MATHEUS DE MORAIS SANTOS

POPULATION GENOMICS OF VIRUSES AND ITS ANALYTICAL TOOLS

Dissertação apresentada à Universidade Federal de Uberlândia, como parte das exigências do Programa de Pós-Graduação em Agronomia – Mestrado, área de concentração em Fitopatologia, para obtenção do título de “Mestre”.

Orientador
Prof. Dr. Alison Talis Martins Lima

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Reuniu-se na sala 212, bloco 1CCG, Campus Glória, da Universidade Federal de Uberlândia, a Banca Examinadora, designada pelo Colegiado do Programa de Pós-graduação em Agronomia, assim composta: Professores Doutores: Flávio Tetsuo Sassaki - UFU; Lisias Coelho - UFU; Alice Kazuko Inoue Nagata - EMBRAPA; Alison Talis Martins Lima - UFU orientador(a) do(a) candidato(a).

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In memory of José Lemos de Morais

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CONTENT

RESUMO

SANTOS, Matheus de Morais. **Genômica de populações de vírus e suas ferramentas analíticas.** 2020. 226p. Dissertação (Mestrado em Agronomia/Fitopatologia) – Universidade Federal de Uberlândia, Uberlândia.[1]

A genômica comparativa permite estudar populações virais com alta acurácia, por utilizar o maior número possível de marcadores moleculares. O entendimento acerca dos processos evolutivos que atuam sobre estas populações tem importância ecológica e epidemiológica, visto que apresentam altos níveis de diversidade genética. Os begomovírus (gênero *Begomovirus*, Família *Geminiviridae*) possuem genomas compostos por uma única molécula de DNA de fita simples (begomovírus monopartidos) ou duas (begomovírus bipartidos, componentes DNA-A e DNA-B), infectam plantas dicotiledôneas e evoluem tão rapidamente quanto os vírus com genomas compostos por RNA. A estrutura genética da metapopulação global dos begomovírus foi determinada em um estudo prévio baseado em sequências de DNA-A e revelou ser composta por grandes subpopulações geneticamente diferentes e coesas em decorrência da existência de barreiras geográficas, pela gama de hospedeiros e por barreiras genéticas à recombinação. Contudo, a estrutura da metapopulação global dos begomovírus baseada no DNA-B ainda não foi determinada. Nos bancos de dados públicos há um número de sequências suficiente para realização de tal estudo. Mas a comparação de três ou mais sequências biológicas requer a construção de alinhamentos múltiplos de sequências (AMSs). Todos os programas computacionais utilizados na construção de AMSs utilizam estratégias heurísticas e, por isso, apresentam diferenças em seus níveis de acurácia. A acurácia é um parâmetro crítico para a escolha de um programa de AMSs. Também, notavelmente, há uma certa escassez de estudos que avaliem o nível de acurácia destes programas quando os conjuntos de dados são compostos por genomas virais. Assim, este trabalho teve como objetivos: *(i)* determinar a estrutura genética da metapopulação global dos begomovírus baseada em sequências do DNA-B, comparando os padrões de recombinação entre suas subpopulações; e *(ii)* avaliar o nível de acurácia dos principais programas para construção de AMSs sobre genomas virais e suas implicações práticas em estudos de genômica. Para cumprir o primeiro objetivo, sequências completas de DNA-B foram obtidas do GenBank, subdivididas em oito subpopulações por meio da análise discriminante de componentes principais e analisadas por sete métodos de detecção de recombinação. As subpopulações inferidas foram geneticamente diferentes e apresentaram dois padrões de recombinação distintos. O segundo objetivo foi cumprido pela avaliação do nível de acurácia de 13 programas/ajustes para construção de AMSs sobre seis conjuntos de dados compostos pelos genomas completos de espécies pertencentes a cinco gêneros de vírus e um gênero de um agente subviral. Os programas apresentaram níveis de acurácia diferentes dependendo do conjunto de dados. Notavelmente, AMSs gerados pelos programas mais acurados (determinados neste estudo) e aqueles gerados por programas amplamente utilizados em estudos genômicos na área da Virologia renderam árvores filogenéticas incongruentes, sugerindo que as histórias evolutivas frequentemente apresentadas na literatura podem não ser as mais verossímeis.

Palavras-chave: Evolução molecular; Begomovírus; Bioinformática.

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[1] Orientador: Prof. Alison Talis Martins Lima

ABSTRACT

SANTOS, Matheus de Morais. **Population genomics of viruses and its analytical tools.** 2020. 226p. Dissertation (Master in Agronomy/Plant Pathology) – Universidade Federal de Uberlândia, Uberlândia.[2]

Comparative genomics makes possible to study virus populations with high degree of accuracy, by using the largest possible number of molecular markers. The knowledge of evolutionary processes that affect these populations is of ecological and epidemiological importance, since they show high degrees of genetic diversity. Begomoviruses (genus *Begomovirus*, Family *Geminiviridae*) have genomes composed of one single-stranded DNA molecule (monopartite begomoviruses) or two (bipartite begomoviruses, DNA-A and DNA-B components), infect dicotyledonous plants and evolve as quickly as viruses with genomes composed of RNA. The genetic structure of the global metapopulation of begomoviruses was determined in a previous study based on DNA-A sequences and revealed to consist of large, genetically different and cohesive subpopulations due to the existence of geographical barriers, host range and genetic barriers to recombination. However, the structure of the global metapopulation based on DNA-B sequences has not been determined. There is a enough sequences in public databases to carry out such a study. Nevertheless, comparing three or more biological sequences requires the construction of multiple sequence alignments (MSAs). All computer programs used in MSAs construction use heuristic strategies and, therefore, show differences in their degrees of accuracy. Accuracy is a critical parameter for choosing a MSA program. Also, notably, there is a scarcity of studies that assess the level of accuracy of these programs when data sets are composed of viral genomes. Thus, this work (*i*) determined the genetic structure of the global metapopulation of begomoviruses based on DNA-B sequences, comparing the recombination patterns from their subpopulations; and (*ii*) evaluated the degree of accuracy of the main MSA programs on viral genomes and their practical implications in genomics studies. To achieve the first objective, full-length DNA-B sequences were obtained from GenBank, subdivided into eight subpopulations by discriminant analysis of principal components and analyzed by seven methods of recombination detection. The inferred subpopulations were genetically different and presented two distinct recombination patterns. The second objective was achieved by estimating the degree of accuracy of 13 MSA programs/settings on six data sets composed of the full-length genomes of species belonging to five genera of viruses and one genus of a subviral agent. The programs showed distinct degrees of accuracy depending on the data set. Notably, MSAs generated by the most accurate programs (determined in this study) and those generated by programs widely used in genomic studies in the field of Virology yielded incongruent phylogenetic trees, suggesting that the evolutionary histories frequently presented in the literature may not be the most likely ones.

