevirus* and *Curtovirus* taxonomy revisions [12, 13], pairwise sequence identities for any particular pair of sequences may be calculated in different ways and therefore can result in differences in identity scores depending on the algorithm employed. Such discrepancies have made it highly desirable to establish a standard procedure to perform pairwise alignments and to calculate identity scores in order to eliminate (or at least minimize) taxonomic uncertainties and/or misplacements.

The concerns raised by the ICTV EC regarding begomovirus taxonomy encouraged the *Geminiviridae* SG to perform a comprehensive re-evaluation of the species demarcation criteria for the genus *Begomovirus*. The results of this re-evaluation have demonstrated that the current pairwise-identity-based taxonomy is sound, that it accurately reflects the biology of begomoviruses, that it will be stable, and that it will be easy to understand and to be adopted by geminivirologists worldwide. Here, we present the specific guidelines for the classification of begomoviruses, following those recently published for the

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genera *Mastrevirus* [12] and *Curtovirus* [13] of the family *Geminiviridae*.

A comprehensive analysis of the species demarcation criteria for the begomoviruses

Since a significant proportion of begomoviruses do not have a cognate DNA-B component, this component is not considered for species demarcation. A total of 3,123 full-length begomovirus genomic sequences (or DNA-A sequences) were downloaded from the NCBI-GenBank database on 31 Dec 2012. They corresponded to viruses belonging to 283 species according to the currently accepted 89 % species demarcation criterion (for comparison, see the 9th Report of the ICTV, which lists 192 species in the genus [1]). To reduce computing time, only the oldest sequences (full-length genomes or DNA-A components) from groups of sequences that shared >99.5 % genome-wide nucleotide (nt) sequence identity were included in the analysis. To the best of our knowledge, the analysis included sequences of members of all ICTV-recognized species and unclassified begomoviruses for which at least one full-length sequence was available in GenBank at that time (for many, there were multiple sequences per virus/strain). Using this data set (1,826 sequences), a preliminary phylogeny using the neighbor-joining (NJ) method was constructed (data not shown). The purpose of the NJ phylogenetic analysis was not to construct a definitive phylogeny but rather to identify groups of most closely related sequences that could be combined for pairwise sequence comparisons and maximum-likelihood (ML) phylogenetic analyses.

Based on the NJ phylogenetic tree, 38 groups were identified, each of which contained sequences that did not obviously correspond to the same viral species but also did not obviously correspond to distinct species. This approach was employed to more easily delineate distinct groups. Some groups consisted of as few as 2–3 sequences, whereas, others were represented by >30 sequences (Supplementary File S1). Pairwise sequence comparisons were carried out separately for each one of the 38 groups, using Sequence Demarcation Tool (SDT) v. 1.0 [14] with the MUSCLE [15] alignment option. Also, ML phylogenetic trees were predicted for each group using the PHYML3.0 method implemented in MEGA 5.2 [16] with the GTR+I+G nucleotide (nt) substitution model and branch support being tested with 3,000 bootstrap iterations.

Simulations were performed based on the results of pairwise sequence comparisons, using different cutoff values (rounded to the nearest full percentile) to delineate potential species so as to determine which sequences

corresponded to virus isolates belonging to the same species, and which were isolates of distinct species. For this, we looked for the optimum cutoff value that placed each sequence into a given species without “outliers” (sequences that displayed identity levels above the cutoff value with two or more species).

Analysis of all 38 groups indicated that the best nt sequence identity cutoff value to separate isolates from different species was 91 %. This value is proposed here as the new species demarcation criterion for viruses of the genus *Begomovirus* using the outlined methodology. Implementing this value yielded the lowest number of outlier sequences compared to any other value within the range of 86 % to 94 % nt sequence identity. The cutoff for strain demarcation is 94 %. Parameters used for comparison are crucial. It is important to note that percent nt sequence identities must be calculated from true pairwise sequence alignments, with the exclusion of sites with gap characters. Ideally, the SDT software that is freely available [14] (<http://web.cbio.uct.ac.za/SDT>) should be used, as it was developed specifically for this purpose.

Phylogenetic support was found to be robust for all new species analyzed across the 38 groups. The 91 % cutoff value is actually quite conservative, as is indicated by the trees for groups 3, 5, 7, 11, 16, 30 and 33 (Supplementary File S1). However, several groups (1, 2, 6, 27, 34 and 36; Supplementary File S1) required additional consideration because the pairwise sequence comparisons and phylogenetic results are conflicting, possibly due to recombination.

Dealing with outliers

The resulting taxonomic framework resulted in the delineation of a small number of outliers. Nevertheless, as the number of sequenced begomoviral genomes continues to increase, additional “conflicting” sequences will become evident. To address this problem, we propose the adoption of the approach described for viruses of the genera *Mastrevirus* [12] and *Curtovirus* [13]. In this light, the four possible conflicts are as follows:

1. An isolate having ≥ 91 % identity (full-length genome or DNA-A component) to isolates assigned to two (or more) species.
2. An isolate having ≥ 91 % identity to one or a few isolates from a particular species, even though it shares <91 % identity with the majority of isolates in that species.
3. An isolate having ≥ 94 % identity to isolates of two (or more) strains of a given species.
4. An isolate having ≥ 94 % identity to one or a few isolates from a particular strain, even though it shares

<94 % identity with the majority of isolates from that strain.

The corresponding conflict-resolution criteria are as follows:

1. The new isolate should be considered to belong to the species that includes the isolate with which it shares the highest percentage of pairwise identity (full-length genome or DNA-A component).
2. The new isolate should be classified as belonging to the species with which it shares ≥ 91 % nt sequence identity with any one isolate from that species, even if it is <91 % identical to all other isolates from that species.
3. The new isolate should be considered to belong to the strain that includes the isolate with which it shares the highest percent identity.
4. The new isolate should be classified as belonging to the strain with which it shares ≥ 94 % nt sequence identity with any one isolate from that strain, even if it has <94 % identity to all other isolates from that strain.

Naturally, any working cutoff value established for viruses, particularly when rapid divergence is occurring (as appears to be the case for begomoviruses), will yield a number of outliers. By adopting these four conflict-resolution criteria, all outliers identified so far could be readily placed into an extant species group.

Exceptions to these rules can include recombinant viruses such as tomato yellow leaf curl Malaga virus (TYLCMaV) and tomato yellow leaf curl Axarquia virus (TYLCAxV), which have ≥ 91 % identity to both parental viruses (tomato yellow leaf curl virus, TYLCV, and tomato yellow leaf curl Sardinia virus, TYLCSV), thus leading to conflict #1 and causing the two parental species to merge into a single species, even though all isolates of the parental viruses have <91 % identity. Such recombinant viruses will have to be examined on a case-by-case basis for species assignment.

The new species demarcation criterion of <91 % nt sequence identity (for full-length genomes or DNA-A components) is more stringent than the previously used 89 %

At first, the higher value, at 91 %, compared to the previously implemented working cutoff of 89 %, may give the impression of a more relaxed species demarcation scenario that might delineate an even greater number of begomovirus species. However, this is not the case. Rather, the pairwise cutoff value at 91 % is a consequence of the

implementation of a more robust approach (now standardized for the entire family *Geminiviridae*) for calculating pairwise identities: true pairwise alignments (compared to global alignment-based pairwise identities) without gaps. This proved to be more stringent than previous approaches based on multiple sequence alignments with gaps treated as a fifth character, which yielded a working cutoff of 89 %.

One group of begomoviruses that has been affected the most by applying the revised analysis is the “sweepovirus” group, a divergent clade of whitefly-transmitted geminiviruses that infect sweet potato and wild species in the Convolvulaceae. Previously, the group was proposed to include 17 species [17]. The new system reduces the number of species by more than half, delineating 8 species (Table 1; Fig. 1).

Results of pairwise sequence comparisons accurately reflect the biology of begomoviruses

It has been claimed that begomoviral species are artificial because they are arbitrarily defined based on sequence alone, and therefore their biological characteristics have been ignored [11]. This is a misconception. Sequence-based taxonomy is possible only because it relies on the knowledge of the biological properties of these well-studied viruses. Therefore, sequence comparisons among related begomovirus isolates can accurately reflect differences in their biology. Several examples can be drawn upon to argue this point. One well-known example involves bean golden mosaic disease, an important disease of bean crops in Latin America. The disease is caused by at least two distinct, well-characterized begomoviruses, bean golden mosaic virus (BGMV), which occurs in Brazil and Argentina, and bean golden yellow mosaic virus (BGYMV), which occurs in Central/North America and the Caribbean Basin [18]. The symptoms of the disease are nearly indistinguishable, the whitefly vector species is the same for both pathogens, and the economic importance with respect to crop loss is comparable as well. In fact, initially, the same begomoviral etiology was suspected for the disease occurring in the two regions. However, when the causal agents from plants collected in Puerto Rico (USA) and Brazil were sequenced, the results indicated that they had substantially different genome sequences [19, 20]. Later, it was demonstrated that the two agents differed in at least one relevant biological property: tissue tropism. BGMV is phloem-restricted in beans, while BGYMV is not [20, 21]. Thus, the species cutoff based on sequence alone was accurate and reflected the biological differences between the viruses belonging to these two species.

Table 1 List of begomovirus species, as of January 2015. Species names are shown in ***bold italics***, and isolate names are given in regular font. For species that do not have any known strains, only one isolate is listed, and that isolate is recognized as the “type” isolate. For species that have known strains, one isolate from each strain is

shown, and the type isolate is the first one listed. Sequence accession numbers and assigned abbreviations are also listed. An expanded table including all begomovirus isolates in GenBank is available for download at the ICTV website (talk.ictvonline.org/ictv_wikis/m/files_begomo/default.aspx)

<i>Abutilon golden mosaic Yucatan virus</i>			
Abutilon golden mosaic Yucatan virus - [Mexico-Yucatan-2007]	AbGMYV-[MX-Yuc-2007]	KC430935	
<i>Abutilon mosaic Bolivia virus</i>			
Abutilon mosaic Bolivia virus - [Bolivia-2007]	AbMBoV-[BO-07]	HM585445	HM585446
<i>Abutilon mosaic Brazil virus</i>			
Abutilon mosaic Brazil virus - [Brazil-BgV01A.1.C21]	AbMBV-[BR-BgV01A.1.C21]	JF694480	JF694483
<i>Abutilon mosaic virus</i>			
Abutilon mosaic virus - [Germany]	AbMV-[DE]	X15983	X15984
<i>African cassava mosaic virus</i>			
African cassava mosaic virus - [Cameroon-1998]	ACMV-[CM-98]	AF112352	AF112353
<i>Ageratum enation virus</i>			
Ageratum enation virus - Nepal [Nepal-1999]	AEV-NP[NP-99]	AJ437618	
Ageratum enation virus - India [India-Kangra-2008]	AEV-IN[IN-Kan-08]	FN543099	
Ageratum enation virus - Uttar Pradesh [India-Uttar Pradesh-SKS-P-2010]	AEV-UP[IN-UP-Ag10-10]	HM149260	
<i>Ageratum leaf curl virus</i>			
Ageratum leaf curl virus - [China-Guangxi 52-2003]	ALCuV-[CN-Gx52-03]	AJ851005	
<i>Ageratum yellow vein Sri Lanka virus</i>			
Ageratum yellow vein Sri Lanka virus - [Sri Lanka-1999]	AYVSLV-[LK-99]	AF314144	
<i>Ageratum yellow vein virus</i>			
Ageratum yellow vein virus - Guangxi [China-Guangxi 129-2005]	AYVV-Gx[CN-Gx129-05]	AM940137	
Ageratum yellow vein virus - [Japan-Soybean crinkle leaf]	AYVV-[JP-Soy]	AB050781	
Ageratum yellow vein virus - China [China-Tomato-2012]	AYVV-CN[CN-Tom-12]	KC172826	
Ageratum yellow vein virus - Hsinchu [Taiwan-Hsinchu-Tom-2003]	AYVV-Hsi[TW-Hsi-Tom-03]	DQ866124	
Ageratum yellow vein virus - Hualian [Taiwan-Hualian 4-2000]	AYVV-Hua[TW-Hua4-00]	DQ866132	
Ageratum yellow vein virus - Indonesia [Indonesia-Tomato]	AYVV-ID[ID-Tom]	AB100305	
Ageratum yellow vein virus - Kamphaengsaen [Thailand-Kamphaengsaen-AFSP3d-2010]	AYVV-Ka[TH-Ka-AFSP3d-10]	JN809816	
Ageratum yellow vein virus - Nanning [China-Nanning-NN1-2009]	AYVV-NN[CN-Nan-NN1-09]	JQ804985	
Ageratum yellow vein virus - Philippines [Philippines-Mindanao-2007]	AYVV-PH[PH-Min-07]	EU487045	
Ageratum yellow vein virus - Singapore [Japan-Ishigaki-2005]	AYVV-SG[JR-Ish-05]	AB306314	
Ageratum yellow vein virus - Taiwan [Taiwan-Tainan-1999]	AYVV-TW[TW-Tai-99]	AF307861	
Ageratum yellow vein virus - Thailand [Thailand-Kamphaengsaen-AFSP6b-2010]	AYVV-TH[TH-Ka-AFSP6b-10]	JN809820	
<i>Allamanda leaf curl virus</i>			
Allamanda leaf curl virus - [China-Guangdong 10-2006]	AILCV-A[CN-Gd10-06]	EF602306	
<i>Alternanthera yellow vein virus</i>			
Alternanthera yellow vein virus - A [China-Fujian 22-2006]	AIYVV-A[CN-Fj22-06]	EF544604	
Alternanthera yellow vein virus - B [China-Fujian-PT1-2006]	AIYVV-B[CN-Fj-PT1-06]	EF544602	
<i>Bean calico mosaic virus</i>			
Bean calico mosaic virus - [Mexico-Sonora-1986]	BCaMV-[MX-Son-86]	AF110189	AF110190
<i>Bean chlorosis virus</i>			
Bean chlorosis virus - [Venezuela-LaBarinesa459-2006]	BChV-[VE-LaB459-06]	JN848770	JN848771
<i>Bean chlorotic mosaic virus</i>			
Bean chlorotic mosaic virus - [Venezuela-Rubio932-2007]	BChMV-[VE-Rub932-07]	JN848772	JN848773
<i>Bean dwarf mosaic virus</i>			
Bean dwarf mosaic virus - [Colombia-1987]	BDMV-[CO-87]	M88179	M88180