Keywords: Molecular evolution; Begomoviruses; Bioinformatics.

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[2] Advisor: Prof. Alison Talis Martins Lima

GENERAL INTRODUCTION

Historically, the evolutionary relationship among the biological entities has been inferred from morphological characters, which are influenced by environmental factors and led to subjective and often inaccurate conclusions. The use of molecular data (protein and nucleotide sequences) and the development of high performance computers (HPCs) revolutionized the biological sciences by making possible to reconstruct accurately the evolutionary histories even at high-level taxonomic categories (HILLIS, 1987; SCOTLAND; OLMSTEAD; BENNETT, 2003). More recently, the high-throughput DNA sequencing platforms added to new bioinformatics tools (HEATHER; CHAIN, 2016; ORTON *et al.*, 2016; SOHN; NAM, 2018; WEE *et al.*, 2019) allowed the extraction of biological information on a genomic scale for different biological entities (BLATTNER, 1997; ELLIS *et al.*, 2014; GREILHUBER *et al.*, 2006; PHILIPPE *et al.*, 2013; VENTER *et al.*, 2001).

Over the last years, the decreased operating costs in DNA sequencing (HERNAEZ *et al.*, 2019; STEPHENS *et al.*, 2015) led to a drastic increase of fully sequenced genomes available in public databases, such as GenBank, EMBL and the DNA Data Bank of Japan. All these combined factors allowed the conduction of comparative genomic studies on a population, sometimes at a global scale (CAO *et al.*, 2019; DOGANTZIS; ZAYED, 2019; GONZÁLEZ-CANDELAS; PATIÑO-GALINDO; VALIENTE-MULLOR, 2018; KACHROO *et al.*, 2019; RANNALA; YANG, 2008; ROUGEMONT *et al.*, 2019; SHEPPARD; GUTTMAN; FITZGERALD, 2018).

Genomes are the most holistic materials for studying populations; each nucleotide site (locus) is a character that can be used in comparisons of two or more individuals; *i.e.*, there is a drastic increase in accuracy due to the use of many genetic markers

(ALLENDORF; HOHENLOHE; LUIKART, 2010). Population genomics is the study of the effects of evolutionary processes or mechanisms that act on individuals to understand the variations on a population scale (BLACK IV *et al*., 2001; LUIKART *et al*., 2003). Therefore, population genomic studies are of fundamental importance to elucidate the evolution based on the highest level of information possible.

Virus populations are usually large (GUTIÉRREZ; MICHALAKIS; BLANC, 2012) and have high degree of genetic variability (CUDINI *et al*., 2019; PAULY; PROCARIO; LAURING, 2017; TROMAS *et al*., 2014; YOKOYAMA; STARMER, 2017; ZANINI *et al*., 2017), which implicate in a rapid adaptation and, consequently, rapid evolution (DENNEHY, 2017; DOLAN; WHITFIELD; ANDINO, 2018; ILLINGWORTH, 2015; XIAO *et al*., 2016). Mutation and recombination are, respectively, the main forces responsible for creating and randomizing the genetic variation in virus populations (DUFFY; SHACKELTON; HOLMES, 2008). Mutation is driven by physical or chemical changes throughout the genome during the replication process, which results in nucleotide substitutions, insertions or deletions (“indels”) (LOEWE; HILL, 2010). Recombination refers to the exchange of parts of genomic segments between viruses. Also, viruses with segmented genomes can exchange their entire genomic segments, a process known as pseudo-recombination (PÉREZ-LOSADA *et al*., 2015). The evolutionary mechanisms of selection, genetic drift and migration, drive the number and frequency of variant genotypes in a given population (DUFFY; SHACKELTON; HOLMES, 2008).

The family *Geminiviridae* consists of circular single-stranded (ss)DNA viruses, encapsidated into quasi-icosahedral particles. Their genera are defined based on genome organization, insect vector and phylogenomic relationships (ZERBINI *et al*., 2017). The genus *Begomovirus*, the largest in number of species, is composed of monopartite or bipartite viruses (segmented into two molecules, DNA-A and DNA-B) (BROWN *et al.*, 2015).

Population genomics studies based on DNA-A sequences (BRIDDON *et al.*, 2010; PRASANNA *et al.*, 2010) confirm the geographic subdivision of begomovirus metapopulation into two large clusters (RYBICKI, 1994): the ‘Old World’ (OW; Africa, Asia, Europe and Oceania), composed of monopartite and bipartite begomoviruses; and ‘New World’ (NW; Americas), with a predominance of bipartite begomoviruses. Both major subpopulations can be further subdivided from seven to thirty-four genetically differentiated and cohesive subpopulations due to geographical barriers, host range or genetic isolation to recombination (PRASANNA *et al.*, 2010). Population genomics studies of begomoviruses on global scale are mostly based on DNA-A sequences hypothetically for two reasons: this component (i) is present equivalently in both monopartite begomoviruses and bipartite begomoviruses (BROWN *et al.*, 2015); and (ii) it is used in the demarcation of its species (BROWN *et al.*, 2015). Therefore, the genetic structure of the global metapopulation of begomoviruses based on the DNA-B sequences remains to be determined.

Comparative genomic analyses, involving two or more sequences, require the construction of multiple sequence alignments (MSAs) (HARDISON, 2003). The construction of an exact MSA involves the simulation of all possible arrangements varying the number and position of gaps and the use of a scoring criterion (objective function) to estimate the degree of accuracy of each one; the best one is the final MSA. Even using HPCs, the construction of an exact MSA is an NP-complete problem (JUST, 2001; WANG; JIANG, 1994), limiting the construction of exact MSAs to a few sequences (EDGAR; BATZOGLOU, 2006; KEMENA; NOTREDAME, 2009). As a consequence, all algorithms designed for MSAs construction use heuristic strategies

(CHATZOU *et al.*, 2016; CHOWDHURY; GARAI, 2017), which allow to obtain the best arrangement in a set of computational viable options; therefore, the final product is considered to be an optimized MSA (CHATZOU *et al.*, 2016; CHOWDHURY; GARAI, 2017).

The programs that incorporate MSA algorithms differ in their heuristic processes and, consequently, are classified into methods. The progressive alignment method was the first to be designed (CORPET, 1988; FENG; DOOLITTLE, 1987; HIGGINS; SHARP, 1988; HOGEWEG; HESPER, 1984; TAYLOR, 1988) and its use was widely disseminated by the Clustal program (HIGGINS; SHARP, 1988; THOMPSON; HIGGINS; GIBSON, 1994). Under the progressive method, the first step in the MSA construction is to calculate the distances between all possible sequence pairs; these distances are stored in a matrix that is converted into a phylogenetic tree (the guide tree) (FENG; DOOLITTLE, 1987; HOGEWEG; HESPER, 1984). In the second step, which is guided by the tree generated in the first step, the most similar sequence pair is aligned; the remaining sequences are added one by one progressively to the partial alignment, until all sequences have been added to it (FENG; DOOLITTLE, 1987; HOGEWEG; HESPER, 1984). In this step, a specific pairwise algorithm is used, for example, the Needleman-Wunsch (NEEDLEMAN; WUNSCH, 1970) or the Smith-Waterman (SMITH; WATERMAN, 1981), to align/score the partial alignments.

The progressive method has the disadvantage in which divergent sequences may lead to low similarity sequence pairs in the guide tree, decreasing the overall accuracy. In addition, any errors in the initial steps of the MSA construction are maintained in the final MSA (CHATZOU *et al.*, 2016). In order to reduce such errors, methods based on this strategy were improved by adding steps of consistency (consistency methods)

(NOTREDAME; HIGGINS; HERINGA, 2000) or iterative refinement (iterative methods) (EDGAR, 2004; GOTOH, 1996; KATOH *et al*., 2002).

Consistency is achieved in the step of guide tree construction in which each pairwise alignment (primary library) is aligned and scored after adding a third sequence (extended library). The primary pairs are extracted from the highest scoring sub-alignments and used for the guide tree inference (NOTREDAME; HIGGINS; HERINGA, 2000). The consistency step avoids low similarity sequence pairs in the guide tree and is incorporated in MSAs programs such as T-Coffee (NOTREDAME; HIGGINS; HERINGA, 2000) and ProbCons (DO, 2005). The consistency steps lead to a higher degree of accuracy in detriment of the execution time (DO, 2005; NOTREDAME; HIGGINS; HERINGA, 2000).

Iterative refinement is performed by repeating the process of MSA construction until obtaining an improved MSA (GOTOH, 1996). The setting [FFT-NS-2] in MAFFT program uses the first complete MSA to recalculate the distance matrix of its guide tree and build a new improved MSA (KATOH *et al*., 2002). The Muscle program is also based on an iterative refinement but applies the Kimura correction in the recalculated distance matrix. Then, it compares the second MSA with the first one and uses the best one to repeat the process for a number of times that can be defined by the user, producing as the final MSA, the best amongst all (EDGAR, 2004).

Accuracy estimates are usually of comparative nature, involving ‘reference’ data sets (benchmarks), which are highly accurate MSA built from real or computationally created sequences to simulate specific scenarios (ANIBA; POCH; THOMPSON, 2010). The sum of pairs (SP) and total columns are parameters used to quantify the similarities shared between benchmarks and MSAs with the same sequence composition but constructed by another program (MIRARAB; WARNOW, 2011; SAUDER; ARTHUR; DUNBRACK JR., 2000; THOMPSON; PLEWNIAK; POCH, 1999).

There are no benchmarks based on viral genomes, which show unusual features compared with those of other biological entities. Their reduced size (KOONIN; DOLJA; KRUPOVIC, 2015), high mutation rates (SANJUAN *et al*., 2010) and a number of novel and compacted genes (BRANDES; LINIAL, 2016; FIRTH; BROWN, 2006; KOONIN, 2010) make inviable to assume the accuracy results of MSA programs obtained for other classes of molecules and genomes. In this context, this study: *(i)* determined the genetic structure of the global metapopulation of begomoviruses based on a large data set comprised of DNA-B sequences and; *(ii)* estimated the degree of accuracy from MSA programs, including those widely used in the field of Virology. Our results indicate that among eigth genetically different subpopulation of global metapopulation of begomoviruses based on DNA-B sequence there are two distinct recombination patterns, and that the accuracy of MSA programs is strongly affected by intrinsic factors of each viral data set and that subsequent analyses using low accuracy MSAs might give rise to spurious results.

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CHAPTER 1

Genetic structure of the global meta-population of begomoviruses based on DNA-B sequences[3]

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Genetic structure of the global meta-population of begomoviruses based on DNA-B sequences

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Abstract

Begomoviruses are single-stranded DNA plant viruses that emerged in the last few decades as threats to important crops, especially in tropical and subtropical countries. Their genomes are comprised of one (monopartite) or two genomic components (DNA-A and DNA-B; referred to as bipartite begomoviruses). The global meta-population of begomoviruses is composed by 409 species, structured into two main subpopulations (the Old and New World) that can be further subdivided into smaller genetically different subpopulations due to geographical barriers and differences in their host ranges. Recombination is thougth to contribute for a significant portion of the genetic polymorphisms in begomovirus subpopulations. Due to geographical isolation, begomovirus subpopulations may exhibit distinct recombination patterns based on sampling location and timing. Due to the importance of the DNA-A component for replication, encapsidation and its use for taxonomic purposes, it has been exhaustively used in population genomic studies. However, the structure of the global meta-population of begomoviruses based on DNA-B sequences has not been determined. In this context, this study determined the genetic structure of begomovirus meta-population based on DNA-B sequences, taking advantage of the currently available large genomic data set, and contrasted the recombination patterns of the main subpopulations. The meta-population, 1,248 sequences representating of 218 species, was divided into eight subpopulations using the discriminant analysis of principal components (DAPC). Three of eigth subpopulations of begomoviruses based on DNA-B formed a large cluster of 'New World' begomoviruses. 'Old World' begomovirus subpopulations were considerably more divergent, Asian and African begomovirus composed two subpopulations each one and one subpopulation was composed by Asian and African begomovirus. The DAPC-inferred begomovirus subpopulations were analyzed for their recombination breakpoints distribution patterns using the Recombination Detection Program (RDP). Our recombination results indicate that the global meta-population of begomoviruses based on DNA-B sequences involves a combination of at least two unique recombination patterns.

Key words: Evolution; Geminivirus; Genetic structure.

Introduction

The genus *Begomovirus* (family *Geminiviridae*), the largest in number of species (409) of plant virus, is composed of circular single-stranded DNA (ssDNA) viruses, comprised of one (DNA-A-like component) or two molecules (DNA-A and DNA-B) genome segments (Brown *et al.*, 2015) encapsidated within quasi-icosahedral geminate particles. Cryptic species complex of the whitefly *Bemisia tabaci* are (De Barro *et al.*, 2011; Brown *et al.*, 2015) involved in the transmission of begomoviruses to cultivated and non-cultivated dicotyledonous plants (Rojas *et al.*, 2005). DNA-A and DNA-B molecules have 2,600 – 2,800 nucleotides (nt) each, with a highly conserved 200 nt-commom region (CR), which contains the functional motif of the origin of replication, the highly conserved nonanucleotide (5’ TAATATT↓AC 3’) (Brown *et al.*, 2015; Zerbini *et al.*, 2017).