Table 1 continued

<i>Bean golden mosaic virus</i>			
Bean golden mosaic virus - [Brazil-Campinas 1-1978]	BGMV-[BR-Cam1-78]	M88686	M88687
Bean golden mosaic virus - Alagoas [Brazil-Mac2-2010]	BGMV-Ala[Brazil-Mac2-2010]	JN419006	
<i>Bean golden yellow mosaic virus</i>			
Bean golden yellow mosaic virus - [Dominican Republic-1987]	BGYMV-[DO-87]	L01635	L01636
<i>Bean yellow mosaic Mexico virus</i>			
Bean yellow mosaic Mexico virus - [Mexico-Mac2-2011]	BYMMxV-[MX-Mac2-11]	FJ944023	
<i>Bhendi yellow vein Bhubhaneswar virus</i>			
Bhendi yellow vein Bhubhaneswar virus - [India-Orissa-2003]	BYVBhV-[IN-Ori-03]	FJ589571	
<i>Bhendi yellow vein mosaic virus</i>			
Bhendi yellow vein mosaic virus - India [India-Madurai]	BYVMV-IN[IN-Mad]	AF241479	
Bhendi yellow vein mosaic virus - [India-Maharashtra-NOL751]	BYVMV-[IN-Mah-NOL751]	EU589392	
Bhendi yellow vein mosaic virus - Haryana [India-Haryana-2007]	BYVMV-Har[IN-Har-07]	FN645923	
Bhendi yellow vein mosaic virus - Pakistan [Pakistan-Faisalabad 201-1995]	BYVMV-[PK-Fai201-95]	AJ002451	
Bhendi yellow vein mosaic virus - Tamil Nadu [India-Coimbatore 4-2004]	BYVMV-TN[IN-Coi4-04]	FJ179372	
Bhendi yellow vein mosaic virus - Thanagan [India-Thanagan-2005]	BYVMV-Tha[IN-Tha-05]	FJ176235	
<i>Blainvillea yellow spot virus</i>			
Blainvillea yellow spot virus - [Brazil-Coi25-2007]	BIYSV-[BR-Coi25-07]	EU710756	EU710757
<i>Blechum interveinal chlorosis virus</i>			
Blechum interveinal chlorosis virus - [Mexico-Campeche-2011]	BleICV-[MX-Cam-11]	JX827487	JX827488
<i>Boerhavia yellow spot virus</i>			
Boerhavia yellow spot virus - [Mexico-Yucatan-2005]	BoYSV-[MX-Yuc-05]	EF121755	
<i>Cabbage leaf curl Jamaica virus</i>			
Cabbage leaf curl Jamaica virus - [Jamaica-CUc3-2005]	CabLCJV-[JM-CUc3-05]	DQ178608	DQ178609
<i>Cabbage leaf curl virus</i>			
Cabbage leaf curl virus - [United States-Florida-1996]	CabLCV-[US-Flo-96]	U65529	U65530
<i>Capraria yellow spot Yucatan virus</i>			
Capraria yellow spot Yucatan virus - [Mexico-Yucatan-Conkal-2007]	CarYSYV-[MX-Yuc-Con-07]	KC426927	KC426928
<i>Cassava mosaic Madagascar virus</i>			
Cassava mosaic Madagascar virus - [Madagascar-Toliary-2006]	CMMGV-[MG-Tol-06]	HE617299	HE617300
<i>Catharanthus yellow mosaic virus</i>			
Catharanthus yellow mosaic virus - [Pakistan-Lahore-KN4]	CaYMV-[PK-Lah-KN4]	HE580234	
<i>Centrosema yellow spot virus</i>			
Centrosema yellow spot virus - [Brazil-Car1-2009]	CeYSV - [BR-Car1-09]	JN419002	
<i>Chayote yellow mosaic virus</i>			
Chayote yellow mosaic virus - [Nigeria-Ibadan]	ChaYMV-[NG-Iba]	AJ223191	
<i>Chenopodium leaf curl virus</i>			
Chenopodium leaf curl virus - [USA-Florida-Citra-2007]	ChLCV-[USA-FL-Cit-07]	HM626515	
<i>Cherry tomato leaf curl virus</i>			
Cherry tomato leaf curl virus - [India-CTM-2005]	CToLCV-[IN-CTM-06]	DQ629102	
<i>Chilli leaf curl Pakistan virus</i>			
Chilli leaf curl Pakistan virus - Pakistan [Pakistan-Shorkot-2004]	ChiLCPKV-PK[PK-Sho-04]	DQ114477	
Chilli leaf curl Pakistan virus - China [China-Yunnan 1045-2009]	ChiLCPKV-CN[CN-Yn1045-09]	HM587709	
<i>Chilli leaf curl India virus</i>			
Chilli leaf curl India virus - [India-2008]	ChiLCINV-[IN-08]	FM877858	
<i>Chilli leaf curl Kanpur virus</i>			
Chilli leaf curl Kanpur virus [India-Kanpur-2008]	ChiLCKV-[IN-Kan-08]	HM007106	

Table 1 continued

<i>Chilli leaf curl Vellnad virus</i>			
Chilli leaf curl Vellnad virus - [India-Vellnad-2008]	ChiLCVV-[IN-Vel-08]	HM007121	
<i>Chilli leaf curl virus</i>			
Chilli leaf curl virus - India [India-Amritsar-Papaya-2009]	ChiLCV-IN[IN-Amr-Pap-09]	GU136803	
Chilli leaf curl virus - [Bangladesh-Gazipur]	ChiLCV-[BD-Gaz]	AJ875159	
Chilli leaf curl virus - Chilli [India-Chilli-2005]	ChiLCV-Chi[IN-Chi-05]	DQ673859	
Chilli leaf curl virus - Joydebpur [India-Pondalu-Hibiscus-2007]	ChiLCV-JO[IN-Pon-Hib-07]	FJ345402	
Chilli leaf curl virus - Khanewal [Pakistan-Khanewal-2004]	ChiLCV-Kha[PK-Kha-04]	DQ116878	
Chilli leaf curl virus - Pakistan [Pakistan-Multan-1998]	ChiLCV-PK[PK-Mul-98]	AF336806	
<i>Chino del tomate Amazonas virus</i>			
Chino del tomate Amazonas virus - [Brazil-AM10-2007]	CdTAV-[BR-AM10-07]	HM357461	
<i>Chino del tomate virus</i>			
Chino del tomate virus - Tomato [Mexico-Sinaloa IC-1983]	CdTV-To[MX-SinIC-83]	AF101476	AF101478
Chino del tomate virus - [Mexico-Iguala]	CdTV-[MX-Igu]	AY751753	
Chino del tomate virus - Soybean [Mexico-Sinaloa-2005]	CdTV-Sb[MX-Sin-05]	DQ347945	
<i>Cleome golden mosaic virus</i>			
Cleome golden mosaic virus - [Brazil-BA 05-2007]	CleGMV-[BR-BA05-07]	HQ396465	
<i>Cleome leaf crumple virus</i>			
Cleome leaf crumple virus - [Brazil-BgV05A.1.C75]	CleLCrV-[BR-BgV051C75]	JF694461	JF694465
<i>Clerodendron yellow mosaic virus</i>			
Clerodendron yellow mosaic virus - [India-Iari-2006]	CIYMV-[IN-Iari-06]	EF408037	
<i>Clerodendrum golden mosaic China virus</i>			
Clerodendron golden mosaic China virus - Fuzon [China-Fuzhou 7-2007]	CIGMCNV-Fu[CN-Fz7-07]	FJ011668	FJ011669
Clerodendron golden mosaic China virus - Jiangsu [China-Jiangsu XY1-2008]	CIGMCNV-Ji[CN-JsXY1-08]	FN396962	FN396963
<i>Clerodendrum golden mosaic Jiangsu virus</i>			
Clerodendron golden mosaic Jiangsu virus - [China-Jiangsu XY2-2008]	CIGMJsV-[CN-JsXY2-08]	FN396966	
<i>Clerodendrum golden mosaic virus</i>			
Clerodendron golden mosaic virus - [Vietnam-Sonla-2005]	CIGMV-[VN-Son-05]	DQ641692	DQ641693
<i>Corchorus golden mosaic virus</i>			
Corchorus golden mosaic virus - India [India-Bahraich-2008]	CoGMV-Ba[IN-Bah-08]	FJ463902	FJ463901
Corchorus golden mosaic virus - Hanoi [Vietnam-Hanoi-2005]	CoGMV-Ha[VN-Han-05]	DQ641688	DQ641689
<i>Corchorus yellow spot virus</i>			
Corchorus yellow spot virus - [Mexico-Yucatan-2005]	CoYSV-[MX-Yuc-05]	DQ875868	DQ875869
<i>Corchorus yellow vein mosaic virus</i>			
Corchorus yellow vein mosaic virus - [India-Maharashtra-2011]	CoYV-[IN-Mah-11]	KC196077	
<i>Corchorus yellow vein Vietnam virus</i>			
Corchorus yellow vein Vietnam virus - [Vietnam-Hoa Binh-2000]	CoYVV-[VN-Hoa-00]	AY727903	AY727904
<i>Cotton chlorotic spot virus</i>			
Cotton chlorotic spot virus - [Brazil-CampinaGrandeB012-2009]	CoChSpV-[BR-Cam-09]	KF358470	
<i>Cotton leaf crumple virus</i>			
Cotton leaf crumple virus - Arizona [Mexico-Sonora-1991]	CLCrV-AZ[MX-Son-91]	AF480940	AF480941
Cotton leaf crumple virus - Texas [United States-Texas-1991]	CLCrV-TX[US-Tex-91]	AY083351	
<i>Cotton leaf curl Alabad virus</i>			
Cotton leaf curl Alabad virus - Alabad [Pakistan-Alabad 804a-1996]	CLCuAIV-Al[PK-Ala804a-96]	AJ002452	
Cotton leaf curl Alabad virus - Haryana [India-Karnal-OY77-Okra-2005]	CLCuAIV-Ha[IN-Kar-OY77-Okr-05]	GU112081	
Cotton leaf curl Alabad virus - Karnal [India-Karnal-OY81B-Okra-2005]	CLCuAIV-Ka[IN-Kar-OY81B-Okr-05]	GU112004	
Cotton leaf curl Alabad virus - Lobatum [Pakistan-Multan-Lobatum-2006]	CLCuAIV-Lo[PK-Mul-Lob-06]	FJ210467	FJ218488

Table 1 continued

Cotton leaf curl Alabad virus - Multan [Pakistan-Multan-Punctatum-2006]	CLCuAIV-Mu[PK-Mul-Pun-06]	EU384575	EU384578
<i>Cotton leaf curl Bangalore virus</i>			
Cotton leaf curl Bangalore virus - [India-Bangalore-2004]	CLCuBaV-[IN-Ban-04]	AY705380	
<i>Cotton leaf curl Gezira virus</i>			
Cotton leaf curl Gezira virus - Sudan [Sudan-Gezira-1996]	CLCuGeV-SD[SD-Gez-96]	AF260241	
Cotton leaf curl Gezira virus - Burkina Faso [Burkina Faso-Bazega-Okra-2009]	CLCuGeV-BF[BF-Baz-Ok-09]	FN554540	
Cotton leaf curl Gezira virus - Cairo [Egypt-Cairo-Hollyhock]	CLCuGeV-Ca[EG-Cai-Hol]	AJ542539	
Cotton leaf curl Gezira virus - Cameroon [Cameroon-Muea-Okra-2008]	CLCuGeV-CM[CM-Mue-Ok-08]	FM210276	
Cotton leaf curl Gezira virus - Egypt [Egypt-Aswan-Okra]	CLCuGeV-EG[EG-Asw-Ok-08]	AF155064	
Cotton leaf curl Gezira virus - Hollyhock [Egypt-Giza-Hollyhock]	CLCuGeV-Ho[EG-Giz-Hol]	AF014881	
Cotton leaf curl Gezira virus - Lysoka [Cameroon-Lysoka11-Okra-2008]	CLCuGeV-Ly[CM-Lys11-Ok-08]	FM164726	
Cotton leaf curl Gezira virus - Madagascar [Madagascar-Fort Dauphin-bean-2001]	CLCuGeV-MG[MG-FtD-Bea-01]	AM701757	
Cotton leaf curl Gezira virus - Mali [Mali-Bamako-Okra-2006]	CLCuGeV-ML[ML-Bam-Ok-06]	EU024120	
Cotton leaf curl Gezira virus - Niger [Niger-Niamey2-Okra-2007]	CLCuGeV-NENE-Nia2-Ok-07]	EU432373	
Cotton leaf curl Gezira virus - Okra [Sudan-Okra-2007]	CLCuGeV-Ok[SD-Ok-07]	FJ868828	
<i>Cotton leaf curl Kokhran virus</i>			
Cotton leaf curl Kokhran virus - Kokhran [Pakistan-Faisalabad 1]	CLCuKoV-Ko[PK-Fai1]	AJ496286	
Cotton leaf curl Kokhran virus - Burewala [Pakistan-Vehari-2006]	CLCuKoV-Bu[PK-Veh-06]	AM421522	
Cotton leaf curl Kokhran virus - Layyah [Pakistan-Layyah-2011]	CLCuKoV-La[PK-Lay-11]	HF549182	
Cotton leaf curl Kokhran virus - Lucknow [India-Lucknow-Cyamopsis tetragonoloba-Bean-2010]	CLCuKoV-Lu[IN-Luc-Ct-Bea10]	GU385879	
Cotton leaf curl Kokhran virus - Shadadpur [Pakistan-Shadadpur-2005]	CLCuKoV-Sha[PK-Sha-05]	FN552001	
<i>Cotton leaf curl Multan virus</i>			
Cotton leaf curl Multan virus - Darwinii [Pakistan-Multan-Darwinii 1-2006]	CLCuMuV-Dar[PK-Mul-Dar1-06]	EU365613	
Cotton leaf curl Multan virus - Faisalabad [Pakistan-Yazman 62-1995]	CLCuMuV-Fai[PK-Yaz62-95]	AJ002447	
Cotton leaf curl Multan virus - Hibiscus [India-Hibiscus1-2011]	CLCuMuV-Hib[IN-Hib1-11]	JN807763	
Cotton leaf curl Multan virus - Hisar [Pakistan-Multan-H65-1-1997]	CLCuMuV-His[PK-Mul-H65-1-97]	AJ132430	
Cotton leaf curl Multan virus - Pakistan [Pakistan-Multan-Davidsonii-2006]	CLCuMuV-PK[PK-Mul-06]	EU365616	
Cotton leaf curl Multan virus - Rajasthan [India-Sriganganagar-1994]	CLCuMuV-Ra[IN-Sri-94]	AF363011	
<i>Cowpea golden mosaic virus</i>			
Cowpea golden mosaic virus - [Nigeria-Nsukka-1990]	CPGMV-[NG-Nsu-90]	AF029217	
<i>Crassocephalum yellow vein virus</i>			
Crassocephalum yellow vein virus - [China-Jinhong-2005]	CraYVV-[CN-Jin-05]	EF165536	
<i>Cucurbit leaf curl virus</i>			
Cucurbit leaf curl virus - [United States-Arizona-1991]	CuLCuV-[US-Ari-91]	AF256200	AF327559
<i>Dalechampia chlorotic mosaic virus</i>			
Dalechampia chlorotic mosaic virus - [Venezuela-Albarico1020-2007]	DaChMV-[VE-Alb1020-07]	JN848775	JN848776
<i>Datura leaf distortion virus</i>			
Datura leaf distortion virus - [Venezuela-Rubio 933-2007]	DaLDV-[VE-Rub933-07]	JN848773	JN848774
<i>Desmodium leaf distortion virus</i>			
Desmodium leaf distortion virus - [Mexico-Yucatan-2005]	DesLDV-[MX-Yuc-05]	DQ875870	DQ875871
<i>Dicliptera yellow mottle virus</i>			
Dicliptera yellow mottle virus - [United States-Florida-1998]	DiYMoV-[US-Flo-98]	AF139168	AF170101
<i>Dolichos yellow mosaic virus</i>			
Dolichos yellow mosaic virus - [Bangladesh-Gazipur]	DoYMV-[BD-Gaz]	AY271891	