Begomovirus species native from “Old World” (OW: Africa, Asia, Europe and Oceania) have bipartite or monopartite genomes, while species from “New World” (NW: Americas) are predominantly bipartite (Brown *et al.*, 2015; Zerbini *et al.*, 2017). For bipartite species, both genomic components are required for systemic infection of the host plant (Rojas *et al.*, 2005). DNA-A or DNA-A like molecules encode structural and replication associated proteins (Hanley-Bowdoin *et al.*, 1999), while the DNA-B encodes two proteins involved in short and long distance movement (Noueiry *et al.*, 1994; Sanderfoot & Lazarowitz, 1996).

Begomovirus subpopulations show high degrees of genetic variability due to their high nucleotide substitution rates, similar to those of RNA viruses (Drake, 1991; Duffy & Holmes, 2008, 2009) and the frequent occurrence of recombination (Padidam *et al.*, 1999; Rocha *et al.*, 2013; Lefeuvre & Moriones, 2015), an evolutionary mechanism in which parts of the genome are exchanged between distinct viruses during mixed infections (Garcia-Arenal *et al.*, 2003; Roossinck, 2008). Previous studies have demonstrated that DNA-B-based sequence data sets are more variable than those of DNA-A sequences (Briddon *et al.*, 2010; Rocha *et al.*, 2013; Mar *et al.*, 2017). Such results, added to the occurrence of pseudo-recombination, an additional evolutionary mechanism in which complete genome segments are exchanged between viruses (Garcia-Arenal *et al.*, 2003; Seal *et al.*, 2006; Roossinck, 2008), indicate that DNA-A and DNA-B of begomoviruses have distinct evolutionary histories (Briddon *et al.*, 2010). More important, the geographical isolation of begomovirus subpopulations (Ilyas *et al.*, 2010; Rocha *et al.*, 2013; De Bruyn *et al.*, 2016; Mar *et al.*, 2017) corroborates the hypothesis that the evolutionary dynamics of DNA-B components might be unique, depending on the sampling location, because for recombination occurrence, it is necessary that the two parental viruses infect the same plant.

The number of begomovirus genomes available in public databases (*e.g.* GenBank) has increased exponentially over the last years due to novel molecular techniques, such as the circular ssDNA amplification using the Phi29 DNA polymerase (Inoue-Nagata *et al.*, 2004) and the high-throughput DNA sequencing platforms (Reuter *et al.*, 2015). Therefore, there is a substantial range of DNA-B data sets for inferring important population genomic parameters to better describe the evolutionary aspects of begomovirus subpopulations. In this study, we investigated the genetic structure of the global metapopulation of begomoviruses based on DNA-B sequences and characterized their recombination patterns.

Material and Methods

Sequence data sets and multiple sequence alignment

Full-length DNA-B sequences of begomoviruses (N = 1,248, 218 different species) were retrieved from GenBank (Sayers *et al.*, 2019) using Taxonomy Browser (www.ncbi.nlm.nih.gov), on January 2019 (Supplementary Table S1). Each sequence was organized to begin at the nicking site of the conserved nonanucleotide (5' TAATATT↓AC 3'). A multiple sequence alignment containing all DNA-B sequences was constructed using MUSCLE (Edgar, 2004) and manually edited using MEGA X (Kumar *et al.*, 2018).

Genetic structure of begomovirus meta-population based on DNA-B sequences

The DNA-B-based multiple sequence alignment was subjected to a multivariate statistical-based approach of population subdivision using the discriminant analysis of principal components (DAPC) (Jombart *et al.*, 2010). By using K-means, the meta-population of begomoviruses was subdivided from two to ten (K-value) subpopulations, retaining all principal components (PC) in adegenet package (Jombart, 2008; Jombart & Ahmed, 2011) of the R-project (R Foundation for Statistical Computing, 2018). Furthermore, haplotype composition and the average pairwise number of nucleotide differences per site (nucleotide diversity, π) were computed for the meta-population and the DAPC-inferred subpopulations using DnaSP v.6 (Rozas *et al.*, 2017).

Recombination analysis

Detection of recombinant sequences and determination of recombination breakpoints distribution (RBD) were performed using seven methods implemented in RDP4 (Martin *et al.*, 2015): [RDP (Martin & Rybicki, 2000), Geneconv (Padidam *et al.*, 1999), Bootscan (Martin *et al.*, 2005), Maximum Chi Square (Smith, 1992), Chimaera (Posada & Crandall, 2001), Sister Scan (Gibbs *et al.*, 2000) and 3Seq (Lam *et al.*, 2018)].

Statistical significance was inferred by *P*-values lower than a Bonferroni-corrected $\alpha = 0.05$ cutoff. Only recombination events detected by more than three of the analysis methods available in the program were considered in the subsequent analyses. RBD plots were constructed using sliding windows of 200 nucleotides under a permutation test with 5,000 replications to estimate the statistical significance of recombination hotspots and coldspots (Heath *et al.*, 2006). RDP project files are available from the authors upon request.

The occurrence of recombination in DNA-B sequences was further validated by evidence of a reticular network using Neighbor-Net method (Bryant, 2003) implemented in SplitsTree v.4 (Huson & Bryant, 2006).

Results

The genetic structure of begomovirus meta-population

In this study, the DNA-B haplotypes were identified and a single representative sequence was maintained in the data set for the subsequent analyses, totalizing 1,217 unique sequences. We focused on the DAPC-simulation assuming eight genetically different DNA-B begomovirus subpopulations (Supplementary Table S1). On these conditions, the sample sizes of most DNA-B-based begomovirus subpopulations were large enough to provide a detectable and robust signal for subsequent recombination detection analyses.

Three of eight begomovirus subpopulations formed a large cluster containing all 'New World' begomoviruses (Figure 1, top left panel). This large cluster consisted of two small sized subpopulations: one comprised of isolates of the Uruguayan begomovirus *Tomato rugose yellow leaf curl virus* (ToRYLCV) (*N* = 9) (Márquez-Martín *et al.*, 2012), and the other one are comprised by *Euphorbia yellow mosaic virus* (EuYMV) and *Squash leaf curl virus* (SqLCV) isolates (*N* = 80). The largest one contained almost all isolates collected in several countries from Latin America (*N* = 552).

The other subpopulations were considerably more divergent (Figure 1, right panel) and comprised 'Old World' begomoviruses. Two of them (Figure 1, top right panel) consisted of Asian isolates: the India and China (*N* = 206) subpopulation and, a second one, more geographically diverse, with isolates from 10 Asian countries (*N* = 91). Another subpopulation (Figure 1, bottom right panel) was even more geographically diverse consisting of isolates (*N* = 133) from 13 and 9 countries from Asia and Africa, respectively.

The two remaining subpopulations (Figure 1, bottom right panel) were composed predominantly of *African cassava mosaic*-like viruses (*N* = 29) and *East African cassava mosaic*-like viruses (*N* = 117) from 7 and 11 African countries, respectively.

The non-random recombination among isolates of begomoviruses DNA-B

A prerequisite for occurrance of recombination between two or more viruses is a co-existence in time and space; therefore viruses co-exiting in time and exploring a common niche (overlapping host ranges), show greater probability of recombining than those temporally and/or spatially separated. We constructed phylogenetic networks that count for alternative evolutionary histories to further investigate this finding. We analyzed one representative sequence of each species for sake of clarity, which made possible the visualization of the major begomovirus subpopulations. The reticulation in the DNA-B-based networks (Figure 2) showed mostly connected branches leading to isolates sharing very close sampling location. This phylogenetic approach corroborate one of our main hypothesis in this study: virus from a same location sampling are more propense to recombination.

Distinct recombination patterns among subpopulations of begomoviruses

Given the geographic isolation of the major begomovirus subpopulations, we assume that each of them could exhibit a distinct recombination pattern in terms of RBD across their DNA-B sequences. This second hypothesis was tested by counting the number of recombination breakpoints (details on breakpoints location are available in Supplementary Table S2) in 200 nt-sliding windows that spanned the whole length of the DNA-B component (Figure 3).

The number of recombination events detected in a given sequence data set is strongly affected by its sample size; *e.g.*, the more sequences in a data set, the greater is the probability of detecting recombination events. Factors other than sample size also affect the performance of recombination detection (Posada & Crandall, 2001) and are discussed here. To minimize the sample size bias in our RBD analyses, we excluded the small subpopulation “ToRYLCV” and “ACM-like viruses” (N = 9 and 29 sequences, respectively).

Two distinct recombination patterns were observed for the DAPC-inferred subpopulations: the first one in which no recombination hotspots were detected (Figure 3b-d and 3f) and a second one in which a single recombination hotspot was detected in the rigth portion of the CR in the “Latin America” and “EACM-like viruses” (Figure 3a and 3e). The “Latin America” subpopulation had the largest sample size (Table 1, $N = 552$) among all subpopulations, which in fact might favor the detection of more recombination events. However, the contrasting numbers of recombination breakpoints within and outside the hotspot region make it a solid result from this study. In contrast, the “EACM-like viruses” had a sample size similar to that of “Asia-Africa” subpopulation ($N = 117$ and 133, respectively) and smaller than that of “India-China” ($N = 206$) in which no recombination hotspots were detected.

The nucleotide diversity calculated for the “Latin America” subpopulation (Table 1, $\pi = 0.23484$) indicated that it is one of the most variable amongst all DNA-B-based subpopulations. Similarly, the “Asia” subpopulation showed a high degree of genetic variability ($\pi = 0.27227$) and no recombination hotspots were detected. In contrast, the “EACM-like viruses” subpopulation was the least variable one ($\pi = 0.08144$) but provided a robust signal for the hotspot detection.

Therefore, given the robustness of our recombination analyses, the hotspots detected in two virus subpopulations and the lack of hotspots in the other six DAPC-inferred subpopulations, we concluded that the genetic structure in subpopulation leads to the existence of distinct recombination patterns amongst in DNA-B sequences of begomoviruses.

Discussion

The geographical subdivision of begomoviruses into 'OW' and 'NW' begomoviruses has been shown in previous phylogenetic and population genomic studies focusing on DNA-A component (Rybicki, 1994; Paximadis *et al.*, 1999; Brown, 2000; Rojas *et al.*, 2005). Our DNA-B-based results also support a similar scenario. However, the segregation of American begomoviruses seems to involve genetic and/or host range rather than geographical barriers since the "Latin America" subpopulation harbored almost all NW begomoviruses, except the smaller and mostly intraspecific "EuYMV-SqLCV" and "ToRYLCV" subpopulations. The closer relationship between 'NW' subpopulations and the genetic divergence among 'OW' subpopulations corroborate with the hypothesis that DNA-B component originated from this latter macro-region (Nawaz-ul-Rehman & Fauquet, 2009; Briddon *et al.*, 2010).

The diversification of begomovirus populations is predominantly driven by the evolutionary mechanism of mutation (Lima *et al.*, 2017). However, recombination still plays an important role in their evolution, randomizing the mutations into new genomic combinations (Martin *et al.*, 2011a). The impact of recombination may be measured by reports of recombinant begomoviruses that proved to be more adapted than their parents under field conditions (Pita *et al.*, 2001; Monci *et al.*, 2002; Silva *et al.*, 2014). However, the occurrence of recombination requires the co-existence in time and space of the parental viruses (mixed infection in a single host plant). Thus, it is reasonable to assume that recombination is strongly affected by the geographical structure of the virus meta-population. In addition, evidences indicate that recombination events occur differently along the genomic components of begomoviruses; such differences might be driven by intrinsic factors in the ssDNA genome of begomoviruses and, or, be a by-product of the evolutionary mechanism of selection acting against recombinant viruses in which the intra-genome interaction network has been disrupted (Lefeuvre *et al.*, 2007; Melzer *et al.*, 2010; Martin *et al.*, 2011b).

The mechanic aspects of recombination in ssDNA viruses have not been elucidated. However, the recombination-dependent replication (RDR) (Jeske, 2001) might explain the recurrent recombination in the CR, which contains the origin of replication (*v*-ori). Nevertheless, additional factors might be involved in the differential predisposition of the CR as a target of recombination breakpoints in specific virus subpopulations, as observed in our results. Taking into account only the subpopulations in which a single recombination hotspot has been detected, the rigth CR portion seems to be the most after-selection recombination-prone region in the DNA-B molecule.

Finally, it is important to emphasize that our results split the recombination pattern of the global meta-population of begomoviruses into two sub-patterns for their genetically differentiated and cohesive subpopulations. Nevertheless, no recombination hotspots were detected in the left CR portion, for any DNA-B-based subpopulation, as shown in a previous study (Lefeuvre *et al.*, 2009) in which the whole meta-population was analyzed, ignoring the geographical isolation of its composing subpopulations. Given the several studies that show a strong geographic structuring for begomovirus subpopulations, even on a small geographic scale (within a country, for example) (Prasanna *et al.*, 2010; Rocha *et al.*, 2013; Sobrinho *et al.*, 2014; Mar *et al.*, 2017), it is questionable to assume a single recombination pattern for large subpopulations that are separated geographically on a large time scale.