Table 1 continued

<i>East African cassava mosaic virus</i>			
East African cassava mosaic virus - Kenya [Kenya-Boa-K48-2001]	EACMV-KE[KE-Boa-K48-01]	AJ1717542	AJ704949
East African cassava mosaic virus - [Malawi-8N-2007]	EACMV-[MW-8N-07]	JX473582	
East African cassava mosaic virus - Cameroon [Cameroon-1998]	EACMV-CM[CM-98]	AF112354	AF112355
East African cassava mosaic virus - Tanzania [Tanzania-1-2001]	EACMV-TZ[TZ-1-01]	AY795983	AY795989
East African cassava mosaic virus - Uganda [Uganda-Mld2-1997]	EACMV-UG[UG-Mld2-97]	AF126804	
<i>East African cassava mosaic Kenya virus</i>			
East African cassava mosaic Kenya virus - [Kenya-Kathiana-K300-2002]	EACMKV-[KE-Kat-K300-02]	AJ1717580	AJ704965
<i>East African cassava mosaic Malawi virus</i>			
East African cassava mosaic Malawi virus - [Malawi-K-1996]	EACMMV-[MW-K-96]	AJ006460	
<i>East African cassava mosaic Zanzibar virus</i>			
East African cassava mosaic Zanzibar virus - [Kenya-Felunzi-K19-2001]	EACMZV-[KE-Fel-K19-01]	AJ1717562	AJ704942
<i>Emilia yellow vein virus</i>			
Emilia yellow vein virus - [China-Fuzhou 1-2007]	EYVV-[CN-Fz1-07]	U377539	
<i>Erectites yellow mosaic virus</i>			
Erectites yellow mosaic virus - [Vietnam-Hoabinh-2005]	ErYMV-[VN-Hoa-05]	DQ641698	
<i>Eupatorium yellow vein virus</i>			
Eupatorium yellow vein virus - A [Japan-Kumamoto]	EpYVV-A[JR-Kum]	AB007990	
Eupatorium yellow vein virus - [Japan-SOJ3-2000]	EpYVV-[JR-SOJ3-00]	AJ438937	
Eupatorium yellow vein virus - B [Japan-MNS2-2000]	EpYVV-B[JR-MNS2-00]	AJ438936	
Eupatorium yellow vein virus - C [Japan-Yamaguchi]	EpYVV-C[JR-Yam]	AB079766	
Eupatorium yellow vein virus - D [Japan-Suya-2007]	EpYVV-D[JR-Suy-07]	AB300463	
Eupatorium yellow vein virus - E [Japan-Kagawa-Tomato-1997]	EpYVV-E[JR-Kag-97]	AB433979	
<i>Euphorbia leaf curl Guangxi virus</i>			
Euphorbia leaf curl Guangxi virus - A [China-Guangxi 35-1-2002]	EuLCGxV-A[CN-Gx35-1-02]	AM411424	
<i>Euphorbia leaf curl virus</i>			
Euphorbia leaf curl virus - [China-Fujian-2006]	EuLCuV-[CN-Fuj-06]	FJ487911	
<i>Euphorbia mosaic virus</i>			
Euphorbia mosaic virus - [Cuba-Tobacco-2007]	EuMV-[CU-Tb-07]	FJ807782	FJ807783
<i>Euphorbia yellow mosaic virus</i>			
Euphorbia yellow mosaic virus - [Brazil-2008]	EuMV-[BZ-08]	FJ619507	FJ619508
Euphorbia yellow mosaic virus - Goias [Brazil-GO-Luziania 8675-2009]	EuYMV-GO[BR-GO-Luz 8675-09]	JF756676	
<i>French bean leaf curl virus</i>			
French bean leaf curl virus - [India-Kanpur-2011]	FbLCV-[IN-Kan-11]	JQ866297	
<i>Hedyotis uncinella yellow mosaic virus</i>			
Hedyotis uncinella yellow mosaic virus - [Vietnam-VN1]	HeuYMV-[VN-VN1]	KF429251	
<i>Hemidesmus yellow mosaic virus</i>			
Hemidesmus yellow mosaic virus - [India-Tirupati-H1-2012]	HemYMV-[IN-Tir-H1-12]	KC898543	
<i>Hollyhock leaf curl virus</i>			
Hollyhock leaf curl virus - [Pakistan-Faisalabad-20-4-06]	HoLCV-[PK-Fai-20-4-06]	FR772082	
<i>Honeysuckle yellow vein virus</i>			
Honeysuckle yellow vein virus - Japan [Japan-Sapporo 1-2000]	HYVV-JR[JR-SP1-00]	AB182261	
Honeysuckle yellow vein virus - [Australia-Ayr-BRIP57501-1983]	HYVV-[AU-Ayr-BRIP57501-83]	JX416174	
Honeysuckle yellow vein virus - A [Japan-Fukuoka 1]	HYVV-A[JR-Fuk1]	AB178945	
Honeysuckle yellow vein virus - B [Japan]	HYVV-B[JR]	AB020781	
Honeysuckle yellow vein virus - C [Japan-Yamaguchi]	HYVV-C[JR-Yam]	AB079765	
Honeysuckle yellow vein virus - D [Japan-Nara 2-2006]	HYVV-D[JR-Nar2-06]	AB287441	
Honeysuckle yellow vein virus - E [Japan-Nara 1-2006]	HYVV-E[JR-Nar1-06]	AB287440	
Honeysuckle yellow vein virus - Ibaraki [Japan-Ibaraki-Honeysuckle-2006]	HYVV-Iba[JR-Iba-06]	AB287439	
Honeysuckle yellow vein virus - Jeju [South Korea-Jeju 138-Tomato-2008]	HYVV-Je[KR-Jeju138-To-08]	HM164545	
Honeysuckle yellow vein virus - Kobe [Japan-Hyogo 12-2000]	HYVV-Kob[JR-Hyo12-00]	AB178946	

Table 1 continued

Honeysuckle yellow vein virus - Kochi [Japan-Kochi-Tomato-2000]	HYVV-Koc[JR-Koc-Tom-00]	AB055009	
Honeysuckle yellow vein virus - Mas [Japan-Masuda-2006]	HYVV-Mas[JR-Mas-06]	AB236325	
Honeysuckle yellow vein virus - Nara [Japan-Nara3-2001]	HYVV-Nar[JR-Nar3-01]	AB079689	
Honeysuckle yellow vein virus - South Korea 1 [South Korea-2007]	HYVV-KR1[KR-07]	FJ434943	
Honeysuckle yellow vein virus - South Korea 2 [South Korea-KJ-Tomato-2007]	HYVV-KR2[KR-KJ-To-07]	HM164547	
Honeysuckle yellow vein virus - UK [Japan-Fukui-2006]	HYVV-UK[JR-Fuk-06]	AB236321	
<i>Horsegram yellow mosaic virus</i>			
Horsegram yellow mosaic virus - [India-Bangalore-2004]	HgYMV-[IN-Ban-04]	AM932427	AM932428
<i>Indian cassava mosaic virus</i>			
Indian cassava mosaic virus - India [India-Maharashtra 2-1988]	ICMV-IN[IN-Mah2-88]	AY730035	AY730036
Indian cassava mosaic virus - [India-Maharashtra-2009]	ICMV-[IN-Mah-09]	JF496657	
Indian cassava mosaic virus - Jatropha [India-Dhawad-2008]	ICMV-Jat[IN-Dha-08]	GQ924760	GQ924761
Indian cassava mosaic virus - Kerala [India-Kerala 2-2002]	ICMV-Ker[IN-Ker2-02]	AJ575819	
<i>Jacquemontia mosaic Yucatan virus</i>			
Jacquemontia mosaic Yucatan virus - [Mexico-Yucatan-2007]	JacMYuV-[MX-Yuc-07]	JQ821386	JQ821387
<i>Jatropha leaf curl virus</i>			
Jatropha leaf curl virus - New Delhi [India-New Delhi-2007]	JLCuV-ND[IN-ND-07]	EU798996	
Jatropha leaf curl virus - [India-Gujarat-2009]	JLCuV-Gu[IN-Guj-09]	GU451249	
<i>Jatropha mosaic India virus</i>			
Jatropha mosaic India virus - [India-Lucknow-2009]	JMINV-[IN-Luc-09]	HM230683	
<i>Jatropha mosaic Nigerian virus</i>			
Jatropha mosaic Nigerian virus - [Nigeria-2-2011]	JMNV-[NG-2-11]	JX025358	
<i>Jatropha mosaic virus</i>			
Jatropha mosaic virus - [Jamaica-Spanish Town 1-2004]	JMV-[JM-ST1-04]	KF723258	KF723261
<i>Jatropha yellow mosaic India virus</i>			
Jatropha yellow mosaic India virus - [India-Kathaupahadi-2008]	JYMINV-[IN-Kat-08]	FJ177030	
<i>Kudzu mosaic virus</i>			
Kudzu mosaic virus - [China-Fujian-2008]	KuMV-[CN-Fuj-08]	FJ539014	FJ539015
<i>Lindernia anagallis yellow vein virus</i>			
Lindernia anagallis yellow vein virus - [China-Hainan-2004]	LaYVV-[CN-Hn-04]	AY795900	
<i>Ludwigia yellow vein virus</i>			
Ludwigia yellow vein virus - [China-Guangxi 37-2003]	LuYVV-[CN-Gx37-03]	AJ965539	
<i>Luffa yellow mosaic virus</i>			
Luffa yellow mosaic virus - [Vietnam]	LYMV-[VN]	AF509739	AF509740
<i>Macroptilium golden mosaic virus</i>			
Macroptilium golden mosaic virus - [Jamaica- Augusta Town-2004]	MacGMV-[JM-StT-04]	EU158096	EU158097
<i>Macroptilium mosaic Puerto Rico virus</i>			
Macroptilium mosaic Puerto Rico virus - [Puerto Rico-Bean-1998]	MacMPRV-[PR-Bea-98]	AF449192	AF449193
<i>Macroptilium yellow mosaic Florida virus</i>			
Macroptilium yellow mosaic Florida virus - [United States-Florida-1985]	MacYMFV-[US-Flo-85]	AY044135	AY044136
<i>Macroptilium yellow mosaic virus</i>			
Macroptilium yellow mosaic virus - Cuba [Cuba]	MacYMV-CU[CU]	AJ344452	
Macroptilium yellow mosaic virus - Jamaica [Jamaica-Mona-2006]	MacYMV-JM[JM-Mon-06]	EF582840	EF582841
<i>Macroptilium yellow spot virus</i>			
Macroptilium yellow spot virus - [Brazil-Agua das Flores 1-2010]	MaYSV-[BR-Agf1-10]	JN419013	
<i>Macroptilium yellow vein virus</i>			
Macroptilium yellow vein virus - [Brazil-Maceio 4-2010]	MaYVV-[BR-Mac4-10]	JN419021	
<i>Malvastrum leaf curl Philippines virus</i>			
Malvastrum leaf curl Philippines virus - [Philippines-Mc1-2012]	MaLCPHV-[PH-Mc1-12]	KC577540	

Table 1 continued

<i>Malvastrum leaf curl virus</i>			
Malvastrum leaf curl virus - [China-Guangxi 100 -Papaya-2005]	MaLCuV-[CN-Gx100-Pap-05]	AM260699	
<i>Malvastrum yellow mosaic Helshire virus</i>			
Malvastrum yellow mosaic Helshire virus - [Jamaica-2005]	MaYMHeV-[JM-05]	FJ600483	
<i>Malvastrum yellow mosaic Jamaica virus</i>			
Malvastrum yellow mosaic Jamaica virus - [Jamaica-179A73-2003]	MaYMJV-[JM-179A73-03]	FJ601917	FJ600485
<i>Malvastrum yellow mosaic virus</i>			
Malvastrum yellow mosaic virus - [China-Hainan 36-2004]	MaYMV-[CN-Hn36-04]	AM236755	
<i>Malvastrum yellow vein virus</i>			
Malvastrum yellow vein virus - [China-Yunnan 206-Ageratum-2003]	MaYVV-[CN-Yn206-Age-03]	AJ744881	
Malvastrum yellow vein virus - A [China-Yunnan 278-2004]	MaYVV-A[CN-Yn278-04]	FN386459	
Malvastrum yellow vein virus - B [China-Yunnan 340-Sida-2008]	MaYVV-C[CN-Yn340-Sid-08]	FN806779	
<i>Malvastrum yellow vein Yunnan virus</i>			
Malvastrum yellow vein Yunnan virus - [China-Yunnan 160-2003]	MaYVYnV-[CN-Yn160-03]	AJ786711	
<i>Melon chlorotic leaf curl virus</i>			
Melon chlorotic leaf curl virus - Costa Rica [Costa Rica-Guanacaste-1998]	MCLCuV-CR[CR-Gua-98]	AY064391	AF440790
Melon chlorotic leaf curl virus - [Costa Rica-Cucurbita-2A-2003]	MCLCuV-[CR-Cuc-2A-03]	KC153490	
Melon chlorotic leaf curl virus - Guatemala [Guatemala-2000]	MCLCuV-GT[GT-00]	AF325497	AF325498
<i>Melon chlorotic mosaic virus</i>			
Melon chlorotic mosaic virus - [Venezuela-Watermelon-2009]	MCIMV-[VN-Wat-09]	HM163576	HM163577
<i>Merremia leaf curl virus</i>			
Merremia leaf curl virus - [Puerto Rico-N1-2006]	MerLCV-[PR-N1-06]	DQ644561	
<i>Merremia mosaic virus</i>			
Merremia mosaic virus - Venezuela [Venezuela-Trujillo]	MerMV-VE[VE-Tru]	AY508991	AY508992
Merremia mosaic virus - Puerto Rico [Puerto Rico-]	MerMV-PR[PR]	AF068636	AY965899
<i>Merremia mosaic Puerto Rico virus</i>			
Merremia mosaic Puerto Rico virus - [Puerto Rico-89-1998]	MerMPRV-[PR-PR89-98]	FJ944021	FJ944022
<i>Mesta yellow vein mosaic Bahraich virus</i>			
Mesta yellow vein mosaic Bahraich virus - [India-Bahraich-2007]	MeYVMBaV-[IN-Bah-07]	EU360303	
<i>Mesta yellow vein mosaic virus</i>			
Mesta yellow vein mosaic virus - Andhra Pradesh [India-Amadalavalasa 27-2008]	MeYVMV-And[IN-Ama27-08]	FJ159269	
Mesta yellow vein mosaic virus - [Pakistan-Changa Manga-2009]	MeYVMV-[PK-CM-09]	FR715681	
Mesta yellow vein mosaic virus - Bengal [India-Bongaon-Leaf curl-2007]	MeYVMV-Ben[IN-Bon-LC-07]	FJ345400	
<i>Mimosa yellow leaf curl virus</i>			
Mimosa yellow leaf curl virus - [Vietnam-Binhduong-2005]	MiYLCV-[VN-Bin-05]	DQ641695	
<i>Mungbean yellow mosaic India virus</i>			
Mungbean yellow mosaic India virus - [India- Sriganganagar-Mungbean 1-1996]	MYMIV-[IN-Sri-Mg1-96]	AF416742	AF416741
<i>Mungbean yellow mosaic virus</i>			
Mungbean yellow mosaic virus - [India-Madurai-Soybean]	MYMV-[IN-Mad-Sb]	AJ421642	AJ867554
<i>Okra enation leaf curl virus</i>			
Okra enation leaf curl virus - [India-Sonipat EL10-2006]	OELCuV-[IN-SonEL10-06]	GU111996	
<i>Okra mottle virus</i>			
Okra mottle virus - [Brazil-6319-2008]	OMoV-[BR-6319-08]	EU914817	EU914818
<i>Okra yellow crinkle virus</i>			
Okra yellow crinkle virus - Cameroon [Cameroon-Muea-2008]	OYCrV-CM[CM-Mue-08]	FM210275	
Okra yellow crinkle virus - [Cameroon-Njombe 5-2007]	OYCrV-[CM-Njo5-07]	HE793424	
Okra yellow crinkle virus - Mali [Mali-Bamako 4-2006]	OYCrV-ML[ML-Bam4-06]	EU024119	
<i>Okra yellow mosaic Mexico virus</i>			
Okra yellow mosaic Mexico virus - [Mexico-Mazatepec 3-2004]	OYMV-[MX-Maz3-04]	DQ022611	GU972604
<i>Papaya leaf crumple virus</i>			
Papaya leaf crumple virus - [India-Nirulas-2007]	PaLCrV-[IN-Nir-07]	HM140368	

Table 1 continued

<i>Papaya leaf curl China virus</i>			
Papaya leaf curl China virus - Ageratum [China-Guangxi 10-Ageratum-2002]	PaLCuCNV-Age[CN-Gx10-02]	AJ558125	
Papaya leaf curl China virus - [China-Hainan-HK7-2008]	PaLCuCNV-[CN-Hn-HK7-08]	FN256261	
Papaya leaf curl China virus - Guangxi [China-Guangxi 4-Tomato-2008]	PaLCuCNV-Gx[CN-Gx8-To-08]	FN297834	
Papaya leaf curl China virus - Papaya [China-Guangxi 30-Tomato-2002]	PaLCuCNV-Pap[CN-Gx30-Tom-02]	AJ558117	
Papaya leaf curl China virus - Tomato [China-Guangxi 12-Tomato-2002]	PaLCuCNV-To[CN-Gx12-02]	AJ558116	
Papaya leaf curl China virus - Vietnam [Vietnam-Hanoi 112-2007]	PaLCuCNV-VN[VN-Han112-07]	GQ373254	
<i>Papaya leaf curl Guangdong virus</i>			
Papaya leaf curl Guangdong virus - [China-Fujian-Euphorbia-2006]	PaLCuGdV-[CN-Fuj-Eu-06]	FJ495184	
<i>Papaya leaf curl virus</i>			
Papaya leaf curl virus - Lucknow [India-Lucknow]	PaLCuV-Luc[IN-Luc]	Y15934	
Papaya leaf curl virus - A [India-WB-Cr-Croton-2008]	PaLCuV-A[IN-WB-Cr-Cro-08]	JN817517	
Papaya leaf curl virus - Amaranthus [India-Lucknow-Amaranthus-2011]	PaLCuV-Ama[PK-Luc-Am-11]	JN135233	
Papaya leaf curl virus - Aster [India-Lucknow-Aster-2011]	PaLCuV-Ast[PK-Luc-As-11]	JQ954859	
Papaya leaf curl virus - Cirica [India-PaND13-2012]	PaLCuV-Cir[IN-PaND13-12]	KF307208	
Papaya leaf curl virus - Croton[India-Croton]	PaLCuV-Cro[IN-Cro]	AJ507777	
Papaya leaf curl virus - India [India-Pataudi-Radish-2009]	PaLCuV-IN[IN-Pat-Rad-09]	FJ593629	
Papaya leaf curl virus - Lahore [Pakistan-Lahore-HYDNA-Alcea rosea-2006]	PaLCuV-Lah[PK-Lah-HYDNA-Alc-06] FN678906		
Papaya leaf curl virus - Pakistan [Pakistan-Cotton-2002]	PaLCuV-PK[PK-Cot-02]	AJ436992	
Papaya leaf curl virus - Punjab [Pakistan-Punjab-Cro-2006]	PaLCuV-Pun[PK-Pun-Cro-06]	FN543112	
Papaya leaf curl virus - Rhynchosia [Pakistan-Mianwali-Rhynchosia capitata-2007]	PaLCuV-Rh[PK-Mia-Rc-07]	FM955601	
Papaya leaf curl virus - Sikar [India-Sikar-Calotropis procera-2010]	PaLCuV-Sik[In-Sik-Cal-10]	JQ407224	
Papaya leaf curl virus - Soybean [India-Lucknow-Soybean-2011]	PaLCuV-Soy[IN-Luc-Soy-11]	JN807765	
Papaya leaf curl virus - Tobacco[India-Lucknow-Nicotiana glutinosa-2010]	PaLCuV-Tob[IN-Luc-Nic-10]	HM143914	
Papaya leaf curl virus - Tomato [India-CTM-Tomato-2005]	PaLCuV-Tom[IN-CTM-Tom-06]	DQ629102	
<i>Passionfruit severe leaf distortion virus</i>			
Passionfruit severe leaf distortion virus - [Brazil-LSN 2-2001]	PSLDV-[BR-LSN2-01]	FJ972767	FJ972768
<i>Pedilanthus leaf curl virus</i>			
Pedilanthus leaf curl virus - [Pakistan-Multan-2006]	PeLCV-[PK-Mul-06]	AM712436	
Pedilanthus leaf curl virus - Euphorbia [Pakistan-Rahim Yar Khan 1-Tomato-2004]	PeLCV-Eu[PK-RYK1-To-04]	DQ116884	
Pedilanthus leaf curl virus - Soybean [Pakistan-Nawab Shah-Soybean-2009]	PeLCV-Sb[PK-NS-Sb-09]	AM948961	
<i>Pepper golden mosaic virus</i>			
Pepper golden mosaic virus - United States [United States-Mosaic-1987]	PepGMV-US[US-Mos-87]	AY928512	AY928513
Pepper golden mosaic virus - Costa Rica [Costa Rica]	PepGMV-CR[CR]	AF149227	
Pepper golden mosaic virus - [Costa Rica-Llano Grande-2008]	PepGMV-[CR-LG-08]	JQ743486	
<i>Pepper huasteco yellow vein virus</i>			
Pepper huasteco yellow vein virus - [Mexico-Tamaulipas]	PHYVV-[MX-Tam]	X70418	X70419
<i>Pepper leaf curl Bangladesh virus</i>			
Pepper leaf curl Bangladesh virus - Bangladesh [Bangladesh-Bogra-1999]	PepLCBV-BD[BD-Bog-99]	AF314531	
Pepper leaf curl Bangladesh virus - [Pakistan-Lahore-2004]	PepLCBV-[PK-Lah-04]	AM404179	
Pepper leaf curl Bangladesh virus - India [India-Coimbatore-2008]	PepLCBV-IN[IN-Coi-08]	HM007096	
Pepper leaf curl Bangladesh virus - Pakistan [Pakistan-Khanewal-2004]	PepLCBV-PK[PK-Kha-04]	DQ116881	
<i>Pepper leaf curl Lahore virus</i>			
Pepper leaf curl Lahore virus - [India-Lucknow-2011]	PepLCLaV-[IN-Luc-11]	JN135234	
<i>Pepper leaf curl virus</i>			
Pepper leaf curl virus - Malaysia [Malaysia-Klang-1997]	PepLCV-MY[MY-Kla-97]	AF414287	
Pepper leaf curl virus - Thailand [Thailand]	PepLCV-TH[TH]	AF134484	

Table 1 continued

<i>Pepper leaf curl Yunnan virus</i>			
Pepper leaf curl Yunnan virus - [China-Yunnan323-2007]	PepLCYnV-[CN-Yn323-07]	EU585781	
<i>Pepper yellow leaf curl China virus</i>			
Pepper yellow leaf curl China virus - [China-YN65-1-2010]	PepYLCCNV-[CN-YN65-1-10]	KC149938	
<i>Pepper yellow leaf curl Indonesia virus</i>			
Pepper yellow leaf curl Indonesia virus - [Indonesia-2005]	PepYLCIV-[ID-05]	AB267834	AB267835
<i>Pepper yellow vein Mali virus</i>			
Pepper yellow vein Mali virus - [Burkina Faso-Banfora-hot pepper1-2009]	PepYVMLV-[BF-Ban-Hpe1-09]	FN555172	
<i>Potato yellow mosaic virus</i>			
Potato yellow mosaic virus - Potato [Venezuela-1991]	PYMV-Po[VE-91]	D00940	D00941
Potato yellow mosaic virus - [Trinidad and Tobago-Tomato-1996]	PYMV-[TT-Tom-96]	AF039031	AF039032
Potato yellow mosaic virus - Colombia [Colombia-Valle del Cauca-Tomato-2007]	PYMV-Co[CO-VdC-Tom-07]	EU518935	
Potato yellow mosaic virus - Tomato [Puerto Rico-Tomato-2004]	PYMV-To[PR-Tom-04]	AY965897	AY965898
<i>Pouzolzia golden mosaic virus</i>			
Pouzolzia golden mosaic virus - [China-TY01-2012]	PouGMV-[CN-TY01-12]	JX183732	
<i>Pouzolzia mosaic Guangdong virus</i>			
Pouzolzia mosaic Guangdong virus - [Taiwan-Miaoli-ML13W1-2013]	PouMGDV-[TW-Mia-ML13W1-13]	KF414123	
<i>Premna leaf curl virus</i>			
Premna leaf curl virus - [Vietnam-VN7-2011]	PreLCV-[VN-VN7-11]	JQ793786	
<i>Pumpkin yellow mosaic Malaysia virus</i>			
Pumpkin yellow mosaic Malaysia virus - [Malaysia-Negeri Sembilan-2001]	PuYMV-[MY-Neg-01]	EF197941	
<i>Radish leaf curl virus</i>			
Radish leaf curl virus - [India-Varanasi-2005]	RaLCuV-[IN-Var-03]	EF175733	
Radish leaf curl virus - Tomato [Pakistan-Bihar-Tomato-2009]	RaLCuV-To[PK-Bih-To-09]	GU732204	
<i>Rhynchosia golden mosaic Havana virus</i>			
Rhynchosia golden mosaic Havana virus - [Cuba-Havana-2007]	RhGMHaV-[CU-Hav-07]	HM236368	HM236369
<i>Rhynchosia golden mosaic virus</i>			
Rhynchosia golden mosaic virus - Mexico [Mexico-Sinaloa-2005]	RhGMV-MX[MX-Sin-05]	DQ347950	DQ356429
Rhynchosia golden mosaic virus - Honduras [Mexico-Chiapas-Tobacco]	RhGMV-HN[MX-Chi-Tob]	AF408199	
Rhynchosia golden mosaic virus - Soybean [Mexico-Sinaloa 4-Soybean-2007]	RhGMV-Sb[MX-Sin4-Sb-07]	EU339936	EU339937
<i>Rhynchosia mild mosaic virus</i>			
Rhynchosia mild mosaic virus - [Puerto Rico-PR79-1997]	RhMMV-[PR-PR79-97]	FJ944019	
<i>Rhynchosia rugose golden mosaic virus</i>			
Rhynchosia rugose golden mosaic virus - [Cuba-Camaguey-2009]	RhRGMV-[CU-Cam-09]	HM236370	HM236371
<i>Rhynchosia yellow mosaic India virus</i>			
Rhynchosia yellow mosaic India virus - [India-Thiruvananthapuram-JRH1-2009]	RhYMIV-[IN-Thi-JRH1-09]	HM777508	HM777510
<i>Rhynchosia yellow mosaic virus</i>			
Rhynchosia yellow mosaic virus - [Pakistan-Lahore33-2007]	RhYMV-[PK-Lah33-07]	AM999981	AM999982
<i>Rose leaf curl virus</i>			
Rose leaf curl virus - [Pakistan-Faisalabad-2006]	RoLCuV-[PK-Fai-06]	GQ478342	
<i>Sauropus leaf curl virus</i>			
Sauropus leaf curl virus - [Thailand-Kamphaengsaen-AFSP5e-2010]	SauLCuV-[TH-Kam-AFSP5e-10]	JN809820	
<i>Senecio yellow mosaic virus</i>			
Senecio yellow mosaic virus - [China-Guangxi 46-2003]	SeYMV-[CN-Gx46-03]	AJ876550	
<i>Sida ciliaris golden mosaic virus</i>			
Sida ciliaris golden mosaic virus - [Venezuela-Lara-M3-2009]	SicGMV-[VE-Lar-M3-09]	JX857691	
<i>Sida common mosaic virus</i>			
Sida common mosaic virus - [Brazil-Coimbra 4-2007]	SiCMV-[BR-Coi4-07]	EU710751	
<i>Sida golden mosaic Braco virus</i>			
Sida golden mosaic Braco virus - [Jamaica-Liguanea-A4-2008]	SiGMBcV-[JM-Lin-A4-08]	JX162595	