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Table 1. Genetic variability and recombination events detected in global subpopulations of begomoviruses

Subpopulation	**DNA-B**		
	N	**π**	**UREs**
ToRYLCV	9	0.10999	3
Latin America	552	0.23484	140
ACM-like viruses	29	0.09429	1
India – China	206	0.13185	49
EuYMV – SqLCV	80	0.13272	7
Asia	91	0.28997	12
EACM-like viruses	117	0.08144	14
Asia – Africa	133	0.27227	19
Total	1217	0.34631	245

N = sample size;

π = nucleotide diversity;

UREs = number of unique recombination events detected by RDP.

Figure legends

Figure 1. Multivariate statistical clustering analyses of subdivision populations based on full-length DNA-B sequences of bipartite begomovirus isolates collected from around the world. Each dot represents a single begomovirus isolate. Sets of dots of the same color indicate an individual begomovirus subpopulation. The distances between every possible subpopulations pairs in the plot are proportional to the genetic distance between subpopulations.

Figure 2. Network phylogenetic trees based on DNA-B data sets containing a single representative sequence of each begomovirus species. The formation of a reticular network rather than a single bifurcated tree is indicative of alternative evolutionary histories possibly due to the occurrence of recombination events amongst begomovirus isolates.

Figure 3. Breakpoints density across full-length DNA-B sequences of bipartite begomoviruses subdivided into eight genetically differentiated subpopulations. (**a**) Latin America, (**b**) India-China, (**c**) EuYMV-SqLCV, (**d**) Asia, (**e**) EACM-like viruses, (**f**) Asia-Africa. A 200-nt window was moved along the alignment, one nucleotide at a time, and the breakpoints detected within the window length were counted and plotted (solid line). The upper and lower broken lines, respectively, indicate 99% and 95% confidence thresholds for globally significant breakpoint clusters. The light- and dark-gray areas, respectively, indicate local 99% and 95% breakpoint-clustering thresholds, taking into account local regional differences in sequence diversity that influence the abilities of different methods to detect recombination breakpoints.

Figure 1

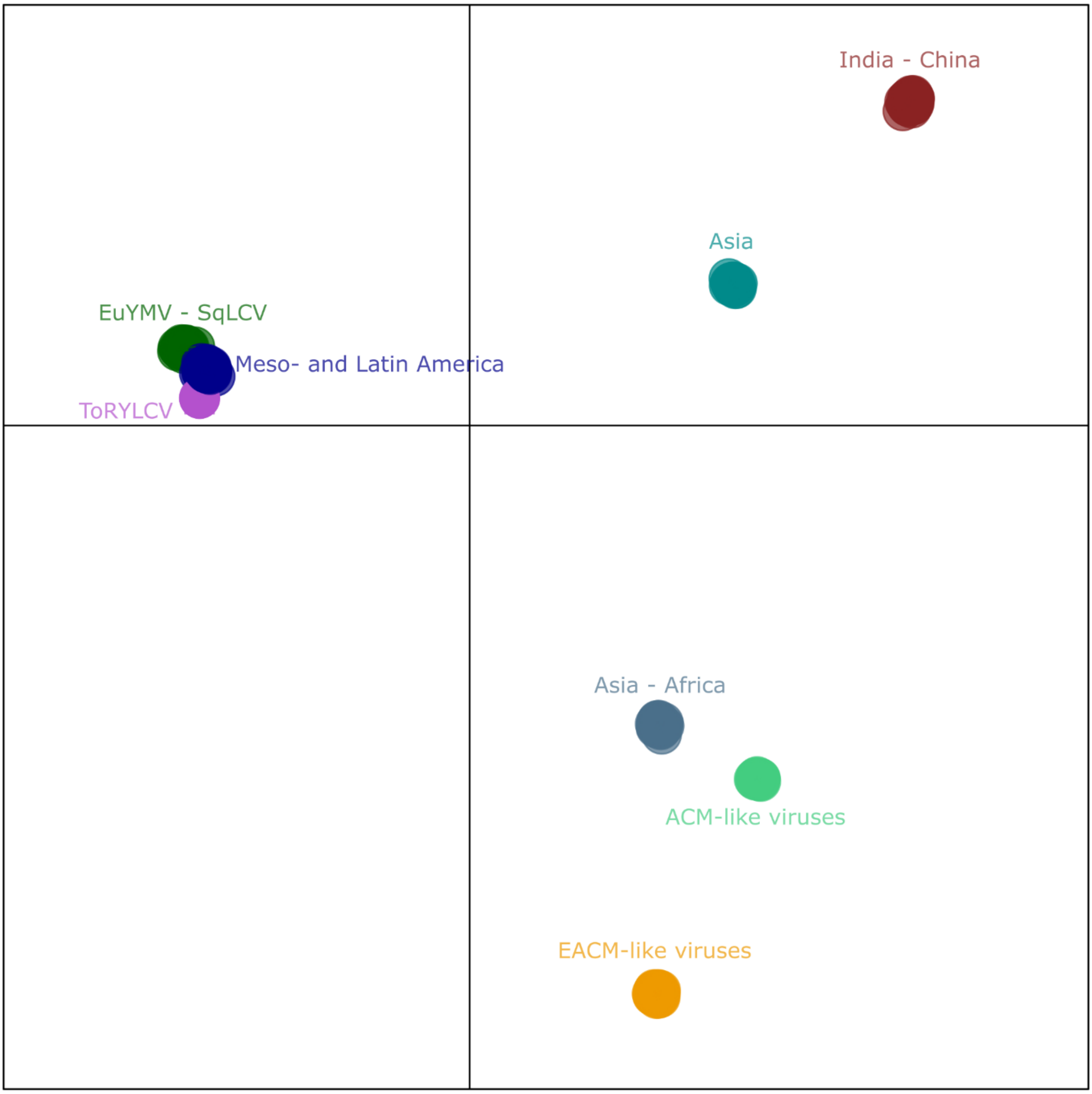

India - China
Asia
EuYMV - SqLCV
Meso- and Latin America
ToRYLCV
Asia - Africa
ACM-like viruses
EACM-like viruses