Table 1 continued

<i>Sida golden mosaic Brazil virus</i>			
Sida golden mosaic Brazil virus - [Brazil-Mato Grosso do Sul-2007]	SiGMBRV-[BR-MS-07]	FN436001	
<i>Sida golden mosaic Backup virus</i>			
Sida golden mosaic Backup virus - [Jamaica-St Elizabeth 1-2004]	SiGMBuV-[JM-SE1-04]	HQ008338	HQ009518
<i>Sida golden mosaic Costa Rica virus</i>			
Sida golden mosaic Costa Rica virus - [Costa Rica]	SiGMCRV-[CR]	X99550	X99551
<i>Sida golden mosaic Florida virus</i>			
Sida golden mosaic Florida virus - Malvastrum [Cuba-Havana-Malvastrum-111-2009]	SiGMFIV-Malv[CU-Hav-Mal-111-09]	HM003779	HM003778
Sida golden mosaic Florida virus - [United States-Homestead-A1]	SiGMFIV-[US-Hom-A1]	U77963	
<i>Sida golden mosaic Lara virus</i>			
Sida golden mosaic Lara virus - [Venezuela-Lara-M1-2009]	SiGMLaV-[VE-Lar-M1-09]	JX857693	
<i>Sida golden mosaic virus</i>			
Sida golden mosaic virus - [United States-Florida]	SiGMV-[US-Flo]	AF049336	AF039841
<i>Sida golden mottle virus</i>			
Sida golden mottle virus - [United States-Florida-Bradenton-1997]	SiGMoV-[US-Flo-Bra-97]	GU997691	GU997692
<i>Sida golden yellow vein virus</i>			
Sida golden yellow vein virus - [Cuba-Havana]	SiGYVV-[CU-Hav]	AJ577395	
<i>Sida leaf curl virus</i>			
Sida leaf curl virus - [China-Hainan 57-2004]	SiLCuV-[CN-Hn57-04]	AM050730	
<i>Sida micrantha mosaic virus</i>			
Sida micrantha mosaic virus - [Brazil-A2B2]	SiMMV-[BR-A2B2]	AJ557451	AJ557453
Sida micrantha mosaic virus - Rhombifolia [Bolivia-Cerro Fraile 2-2007]	SiMMV-Rho[Bo-CF2-07]	HM585439	
Sida micrantha mosaic virus - Santarensi [BR-GO-Luziania 780-2003]	SiMMV-San[BR-GO-Luz780-03]	JX415187	
<i>Sida mosaic Bolivia virus 1</i>			
Sida mosaic Bolivia virus 1 - [Bolivia-Sida micrantha-2007]	SiMBoV1-[BO-mic-07]	HM585441	
<i>Sida mosaic Bolivia virus 2</i>			
Sida mosaic Bolivia virus 2 - [Bolivia-Sida micrantha-2007]	SiMBoV2-[BO-mic-07]	HM585443	
<i>Sida mosaic Sinaloa virus</i>			
Sida mosaic Sinaloa virus - [Mexico-Guasave-2006]	SiMSiV-[MX-Gua-06]	DQ520944	DQ356428
<i>Sida mottle Alagoas virus</i>			
Sida mottle Alagoas virus - [BR-Alagoas-Vicosa 2-2010]	SiMoAV-[BR-AL-Vsa2-10]	JX871385	
<i>Sida mottle virus</i>			
Sida mottle virus - Micrantha [Brazil-A1B3]	SiMoV-Mic[BR-A1B3]	AJ557450	AJ557454
Sida mottle virus - Rhombifolia [Brazil-Vicosa 1-1999]	SiMoV-Rho[BR-Vic1-99]	AY090555	
<i>Sida yellow blotch virus</i>			
Sida yellow blotch virus - [Brazil-Rio Largo 1-2010]	SiYBV-[BR-Rla1-10]	JX871380	
<i>Sida yellow leaf curl virus</i>			
Sida yellow leaf curl virus - [Brazil-Coimbra3-2007]	SiYLCV-[BR-Coi3-07]	EU710750	
<i>Sida yellow mosaic Alagoas virus</i>			
Sida yellow mosaic Alagoas virus - [Brazil-Alagoas-Vicosa 3-2010]	SiYMAV-[BR-AL-Vsa3-10]	JX871383	
<i>Sida yellow mosaic China virus</i>			
Sida yellow mosaic China virus - [China-Hainan 7-Ageratum-2003]	SiYMCNV-[CN-Hn7-Age-03]	AM048837	
<i>Sida yellow mosaic virus</i>			
Sida yellow mosaic virus - [Brazil-Vicosa 2-1999]	SiYMV-[BR-Vic2-99]	AY090558	
<i>Sida yellow mosaic Yucatan virus</i>			
Sida yellow mosaic Yucatan virus - [Mexico-Yucatan-2005]	SiYMYuV-[MX-Yuc-05]	DQ875872	DQ875873
<i>Sida yellow mottle virus</i>			
Sida yellow mottle virus - [Cuba-Sancti Spiritus159-1-2009]	SiYMoV-[CU-SSp159-1-09]	JN411687	JN411688
<i>Sida yellow vein Vietnam virus</i>			
Sida yellow vein Vietnam virus - [Vietnam-Hanoi-2005]	SiYVVV-[VN-Han-05]	DQ641696	

Table 1 continued

<i>Sida yellow vein virus</i>				
Sida yellow vein virus - [Honduras-yellow vein]	SiYVV-[HN-yv]	Y11099	Y11100	
<i>Sidastrum golden leaf spot virus</i>				
Sidastrum golden leaf spot virus - [Brazil-DF334-2010]	SidGLSV-[BR-DF334-10]	HM357458		
<i>Siegesbeckia yellow vein Guangxi virus</i>				
Siegesbeckia yellow vein Guangxi virus - [China-Guangxi 111-2005]	SgYVGxV-[CN-Gx111-05]	AM238692		
<i>Siegesbeckia yellow vein virus</i>				
Siegesbeckia yellow vein virus - [China-Guangdong 13-2004]	SgYVV-[CN-Gd13-04]	AM183224		
<i>Solanum mosaic Bolivia virus</i>				
Solanum mosaic Bolivia virus - [Bolivia-2007]	SoMBoV-[BO-07]	HM585435		
<i>South African cassava mosaic virus</i>				
South African cassava mosaic virus - [Madagascar-12]	SACMV-[MG-12]	AJ422132		
<i>Soybean blistering mosaic virus</i>				
Soybean blistering mosaic virus - [Argentina-NOA-2005]	SbBMV-[AR-NOA-05]	EF016486		
<i>Soybean chlorotic blotch virus</i>				
Soybean chlorotic blotch virus - [Nigeria-Soybean 19-2007]	SbCBV-[NG-Sb19-07]	GQ472985	GQ472986	
<i>Soybean mild mottle virus</i>				
Soybean mild mottle virus - [Nigeria-Soybean 17-2007]	SbMMoV-[NG-Sb17-07]	GQ472984		
<i>Spilanthes yellow vein virus</i>				
Spilanthes yellow vein virus - [Vietnam-Dalat-2005]	SpYVV-[VN-Dal-05]	DQ641694		
<i>Spinach yellow vein Sikar virus</i>				
Spinach yellow vein Sikar virus - [India-Sikar-AS22]	SpiYVSKV-[IN-Sik-AS22]	KF660223		
<i>Squash leaf curl China virus</i>				
Squash leaf curl China virus - China [China-Guangxi25-2005]	SLCCNV-CN[CN-Gx25-05]	AM260206	AM260208	
Squash leaf curl China virus - [Philippines-Benguet-P54]	SLCCNV-[PH-Ben-P54]	EU487031		
Squash leaf curl China virus - India [Pakistan-Lahore-2004]	SLCCNV-IN[PK-Lah-04]	AM286794	AM778959	
Squash leaf curl China virus - Thailand [Thailand-Nakhon Pathom-Wax Gourd-2007]	SLCCNV-TH[TH-NP-WG-07]	EU543562		
<i>Squash leaf curl Philippines virus</i>				
Squash leaf curl Philippines virus - [Philippines-Batangas P133-Pumpkin-2007]	SLCuPV-[PH-BatP133-Pum-07]	EU487041		
<i>Squash leaf curl virus</i>				
Squash leaf curl virus - [Jordan-Malva-2006]	SLCuV-[JD-Mal-06]	EF532620	EF532621	
<i>Squash leaf curl Yunnan virus</i>				
Squash leaf curl Yunnan virus- [China-Yunnan-Y23]	SLCuYV-[CN-Yun-Y23]	AJ420319		
<i>Squash mild leaf curl virus</i>				
Squash mild leaf curl virus - [United States-Imperial Valley-1979]	SMLCuV-[US-IV-79]	AF421552	AF421553	
<i>Sri Lankan cassava mosaic virus</i>				
Sri Lankan cassava mosaic virus - India [India-Adivaram-2003]	SLCMV-IN[IN-Adi-03]	AJ579307	AJ579308	
Sri Lankan cassava mosaic virus - Sri Lanka [Sri Lanka-Colombo-1998]	SLCMV-LK[LK-Col-98]	AJ314737	AJ314738	
<i>Stachytarpheta leaf curl virus</i>				
Stachytarpheta leaf curl virus - [China-Hainan 30-2004]	StaLCuV-[CN-Hn30-04]	AJ810156		
<i>Sunn hemp leaf distortion virus</i>				
Sunn hemp leaf distortion virus - [India-Barrackpore 1-2008]	SHLDV-[IN-Bar-08]	FJ455449		
<i>Sweet potato leaf curl Canary virus</i>				
Sweet potato leaf curl Canary virus - [Spain-Canary Islands-BG4-2002]	SPLCCV-[ES-CI-BG4-02]	EF456742		
<i>Sweet potato leaf curl China virus</i>				
Sweet potato leaf curl China virus - [China-2005]	SPLCCNV-[CN-05]	DQ512731		
<i>Sweet potato leaf curl Georgia virus</i>				
Sweet potato leaf curl Georgia virus - [United States-Georgia-16]	SPLCGV-[US-Geo-16]	AF326775		
<i>Sweet potato leaf curl Henan virus</i>				
Sweet potato leaf curl Henan virus - [China-Henan 10-2012]	SPLCHnV-[CN-Hn10-12]	KC907406		

Table 1 continued

<i>Sweet potato leaf curl Sao Paulo virus</i>		
Sweet potato leaf curl Sao Paulo virus - [Brazil-Sao Paulo-Alvares Machado-2009]	SPLCSPV-[BR-SP-AlvM-09]	HQ393477
<i>Sweet potato leaf curl Sichuan virus 1</i>		
Sweet potato leaf curl Sichuan virus 1 - [China-Sichuan 15-2012]	SPLCSiV-1-[CN-Sc15-12]	KC488316
<i>Sweet potato leaf curl Sichuan virus 2</i>		
Sweet potato leaf curl Sichuan virus 2 - [China-Sichuan 14-2012]	SPLCSiV-2-[CN-Sc14-12]	KF156759
<i>Sweet potato leaf curl South Carolina virus</i>		
Sweet potato leaf curl South Carolina virus - [United States-South Carolina-648-B9-2006]	SPLCSCV-[US-SC-648-B9-06]	HQ333144
<i>Sweet potato leaf curl Uganda virus</i>		
Sweet potato leaf curl Uganda virus - [Uganda-Kampala-2008]	SPLCUV-[UG-KAMP-08]	FR751068
<i>Sweet potato leaf curl virus</i>		
Sweet potato leaf curl virus - China [China-Yunnan-RL31-2006]	SPLCV-CN[CN-Yn-RL31-06]	EU253456
Sweet potato leaf curl virus - [Spain-1998]	SPLCV-[ES-98]	AJ132548
Sweet potato leaf curl virus - Brazil [Brazil-Para-Belem1-2008]	SPLCV-BR[BR-PA-Bel1-08]	FJ969829
Sweet potato leaf curl virus - Fujian [China-Jujian-Fp3-2007]	SPLCV-Fu[CN-Fuj-IP3-07]	FJ515898
Sweet potato leaf curl virus - Italy [Italy-Sicily-2002]	SPLCV-IT[IT-Sic-02]	AJ586885
Sweet potato leaf curl virus - Japan [Japan-Miyazaki-1996]	SPLCV-JP[JP-Miy-96]	AB433786
Sweet potato leaf curl virus - Paraiba [Brazil-Paraiba-Souza1-2008]	SPLCV-PB[BR-PB-Sou1-08]	FJ969830
Sweet potato leaf curl virus - Pernambuco [Brazil-Rondonia-Porto Velho-2008]	SPLCV-PE[BR-RO-PV-08]	HQ393456
Sweet potato leaf curl virus - Puerto Rico [Puerto Rico-80-N2-2006]	SPLCV-PR[PR-80-N2-06]	DQ644562
Sweet potato leaf curl virus - Rondonia [Brazil-Bahia-Utinga-2008]	SPLCV-RO[BR-BA-Uti-08]	HQ393447
Sweet potato leaf curl virus - Sao Paulo [Brazil-Sao Paulo-Alvares Machado-2009]	SPLCV-SP[BR-SP-AlvM-09]	HQ393473
Sweet potato leaf curl virus - South Carolina [United States-South Carolina-646-B11-2006]	SPLCV-SC[US-SC-646-B11-06]	HQ333138
Sweet potato leaf curl virus - Spain [Spain-Canary Islands-BG6-2002]	SPLCV-ES[ES-CI-BG6-02]	EF456744
Sweet potato leaf curl virus - United States [United States- Louisiana-1994]	SPLCV-US[US-Lou-94]	AF104036
<i>Sweet potato mosaic virus</i>		
Sweet potato mosaic virus - [Brazil-Brasilia1-2008]	SPMV-[BR-BSB1-08]	FJ969831
<i>Tobacco curly shoot virus</i>		
Tobacco curly shoot virus - [China-Alternanthera-2008]	TbCSV-[CN-Alt-08]	GU199583
<i>Tobacco leaf curl Comoros virus</i>		
Tobacco leaf curl Comoros virus - [Comoros-Simboussa-2004]	TbLCKMV-[KM-Sim-04]	AM701760
<i>Tobacco leaf curl Cuba virus</i>		
Tobacco leaf curl Cuba virus - [Cuba-Taguasco-2005]	TbLCuCV-[CU-Tag-05]	AM050143
<i>Tobacco leaf curl Pusa virus</i>		
Tobacco leaf curl Pusa virus - [India-Pusa-2009]	TbLCPuV-[IN-Pus-09]	HQ180391
<i>Tobacco leaf curl Thailand virus</i>		
Tobacco leaf curl Thailand virus - [Thailand-Tomato-2005]	TbLCTHV-[TH-To-05]	DQ871221
<i>Tobacco leaf curl Yunnan virus</i>		
Tobacco leaf curl Yunnan virus - China [China-Yunnan 136-2002]	TbLCYnV-CN[CN-Yn136-02]	AJ512761
<i>Tobacco leaf curl Zimbabwe virus</i>		
Tobacco leaf curl Zimbabwe virus - [Comoros-Foumboudziouni-2005]	TbLCZV-[KM-Fou-05]	AM701756
<i>Tobacco leaf rugose virus</i>		
Tobacco leaf rugose virus - [Cuba-Havana-2001]	TbLRV-[CU-Hav-01]	AJ488768
<i>Tobacco mottle leaf curl virus</i>		
Tobacco mottle leaf curl virus - [Cuba-Sanci Spiritus-2003]	TbMoLCV-[CU-SS-03]	FM160943
<i>Tobacco yellow crinkle virus</i>		
Tobacco yellow crinkle virus - [Cuba-2007]	TbYCV-[CU-07]	FJ213931 HQ896204
<i>Tomato bright yellow mosaic virus</i>		
Tomato bright yellow mosaic virus - [Brazil-BA167-2012]	ToBYMV-[BR-BA167-12]	KC791690