Figure 2

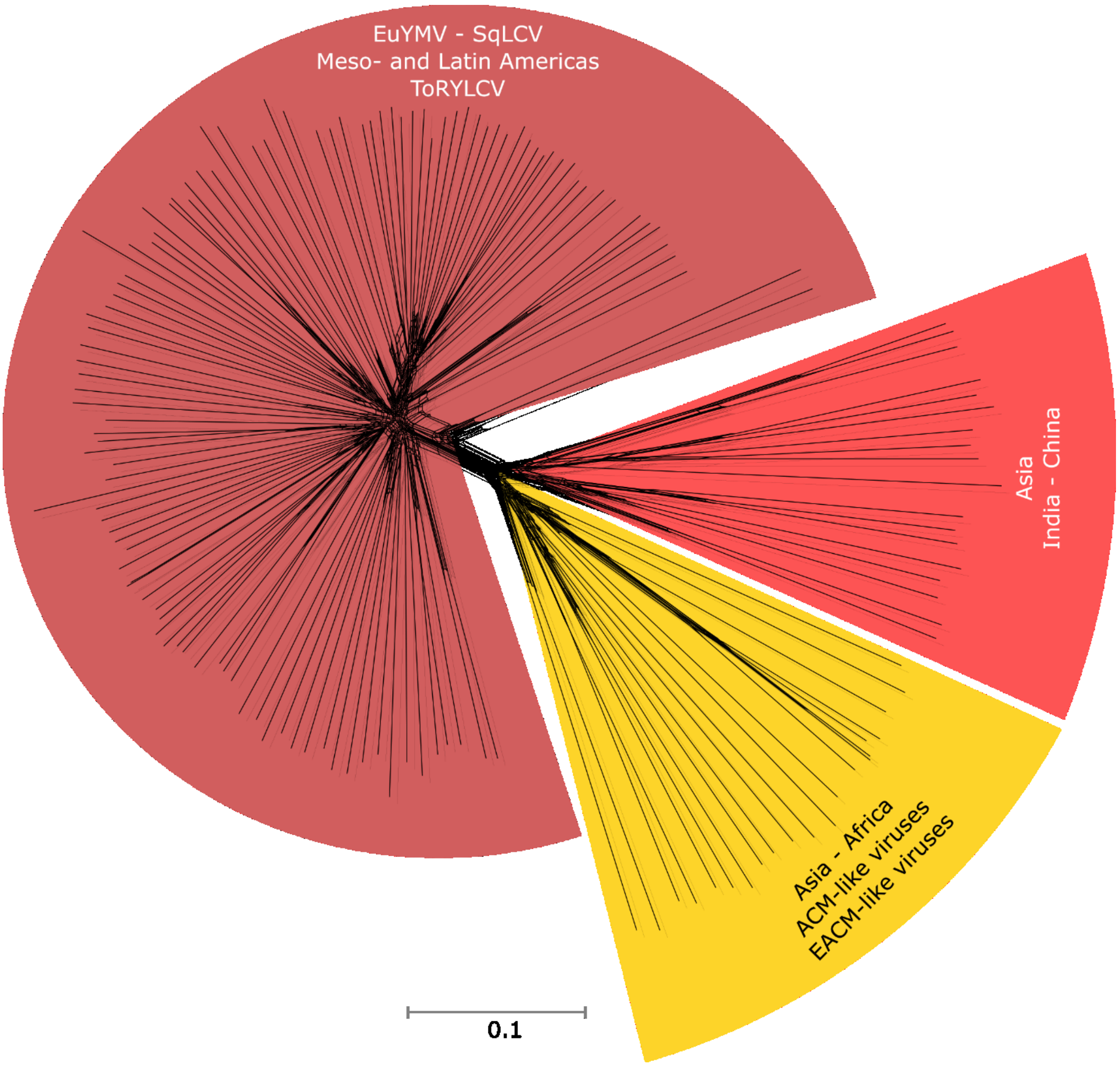
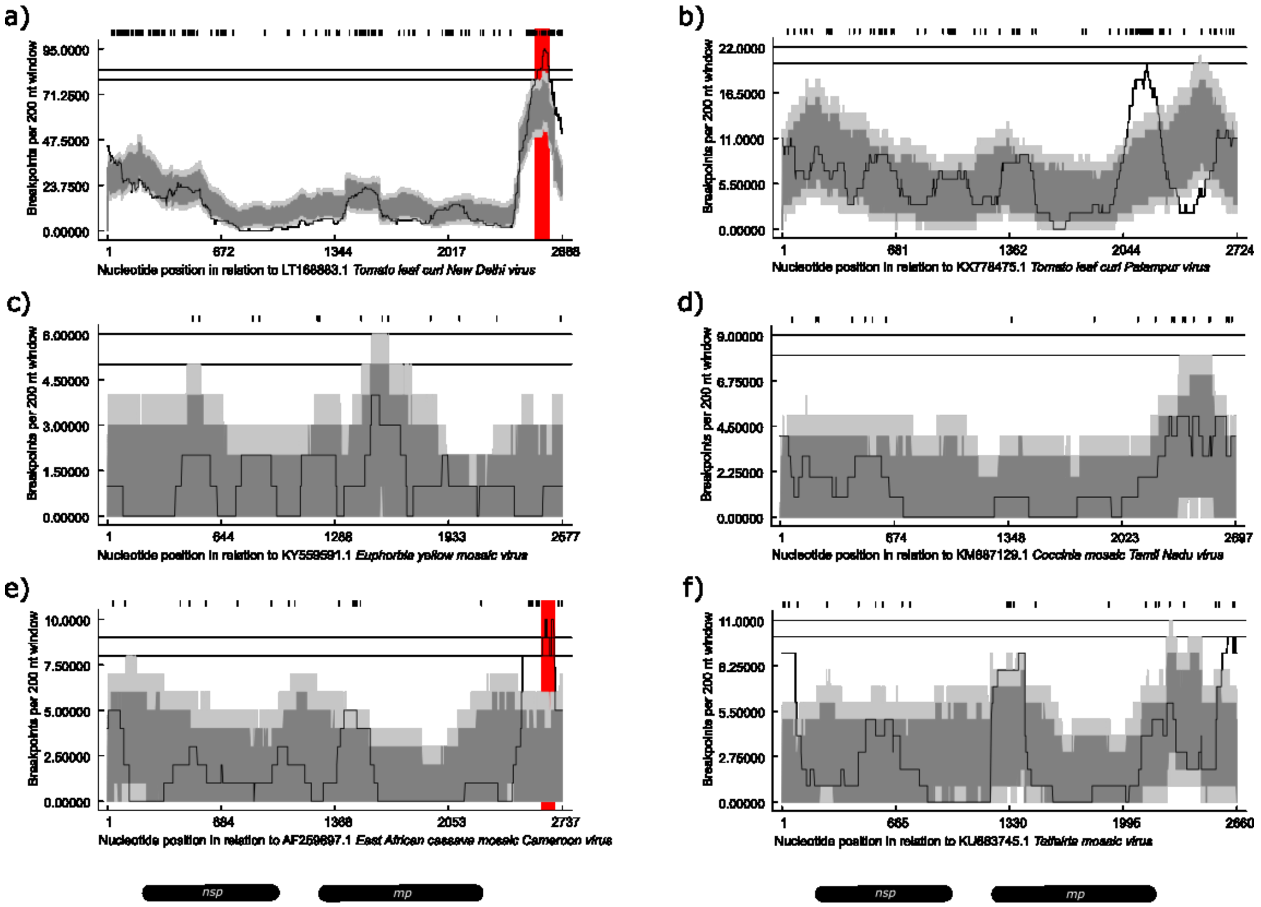