Table 1 continued

<i>Tomato bright yellow mottle virus</i>			
Tomato bright yellow mottle virus - [Brazil-TO167-2008]	ToBYMoV-[BR-TO167-08]	KC791691	
<i>Tomato chino La Paz virus</i>			
Tomato chino La Paz virus - A [Mexico-Baja La Paz-2002]	ToChLPV-A[MX-BLP-02]	AY339618	
Tomato Chino La Paz virus - [Mexico-SLP4-2011]	ToChLPV-[MX-SLP4-11]	JN676150	
Tomato chino La Paz virus - B [Mexico-Baja El Carrizal-2002]	ToChLPV-A[MX-BEC-02]	AY339619	
<i>Tomato chlorotic leaf distortion virus</i>			
Tomato chlorotic leaf distortion virus - [Venezuela-Zulia-2004]	ToCILDV-[VE-Zul-04]	HQ201952	
<i>Tomato chlorotic mottle virus</i>			
Tomato chlorotic mottle virus - Bahia [Brazil-Seabra 1-1996]	ToCMoV-BA[BR-Seal-96]	AF490004	AF491306
Tomato chlorotic mottle virus - [Brazil-Florestal 211-2008]	ToCMoV-[BR-Flo211-08]	KC706561	
Tomato chlorotic mottle virus - Minas Gerais [Brazil-Betim 1-1996]	ToCMoV-MG[BR-Bet1-96]	AY090557	
<i>Tomato common mosaic virus</i>			
Tomato common mosaic virus - [Brazil-Coimbra 22-2007]	ToCmMV-[BR-Coi22-07]	EU710754	EU710755
<i>Tomato curly stunt virus</i>			
Tomato curly stunt virus - [South Africa-Onderberg-1998]	ToCSV-[ZA-Ond-98]	AF261885	
<i>Tomato dwarf leaf virus</i>			
Tomato dwarf leaf virus - [Argentina-Pichanal 397-2008]	ToDfLV-[AR-Pic397-08]	JN564749	
<i>Tomato golden leaf distortion virus</i>			
Tomato golden leaf distortion virus - [Brazil-TO45-2007]	ToGLDV-[BR-TO45-07]	HM357456	
<i>Tomato golden leaf spot virus</i>			
Tomato golden leaf spot virus - [Brazil-Araguaina-TO83-2013]	ToGLSV-[BR-Ara-TO83-13]	KC626021	
<i>Tomato golden mottle virus</i>			
Tomato golden mottle virus - [Mexico-San Luiz Potosi-2005]	ToGMoV-[MX-SLP-05]	DQ520943	DQ406674
<i>Tomato golden mosaic virus</i>			
Tomato golden mosaic virus - [Brazil-Common-1984]	TGMV-[BR-Com-84]	K02029	K02030
<i>Tomato golden vein virus</i>			
Tomato golden vein virus - [Brazil-Ita1220-2003]	TGVV-[BR-Ita1220-03]	JF803254	
<i>Tomato interveinal chlorosis virus</i>			
Tomato interveinal chlorosis virus - [Brazil-Pernambuco-Mdc2681-2004]	ToICV-[BR-PE-Mdc2681-04]	JF803252	
<i>Tomato leaf curl Anjouan virus</i>			
Tomato leaf curl Anjouan virus - [Comoros-Ouani-2004]	ToLCAnV-[KM-Oua-04]	AM701758	
<i>Tomato leaf curl Arusha virus</i>			
Tomato leaf curl Arusha virus - [Tanzania-Kilimandjaro-2005]	ToLCArV-[TZ-Kil-05]	EF194760	
<i>Tomato leaf curl Bangalore virus</i>			
Tomato leaf curl Bangalore virus - A [India-Bangalore 1]	ToLCBaV-A[IN-Ban1]	Z48182	
Tomato leaf curl Bangalore virus - [India-Hessaraghatta-TC265-2010]	ToLCBaV-[IN-Hes-TC265-10]	KF663698	
Tomato leaf curl Bangalore virus - B [India-Bangalore 5]	ToLCBaV-B[IN-Ban5]	AF295401	
Tomato leaf curl Bangalore virus - C [India-Bangalore 4-1997]	ToLCBaV-C[IN-Ban4-97]	AF165098	
Tomato leaf curl Bangalore virus - D [India-Kerala II-2005]	ToLCBaV-D[IN-KerII-05]	DQ852623	
<i>Tomato leaf curl Bangladesh virus</i>			
Tomato leaf curl Bangladesh virus - [Bangladesh-BD2]	ToLCBV-[BD-BD2]	AF188481	
<i>Tomato leaf curl Cebu virus</i>			
Tomato leaf curl Cebu virus - [Philippines-Nueva Ecita P2-1-2007]	ToLCCeV-[PH-NuEP2-1-07]	EU487025	
<i>Tomato leaf curl China virus</i>			
Tomato leaf curl China virus - Baise [China-Guangxi 32-2002]	ToLCCNV-BS[CN-Gx32-02]	AJ558118	
Tomato leaf curl China virus - [China-Guangxi-Tobacco-JX-2-2010]	ToLCCNV-[CN-Gx-Tob-JX-2-10]	JF681158	
Tomato leaf curl China virus - Nanning1 [China-Guangxi 18-2002]	ToLCCNV-NN1[CN-Gx18-02]	AJ558119	
Tomato leaf curl China virus - Nanning2 [China-Guangxi 63-2003]	ToLCCNV-NN2[CN-Gx63-03]	AJ704603	
<i>Tomato leaf curl Diana virus</i>			
Tomato leaf curl Diana virus - [Madagascar-Namakely-2001]	ToLCDiV-[MG-Nam-01]	AM701765	

Table 1 continued

Tomato leaf curl Ghana virus			
Tomato leaf curl Ghana virus - [Ghana-Akumadan-2006]	ToLCGV-[GH-Aku-06]	EU350585	
Tomato leaf curl Ghana virus - Ageratum [Cameroon-AGFG24-2009]	ToLCGV-Ag[CM-AGFG24-09]	FR873228	
Tomato leaf curl Guangdong virus			
Tomato leaf curl Guangdong virus - [China-Guangzhou 2-2003]	ToLCGdV-[CN-Gz2-03]	AY602165	
Tomato leaf curl Guangxi virus			
Tomato leaf curl Guangxi virus - [China-Guangxi 1-2003]	ToLCGxV-[CN-Gx1-03]	AM236784	
Tomato leaf curl Hainan virus			
Tomato leaf curl Hainan virus - [China-FQ12-2012]	ToLCHaV-[CN-FQ12-12]	KF150142	
Tomato leaf curl Hanoi virus			
Tomato leaf curl Hanoi virus - [Vietnam-Hanoi-Tomato-2010]	ToLCHaV-[VN-Han-tom-10]	HQ162270	
Tomato leaf curl Hsinchu virus			
Tomato leaf curl Hsinchu virus - [China-Hainan-Ramie-2007]	ToLCHsV-[CN-Hn-Ram-07]	EU596959	EU596960
Tomato leaf curl Java virus			
Tomato leaf curl Java virus - A [Indonesia]	ToLCJaV-A[ID]	AB100304	
Tomato leaf curl Java virus - B [Indonesia-Ageratum]	ToLCJaV-B[ID-Age]	AB162141	
Tomato leaf curl Joydebpur virus			
Tomato leaf curl Joydebpur virus - [India-Varanasi-Capsicum annum-2010]	ToLCJIV-[IN-Var-Caa-10]	HM991146	
Tomato leaf curl Kerala virus			
Tomato leaf curl Kerala virus - [India-Kerala 3-2007]	ToLCKeV-[IN-Ker3-07]	EU910141	
Tomato leaf curl Laos virus			
Tomato leaf curl Laos virus - [Laos]	ToLCLV-[LA]	AF195782	
Tomato leaf curl Liwa virus			
Tomato leaf curl Liwa virus - [Oman-Liwa-LW1-2012]	ToLCLwV-[OM-Liw-LW1-12]	HF912280	
Tomato leaf curl Madagascar			
Tomato leaf curl Madagascar virus - Atsimo [Madagascar-Toliary-2001]	ToLCMGV-Ats[MG-Tol-01]	AJ865339	
Tomato leaf curl Madagascar virus - Menabe [Madagascar-Morondova-2001]	ToLCMGV-Men[MG-Mor-01]	AJ865338	
Tomato leaf curl Malaysia virus			
Tomato leaf curl Malaysia virus - Malaysia [Malaysia-Klang-1997]	ToLCMYV-MY[MY-Kla-97]	AF327436	
Tomato leaf curl Mali virus			
Tomato leaf curl Mali virus - [Mali]	ToLCMLV-[ML]	AY502936	
Tomato leaf curl Mayotte virus			
Tomato leaf curl Mayotte virus - [Mayotte-Kahani-2003]	ToLCYTV-[YT-Kah-03]	AJ865340	
Tomato leaf curl Mayotte virus - Madagascar [Madagascar-Dimadjou-2006]	ToLCYTV-MG[MG-Dim-06]	AM701761	
Tomato leaf curl Mindanao virus			
Tomato leaf curl Mindanao virus - [Philippines-Mindanao P162-2007]	ToLCMiV-[PH-MinP162-07]	EU487046	
Tomato leaf curl New Delhi virus			
Tomato leaf curl New Delhi virus - [Bangladesh-Jessore- Severe-2005]	ToLCNDV-[BG-Jes-Svr -05]	AJ875157	AJ875158
Tomato leaf curl New Delhi virus 2			
Tomato leaf curl New Delhi virus 2 - [India-IANDS1-2011]	ToLCNDV2-[IN-IANDS1-11]	JQ897969	
Tomato leaf curl New Delhi virus 3			
Tomato leaf curl New Delhi virus 3 - [India-Bijnor-Chilli-2012]	ToLCNDV3-[IN-Bij-Chi-12]	KC465466	
Tomato leaf curl New Delhi virus 4			
Tomato leaf curl New Delhi virus 4 - [India-Junagad-TC306-2011]	ToLCNDV4-[IN-Jun-TC306-11]	KF551592	
Tomato leaf curl Palampur virus			
Tomato leaf curl Palampur virus - [India-Palampur-2007]	ToLCPaV-[IN-Pal-047]	AM884015	AM992534
Tomato leaf curl Patna virus			
Tomato leaf curl Patna virus - [India-Patna-2008]	ToLCPaV-[IN-Pat-08]	EU862323	
Tomato leaf curl Philippines virus			
Tomato leaf curl Philippines virus - A [Philippines-Laguna-2006]	ToLCPV-A[PH-Lag-06]	AB377113	
Tomato leaf curl Philippines virus - B [Philippines-Laguna 1-2006]	ToLCPV-B[PH-Lag1-06]	AB377111	

Table 1 continued

Tomato leaf curl Philippines virus - C [Philippines-Laguna-2006]	ToLCPV-C[PH-Lag-06]	AB307731	
<i>Tomato leaf curl Pune virus</i>			
Tomato leaf curl Pune virus - [India-Pune-2005]	ToLCPuV-[IN-Pun-05]	AY754814	
<i>Tomato leaf curl Rajasthan virus</i>			
Tomato leaf curl Rajasthan virus - [India-Rajasthan-2005]	ToLCRaV-[IN-Raj-05]	DQ339117	
<i>Tomato leaf curl Seychelles virus</i>			
Tomato leaf curl Seychelles virus - [Seychelles-Val d'Endor-2004]	ToLCSCV-[SC-VE-04]	AM491778	
<i>Tomato leaf curl Sinaloa virus</i>			
Tomato leaf curl Sinaloa virus - [Nicaragua-Santa Lucia-NI2]	ToLCSiV-[NI-SL]	AJ608286	AJ508783
<i>Tomato leaf curl Sri Lanka virus</i>			
Tomato leaf curl Sri Lanka virus - [Sri Lanka-Bandarawela-1997]	ToLCLKV-[LK-Ban-97]	AF274349	
<i>Tomato leaf curl Sudan virus</i>			
Tomato leaf curl Sudan virus - Gezira [Sudan-Gezira-1996]	ToLCSDV-Gez[SD-Gez-96]	AY044137	
Tomato leaf curl Sudan virus - [Sudan-WM-2011]	ToLCSDV-[SD-WM-11]	KC763630	
Tomato leaf curl Sudan virus - Shambat [Sudan-Shambat-1996]	ToLCSDV-Sha[SD-Sha-96]	AY044139	
Tomato leaf curl Sudan virus - Yemen [Yemen-2005]	ToLCSDV-YE[YE-05]	EF110891	
<i>Tomato leaf curl Sulawesi virus</i>			
Tomato leaf curl Sulawesi virus - [Indonesia-Sulawesi-Langowan F101-2006]	ToLCSuV-[ID-Sul-LanF101-06]	FJ237614	
<i>Tomato leaf curl Taiwan virus</i>			
Tomato leaf curl Taiwan virus - A [China-Hong Kong T1-2007]	ToLCTV-A[CN-HKT1-07]	EU624503	
Tomato leaf curl Taiwan virus - [China-NS1-2011]	ToLCTV-[CN-NS1-11]	JQ867093	
Tomato leaf curl Taiwan virus - B [Taiwan-Luye 2-4-2009]	ToLCTV-B[TW-Luy2-4-09]	GU723730	
Tomato leaf curl Taiwan virus - C [Taiwan-Chiayi-LJC14-2005]	ToLCTV-C[TW-Cy-LJC14-05]	DQ866128	
<i>Tomato leaf curl Toliara virus</i>			
Tomato leaf curl Toliara virus - [Madagascar-Miandrivazo-2001]	ToLCToV-[MG-Mia-01]	AM701768	
<i>Tomato leaf curl Uganda virus</i>			
Tomato leaf curl Uganda virus - [Uganda-Iganga-2005]	ToLCUV-[UG-Iga-05]	DQ127170	
<i>Tomato leaf curl Vietnam virus</i>			
Tomato leaf curl Vietnam virus - [Vietnam-Dan Xa 2-2007]	ToLCVV-[VN-DX1-07]	EU189149	
<i>Tomato leaf curl virus</i>			
Tomato leaf curl virus - Solanum [Australia-Solanum-D1]	ToLCV-Sol[AU-Sol-D1]	AF084006	
Tomato leaf curl virus - [India-New Delhi-CTS-2006]	ToLCV-[IN-ND-06]	DQ629101	
Tomato leaf curl virus - Bangalore [India-Punjab-Mentha-2007]	ToLCV-Ban[IN-Pun-Me-07]	FJ514798	
Tomato leaf curl virus - Janti [India-Janti-2005]	ToLCV-Jan[IN-Jan-05]	AY754812	
Tomato leaf curl virus - Tomato [Australia]	ToLCV-To[AU]	S53251	
<i>Tomato leaf deformation virus</i>			
Tomato leaf deformation virus - [Peru-Tomato-1-2003]	ToLDeV-[PE-tom-1-03]	GQ334472	
<i>Tomato leaf distortion virus</i>			
Tomato leaf distortion virus - [Brazil-Paty do Alferes 4-2005]	ToLDV-[BR-Pda4-05]	EU710749	
<i>Tomato mild mosaic virus</i>			
Tomato mild mosaic virus - [Brazil-Paty do Alferes 58-2005]	ToMMV-[BR-Pda58-05]	EU710752	EU710753
<i>Tomato mild yellow leaf curl Aragua virus</i>			
Tomato mild yellow leaf curl Aragua virus - [Venezuela-10-2003]	ToMYLCV-[VE-10-03]	AY927277	EF547938
<i>Tomato mosaic Havana virus</i>			
Tomato mosaic Havana virus - [Cuba-Quivicán]	ToMHaV-[CU-Qui]	Y14874	Y14875
<i>Tomato mottle leaf curl virus</i>			
Tomato mottle leaf curl virus - [Brazil-Jaiba 13-2008]	ToMoLCV-[BR-Jai13-08]	KC706615	

Table 1 continued

<i>Tomato mottle Taino virus</i>			
Tomato mottle Taino virus - [Cuba]	ToMoTaV-[CU]	AF012300	AF012301
<i>Tomato mottle virus</i>			
Tomato mottle virus - [United States-Florida-1989]	ToMoV-[US-Flo-89]	L14460	L14461
<i>Tomato mottle wrinkle virus</i>			
Tomato mottle wrinkle virus - [Argentina-Pichanal-400-2008]	ToMoWV-[AR-Pic-400-08]	JQ714137	
<i>Tomato rugose mosaic virus</i>			
Tomato rugose mosaic virus - [Brazil-Uberlandia 1-1996]	ToRMV-[BR-Ube1-96]	AF291705	AF291706
<i>Tomato rugose yellow leaf curl virus</i>			
Tomato rugose yellow leaf curl virus - [Uruguay-Salto Grande-U2-2009]	TRYLCV-[UY-SG-U2-09]	JN381819	
<i>Tomato severe leaf curl virus</i>			
Tomato severe leaf curl virus - Guatemala [Guatemala-Sansirisay-1996]	ToSLCV-GT[GT-San-96]	AF130415	
Tomato severe leaf curl virus - [Mexico-Huasteca-2011]	ToSLCV-[MX-Hua-11]	JN680352	
Tomato severe leaf curl virus - Nicaragua [Nicaragua-Condega]	ToSLCV-NI[NI-Con]	AJ508784	
<i>Tomato severe rugose virus</i>			
Tomato severe rugose virus - [Brazil-Petrolina de Goias 1-Capsicum-2003]	ToSRV-[BR-PG1-Cap-03]	DQ207749	
<i>Tomato yellow leaf curl Axarquia virus</i>			
Tomato yellow leaf curl Axarquia virus - [Spain-Algarrobo-ES-mh800-2000]	TYLCAxV-[ES-Alg-ES-mh800-00]	AY227892	
<i>Tomato yellow leaf curl China virus</i>			
Tomato yellow leaf curl China virus - Baoshan1 [China-Yunnan 10-Tobacco-2000]	TYLCCNV-BS1[CN-Yn10-Tob - 00]	AJ319675	
Tomato yellow leaf curl China virus - [China-Yunnan 25-Tomato-2000]	TYLCCNV-[CN-Yn25-Tom-00]	AJ457985	
Tomato yellow leaf curl China virus - Baoshan3 [China-Yunnan 278-Malvastrum-2007]	TYLCCNV-BS3[CN-Yn278-Mal-07]	AM980509	
Tomato yellow leaf curl China virus - Bean [China-Yunnan-Bean-2004]	TYLCCNV-Bea[CN-Yn-Bea-04]	DQ256460	
Tomato yellow leaf curl China virus - Dali [China-Yunnan 5-Tobacco-1999]	TYLCCNV-DL[CN-Yn5-Tob-99]	AJ319674	
Tomato yellow leaf curl China virus - Datura [China-Yunnan 72- Datura -2005]	TYLCCNV-Dat[CN-Yn72-Dat-05]	EF011559	
Tomato yellow leaf curl China virus - Honghe [China-Guangxi]	TYLCCNV-HH[CN-Gx]	AF311734	
<i>Tomato yellow leaf curl Indonesia virus</i>			
Tomato yellow leaf curl Indonesia virus - [Indonesia-Lembang-2005]	TYLCIDV-[ID-Lem-05]	AF189018	
<i>Tomato yellow leaf curl Kanchanaburi virus</i>			
Tomato yellow leaf curl Kanchanaburi virus - [Thailand-Kanchanaburi 1-2001]	TYLCKaV-[TH-Kan1-01]	AF511529	AF511528
<i>Tomato yellow leaf curl Malaga virus</i>			
Tomato yellow leaf curl Malaga virus - [Spain-421-1999]	TYLCMaV-[ES-421-99]	AF271234	
<i>Tomato yellow leaf curl Mali virus</i>			
Tomato yellow leaf curl Mali virus - Ethiopia [Ethiopia-Melkassa-2005]	TYLCMLV-ET[ET-Mel-05]	DQ358913	
Tomato yellow leaf curl Mali virus - Mali [Mali -2003]	TYLCMLV-ML[ML-03]	AY502934	
<i>Tomato yellow leaf curl Sardinia virus</i>			
Tomato yellow leaf curl Sardinia virus - [Italy-Sardinia-1988]	TYLCSV-[IT-Sar-88]	X61153	
<i>Tomato yellow leaf curl Thailand virus</i>			
Tomato yellow leaf curl Thailand virus - A [Thailand-1]	TYLCTHV-A[TH-1]	X63015	X63016
Tomato yellow leaf curl Thailand virus - B [Thailand-Chiang Mai]	TYLCTHV-B[TH-ChMai]	AY514630	AY514633
Tomato yellow leaf curl Thailand virus - C [China-Yunnan 72-2002]	TYLCTHV-C[CN-Yn72-02]	AJ495812	
Tomato yellow leaf curl Thailand virus - D [Myanmar-Yangon-1999]	TYLCTHV-D[MY-Yan-99]	AF206674	
Tomato yellow leaf curl Thailand virus - E [Thailand-Sakon Nakhon]	TYLCTHV-E[TH-SaNa]	AY514632	AY514635
<i>Tomato yellow leaf curl virus</i>			
Tomato yellow leaf curl virus - [Israel-Rehovot-1986]	TYLCV-[IL-Reo-86]	X15656	
Tomato yellow leaf curl virus - Boushehr [Iran- Genaveh 29-2006]	TYLCV-Bou[IR-Gen29-06]	GU076454	
Tomato yellow leaf curl virus - Iran [Iran-Iranshahr-1998]	TYLCV-IR[IR-Ira-98]	AJ132711	
Tomato yellow leaf curl virus - Kahnoo [Iran-Kahnooj-2007]	TYLCV-Kah[IR-Kah-07]	EU635776	
Tomato yellow leaf curl virus - Kerman [Iran-Hormozgan 32-2006]	TYLCV-Ker[IR-Hor32-06]	GU076442	

Table 1 continued

Tomato yellow leaf curl virus - Mild [Israel-1993]	TYLCV-Mld[IL-93]	X76319	
Tomato yellow leaf curl virus - Oman [Oman-AI-batinah 22-2005]	TYLCV-OM[OM-AIb22-05]	FJ956700	
<i>Tomato yellow leaf curl Yunnan virus</i>			
Tomato yellow leaf curl Yunnan virus - [China-YN2013-2011]	TYLCYnV-[CN-YN2013-11]	KC686705	
<i>Tomato yellow leaf distortion virus</i>			
Tomato yellow leaf distortion virus - [Cuba-5E17-2007]	ToYLDV-[CU-5E17-07]	FJ174698	
<i>Tomato yellow margin leaf curl virus</i>			
Tomato yellow margin leaf curl virus - [Venezuela-Merida-57]	ToYMLCV-[VE-Mer-57]	AY508993	
<i>Tomato yellow mottle virus</i>			
Tomato yellow mottle virus - [Costa Rica-2003]	ToYMoV-[CR-03]	KC176780	
<i>Tomato yellow spot virus</i>			
Tomato yellow spot virus - [Brazil-Bicas 2-1999]	ToYSV-[BR-Bic2-99]	DQ336350	DQ336351
Tomato yellow spot virus - Leonurus [Brazil-PR49-2007]	ToYSV-Le[BR-PR49-07]	JX863081	
<i>Tomato yellow vein streak virus</i>			
Tomato yellow vein streak virus - [Brazil-Potato-1983]	ToYVSV-[BR-Pot-83]	EF417915	EF417916
<i>Velvet bean severe mosaic virus</i>			
Velvet bean severe mosaic virus - [India-Lucknow-2008]	VBSMV-[IN-Luc-08]	FN543425	FN543426
<i>Vernonia yellow vein Fujian virus</i>			
Vernonia yellow vein Fujian virus - [China-Fujian-2009]	VeYVFV-[CN-Fj-09]	JF265670	
<i>Vernonia yellow vein virus</i>			
Vernonia yellow vein virus - [India-Madurai-2005]	VeYVV-[IN-Mad-05]	AM182232	
<i>Vigna yellow mosaic virus</i>			
Vigna yellow mosaic virus - [Mexico-Morelos-Yautepec-2007]	ViYMV-[MX-Mor-Yau-07]	KC430936	
<i>Watermelon chlorotic stunt virus</i>			
Watermelon chlorotic stunt virus - [Iran-1997]	WmCSV-[IR-97]	AJ245652	AJ245653
<i>West African Asystasia virus 1</i>			
West African Asystasia virus 1 - [West Africa-Asystasia1-2011]	WAAV1-[WA-Asy1-11]	JF694486	
<i>West African Asystasia virus 2</i>			
West African Asystasia virus 2 - [West Africa-Asystasia2-2011]	WAAV2-[WA-Asy2-11]	JF694484	
<i>Wissadula golden mosaic virus</i>			
Wissadula golden mosaic virus - [Jamaica-St Thomas-2005]	WGMV-[JM-StT-05]	DQ395343	EU158095

The most obvious benefit to using the SDT-based pairwise identity analysis is that there are fewer species and strains at the interface between the cutoff and the next lower or higher percent nt sequence identity. As such, applying the proposed 91 % cutoff increases reliability owing to the robust stringency.

Why so many begomoviruses?

As noted above, the genus *Begomovirus* includes the largest number of species of all currently established genera, with 288 species currently recognized by the ICTV. Why so many begomoviruses? Are these species “artificial”, the result of flawed taxonomic demarcation criteria? The existence of this large number of species can be explained by natural order relationships based on the characteristics of this genus that set it apart from many other viral genera.

Begomoviruses are transmitted by members of a cryptic species complex, *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae), which is distributed worldwide and colonize a wide array of plants belonging to species in many families [22–25]. *B. tabaci* has emerged as a major threat to agricultural systems in many regions of the world since the 1970s and 1980s [26, 27]. Reports of unprecedented *B. tabaci* infestations have characteristically resulted in outbreaks of previously undescribed begomoviruses and the apparent disappearance of others from cultivated plants [28]. Because *B. tabaci* colonizes so many plant species [25], it potentiates the transfer of begomoviruses between non-cultivated and cultivated hosts (which are most studied by plant virologists). While it is beyond the scope of this proposal to fully explore the hypothesis that most begomoviruses isolated from cultivated hosts likely evolved from viruses originally adapted to infecting non-cultivated

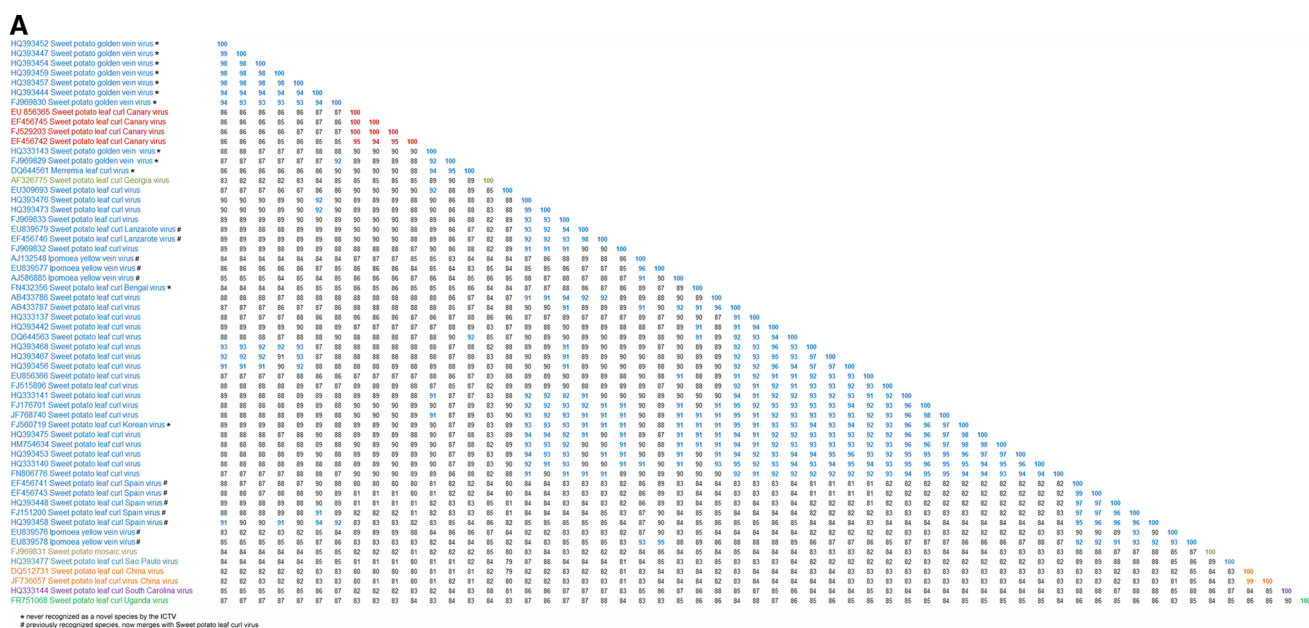


Fig. 1 (A) Pairwise sequence comparisons and (B) maximum-likelihood phylogenetic tree of sequences comprising the "sweep-virus" group. Sequences corresponding to the same species based on

hosts, this hypothesis could explain, at least in part, why there are so many more begomovirus species than are found for other virus genera where virus-host-vector interactions are more evolutionarily ancient.

Another consideration is that virologists working with ssDNA viruses have gained a powerful new tool in the form of rolling circle-amplification (RCA), a method that allows for rapid, sequence-independent sampling of virus populations. The impact of RCA in the field of geminivirology cannot be overstated (for example, see ref. [29]). Using RCA, it is possible to amplify and recover the complete genome of almost any begomovirus from minute amounts of total plant DNA extracted under suboptimal conditions [30]. Presently, tissue samples can be collected, dried, and stored for months or years at room temperature, and thousands of complete begomovirus genomes will be readily amplified using RCA following a quick DNA extraction [31, 32]. In the 1990s it would take months to clone one full-length begomovirus genome, whereas hundreds of genomes can now be cloned in a matter of weeks. Furthermore (and equally relevant), because RCA uses random primers, it reduces sequence amplification biases and enables the detection of most or all unique genome molecules present in a sample. As a result, new begomoviruses and other, often highly divergent, geminiviruses have been discovered that will probably lead to the recognition of additional genera in the family (and perhaps new families as well) [33–36]. Also, this new technology has prompted a significant increase in the numbers of novel

a 91 % cutoff (using the parameters described in the main text) are highlighted in the same color

begomoviruses that are being sought, and found, in non-cultivated plants.

Finally, it should be pointed out that the extent of diversity currently recognized within this genus (and possibly for all viruses) represents only the tip of the iceberg. Metagenomic approaches are rapidly becoming affordable and will probably lead to the discovery of viruses belonging to hundreds of new genera and families, not to mention species [37]. Its impact on geminivirus discovery has already been felt [38–42].

Different cutoff values must be used for the different genera in the family *Geminiviridae*

The approach implemented herein to demarcate species in the genus *Begomovirus* is identical to that used and approved by the ICTV for the other genera in the family [12, 13, 36]. However, for each genus, the working cutoff for species demarcation differs, even though the method applied to determine these cutoffs has been the same. For example, mastrevirus species are demarcated using a 78% cutoff. The 78% species cutoff value for the mastreviruses is demonstrated by the pairwise distance distribution plot (Fig. 2A), in which a clear valley is apparent at 78%. Such a valley is not readily evident in the equivalent plot for the begomoviruses (Fig. 2B and C), leading us to analyze this genus using groups of sequences. The analysis reported herein supported a 91% cutoff value for begomoviruses as

Fig. 1 continued

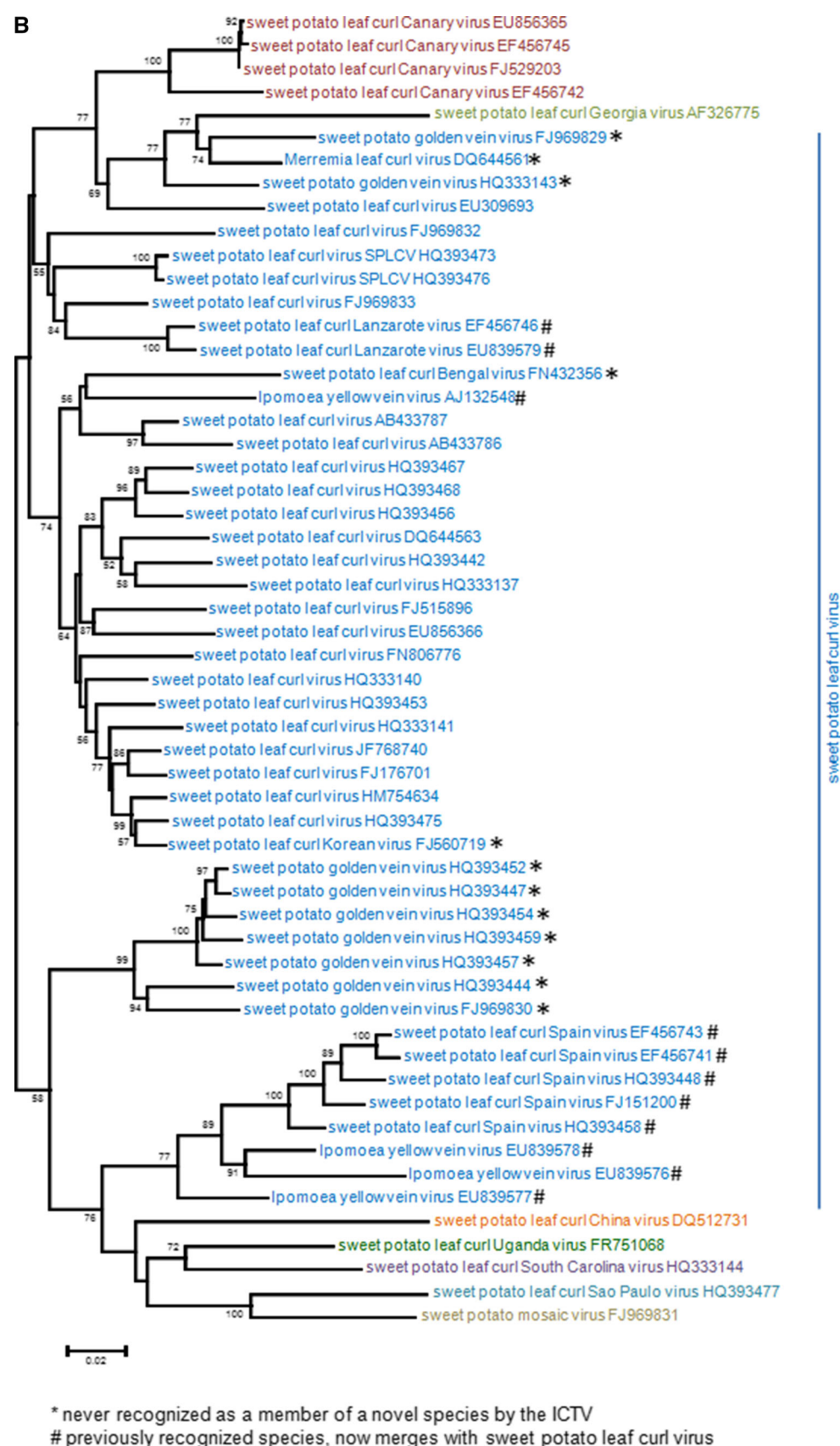
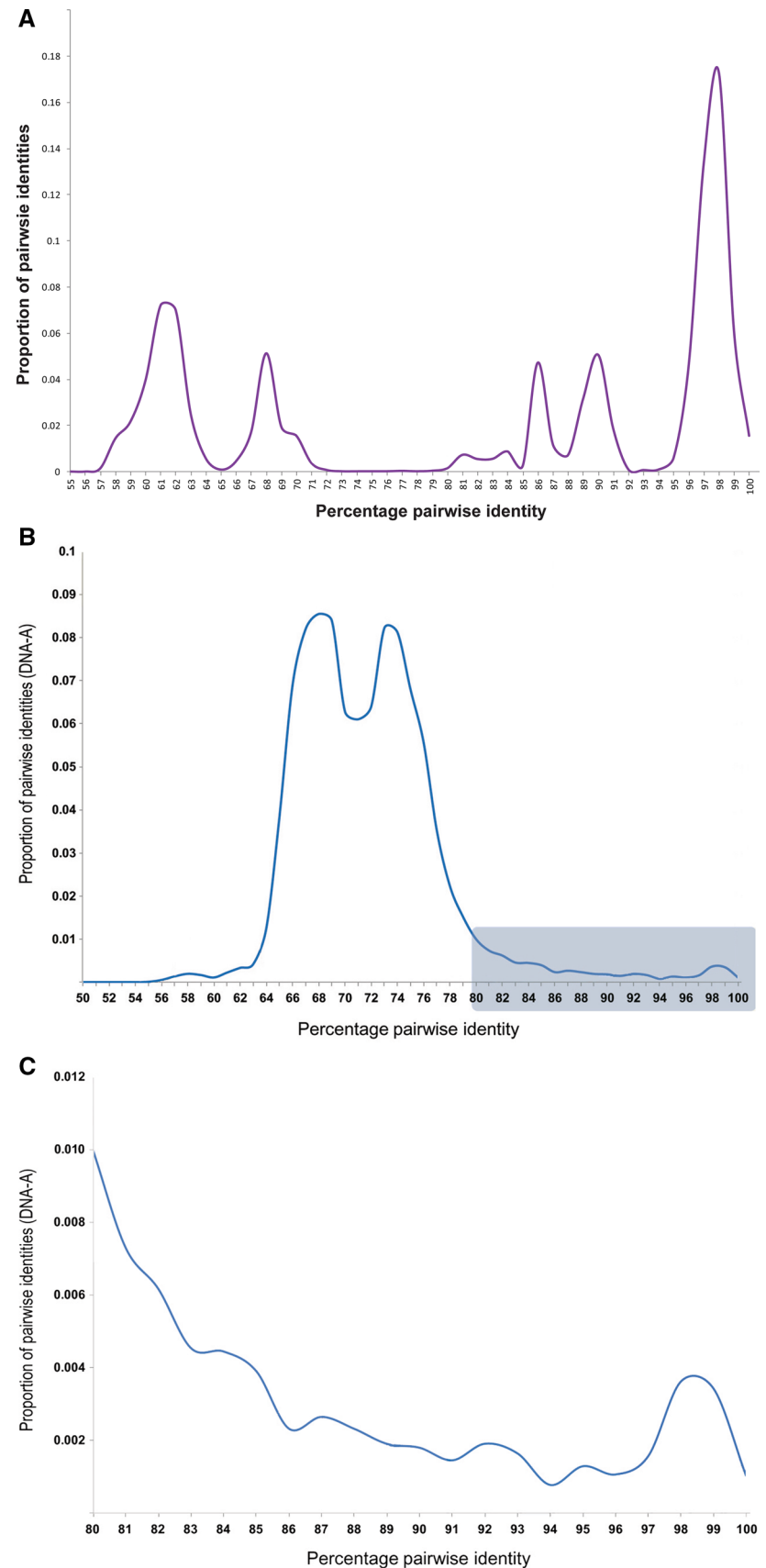


Fig. 2 Distribution of the full-genome pairwise sequence identity scores for members of the genera (A) *Mastrevirus* and (B, C) *Begomovirus* (C corresponds to a higher resolution of the shaded region in B). Note the valley (or gap) corresponding to the 72–78 % frequencies in the *Mastrevirus* plot and the absence of significant valleys in the *Begomovirus* plot



that which best separates the species in the genus, and this is well supported by the SDT analysis.

Several other families and genera have species demarcation thresholds similar to that of the begomoviruses, including *Parvovirus* (95 %), *Microviridae* (80–85 %) and *Sobemovirus* (60–85 %). It is perhaps troubling that a uniform approach for computing species thresholds does not exist across all of viral taxonomy at this time. Currently, various study groups use different algorithms for specific genes, sets of genes, or complete genomes. Further, complete genome sequences are lacking for viruses of many species, particularly those with large genomes. In those instances, the trees represent a gene tree instead of a virus tree, which can create misconceptions about viral genome structure and lead to incorrect evolutionary inferences. It will be interesting to see if our approach may be useful for other viral families.

A step-by-step guide for classifying new begomovirus isolates as members of species or strains

To facilitate the taxonomic placement of newly discovered begomoviruses and to assist in the standardization of this procedure, the following guidelines are proposed for classification into species and strains:

1. A BLAST_n analysis of the “non-redundant nucleotide” database should be performed to identify the species whose members have sequences most similar to the new sequence. The nucleotide sequence database at the NCBI website (<http://www.ncbi.nlm.nih.gov/nucleotide/>) can also be searched using the search term “txid10814 [Organism: exp] AND 2500:3500[SLEN]”, which will return all begomovirus nucleotide sequences that are between 2500 and 3500 nucleotides long.
2. The new sequence should be added to a dataset of full-length genomes or DNA-A components created based on the BLAST results, and saved in FASTA format. All sequences must start at the same genomic coordinate (the first nucleotide after the nicking site within the conserved nonanucleotide at the origin of replication is the recommended standard).
3. The MUSCLE option in SDT v1.2 (freely available at <http://www.cbio.uct.ac.za/SDT>) or any other program that uses the MUSCLE alignment algorithm with pairwise deletion of gaps should be used to calculate identities between every pair of sequences in the dataset. If using SDT, these pairwise identities may be saved in either a column or matrix csv format that can then be viewed in a spreadsheet program such as Microsoft Excel. Percent identities must be rounded to the nearest full percentile.
4. If the new sequence shares <91 % genome-wide pairwise identity to any other known begomovirus sequence, appropriate species and virus names should then be proposed (see below for guidelines on doing so).
5. If the sequence shares <94 % genome-wide pairwise identity to all isolates described for that species, a strain name should then be proposed.

Guidelines for naming new species that include newly discovered begomoviruses

Virus species name

This is the ICTV-accepted name of a group of begomoviruses sharing ≥ 91 % pairwise sequence identity for the full-length genome or DNA-A component. If the sequence has <91 % sequence identity to all begomoviruses previously classified as members of distinct species, the virus should be considered a member of a new species, and a unique name that is not currently in use for any ICTV-recognized species should be assigned. This name should follow the template “Host symptom virus” (e.g., *Bean golden mosaic virus*). Although it was common practice for begomoviruses, the *Geminiviridae* SG recommends that country, city, town, village or province names not be used in naming new viruses and new viral species (e.g., *Tomato yellow leaf curl Thailand virus*), as this may cause misunderstandings when a virus named after a country or city is subsequently found in other locations within that country or in other countries. (Previously accepted names using this practice will not be changed to avoid conflicts in the literature.)

Strain name

Based on ICTV guidelines, there is no practical or standardized approach for differentiating or naming strains (or any other category below the species level). In fact, item 3.3 of the ICTV Statutes states that “The ICTV is not responsible for classification and nomenclature of virus taxa below the rank of species.” Nevertheless, the *Geminiviridae* Study Group has adopted its own guidelines for strain differentiation and nomenclature [43], although there is no formal requirement to do so. Our new analysis indicated a sequence identity threshold of 94 % for strain demarcation.

Ideally (when knowledge is available), strains should follow a nomenclature that reflects biological differences

between the members of the same species. For example, if it is established that a number of BGMV isolates comprising a distinct strain are capable of infecting a host (e.g., lima bean) that other BGMV isolates do not normally infect, it would then be appropriate to name the strain BGMV-Lima bean. Likewise, symptom severity descriptors (e.g., *Tomato golden mosaic virus*-Yellow vein) could also be used. In either case, such strain names should be used only when the phenotype is observed in multiple isolates of the same strain. As recommended for species names, country, city, town, village or province names should not be used in naming new strains. Strain name follows species name separated by a hyphen (“-”).

Isolate descriptor

Following the species/strain name, and within square brackets (“[]”), the isolate descriptor may contain any number of sub-fields separated by hyphens. Although the 9th ICTV Report’s recommendations for geminivirus nomenclature [1] suggested the use of colons (“:”) to separate sub-fields in the isolate descriptor, this can cause problems in various phylogenetic-tree-drawing programs, which, when reading phylogenetic trees in Newick format, will misinterpret numbers after the colon as representing branch length information.

The first sub-field should always be the two-letter international code of the country/territory in which the isolate was sampled (Supplementary Table S2), whereas the last sub-field should always be the year in which the isolate was last present within living tissue. If the year in which the isolate was sampled differs from the date on which it was last present within living tissue (e.g., when isolates are propagated in the laboratory), the date when the isolate was sampled should then be included as an internal sub-field. Between the first and last sub-fields, any additional descriptors can be used (for example, the laboratory code of the sample from which the isolate was obtained, the city nearest to the place where the sample was obtained, the host species from which the virus was isolated).

Conclusions

Since the 1990s begomovirus taxonomy has been based primarily on sequence comparisons methods. In this regard, it was pioneering, helped by the large number of full-length sequences available, and allowed for a robust statistical treatment of the data. Although this approach has been criticized for not taking biology into account, a closer look into the recognized species will show that biology is accurately reflected in the taxonomy. This revision demonstrated the robustness and the reliability of a sequence-based taxonomy, and this was acknowledged by the ICTV with the positive

outcome of the latest taxonomy proposal and the establishment of new begomovirus species (http://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/plant-official/4838.aspx). It should be noted, however, that the ICTV *Geminiviridae* SG has no ulterior motivation for continuing to propose new species. Rather, the number of new species proposed is a genuine reflection of our increasingly effective methods to conceptualize the natural genetic variability of this remarkable group of viruses. By establishing clear guidelines for the analysis of full-length genomic sequences, and following standardized nomenclature for the naming of newly established species and strains, the intention of the ICTV *Geminiviridae* SG is that these changes will improve taxonomic communications among users while also leaving open options for further improvements in the future that will serve the geminivirus community at large.

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