EuYMV - SqLCV
Meso- and Latin Americas
ToRYLCV
Asia
India - China
Asia - Africa
ACM-like viruses
EACM-like viruses
0.1

Figure 3


a)
Breakpoints per 200 nt window
95.0000
71.2500
47.5000
23.7500
0.00000
1
672
1344
2017
2688
Nucleotide position in relation to LT168863.1 Tomato leaf curl New Delhi virus
b)
Breakpoints per 200 nt window
22.0000
16.5000
11.0000
5.50000
0.00000
1
681
1362
2044
2724
Nucleotide position in relation to KX778475.1 Tomato leaf curl Palampur virus
c)
Breakpoints per 200 nt window
6.00000
4.50000
3.00000
1.50000
0.00000
1
644
1288
1933
2577
Nucleotide position in relation to KY559591.1 Euphorbia yellow mosaic virus
d)
Breakpoints per 200 nt window
9.00000
6.75000
4.50000
2.25000
0.00000
1
674
1348
2023
2697
Nucleotide position in relation to KM687129.1 Coccinia mosaic Tamil Nadu virus
e)
Breakpoints per 200 nt window
10.0000
7.50000
5.00000
2.50000
0.00000
1
684
1368
2053
2737
Nucleotide position in relation to AF259897.1 East African cassava mosaic Cameroon virus
f)
Breakpoints per 200 nt window
11.0000
8.25000
5.50000
2.75000
0.00000
1
665
1330
1995
2660
Nucleotide position in relation to KU683745.1 Telfairia mosaic virus
nsp
mp
nsp
mp

Supplementary Material

Supplementary Table S1. Full-length DNA-B sequences used in this study. Lines highlighted in red indicate redundant sequences (same haplotype) that were excluded from the population genomics analyses.

GenBank access #	**Virus**	**Location**	**Host**	**Subpopulation**
AB085794	*Squash leaf curl Philippines virus*	Philippines	*Cucurbita moschata*	India – China
HM585446	*Abutilon mosaic Bolivia virus*	Bolivia	*Abutilon* sp.	Latin America
FN434439	*Abutilon mosaic Brazil virus*	Brazil	*Abutilon* sp.	Latin America
JF694479	*Abutilon mosaic Brazil virus*	Brazil	*Blainvillea rhomboidea*	Latin America
JF694483	*Abutilon mosaic Brazil virus*	Brazil	*Sida rhomboidea*	Latin America
AM886130	*Abutilon mosaic virus*	South Africa	*Abutilon pannosum*	Latin America
JN236209	*Abutilon mosaic virus*	India	*Abutilon pictum*	Latin America
LN611624	*Abutilon mosaic virus*	Germany	*Abutilon megapotamicum*	Latin America
LN611625	*Abutilon mosaic virus*	France	*Abutilon megapotamicum*	Latin America
U51138	*Abutilon mosaic virus*	Hawaii	*Abutilon* sp.	Latin America
X15984	*Abutilon mosaic virus*	-	*Abutilon sellovianum*	Latin America
HE616778	*African cassava mosaic Burkina Faso virus*	Burkina Faso	*Manihot esculenta*	ACM-like viruses
AF126801	*African cassava mosaic virus*	Uganda	-	ACM-like viruses

AF126803	*African cassava mosaic virus*	Uganda	-	ACM-like viruses
AF259895	*African cassava mosaic virus*	Cote d'Ivoire	-	ACM-like viruses
HE979781	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979782	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979783	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979784	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979785	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979786	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979787	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979788	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979789	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979790	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979791	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979792	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979793	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979794	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979795	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HE979796	*African cassava mosaic virus*	Uganda	*Manihot esculenta*	ACM-like viruses
HG530117	*African cassava mosaic virus*	Kenya	*Manihot esculenta*	ACM-like viruses

HG530118	*African cassava mosaic virus*	Kenya	*Manihot esculenta*	ACM-like viruses
HG530119	*African cassava mosaic virus*	Kenya	*Manihot esculenta*	ACM-like viruses
HG530120	*African cassava mosaic virus*	Kenya	*Manihot esculenta*	ACM-like viruses
HG530121	*African cassava mosaic virus*	Kenya	*Manihot esculenta*	ACM-like viruses
HG530122	*African cassava mosaic virus*	Kenya	*Manihot esculenta*	ACM-like viruses
JN165086	*African cassava mosaic virus*	Ghana	*Manihot* sp.	ACM-like viruses
KR476373	*African cassava mosaic virus*	Benin	*Manihot* sp.	ACM-like viruses
KR476374	*African cassava mosaic virus*	Togo	*Manihot* sp.	ACM-like viruses
MG969497	*Allamanda leaf mottle distortion virus*	India	*Allamanda cathartica*	Asia
KP663484	*Asystasia mosaic Madagascar virus*	Madagascar	*Asystasia gangetica*	Asia – Africa
AF110190	*Bean calico mosaic virus*	Mexico	*Phaseolus vulgaris*	Latin America
JN848771	*Bean chlorosis virus*	Venezuela	*Phaseolus vulgaris*	Latin America
JQ283246	Bean chlorotic mosaic virus	Venezuela	*Phaseolus vulgaris*	Latin America
M88180	*Bean dwarf mosaic virus*	-	*Phaseolus vulgaris*	Latin America
JF694455	*Bean golden mosaic virus*	Brazil	*Phaseolus* sp.	Latin America
JF694456	*Bean golden mosaic virus*	Brazil	*Phaseolus* sp.	Latin America
JF694457	*Bean golden mosaic virus*	Brazil	*Phaseolus* sp.	Latin America
JF694458	*Bean golden mosaic virus*	Brazil	*Phaseolus* sp.	Latin America
JF694459	*Bean golden mosaic virus*	Brazil	*Phaseolus* sp.	Latin America

JN419008	*Bean golden mosaic virus*	Brazil	*Macroptilium lathyroides*	Latin America
JN419017	*Bean golden mosaic virus*	Brazil	*Macroptilium lathyroides*	Latin America
M88687	*Bean golden mosaic virus*	Brazil	*Phaseolus vulgaris*	Latin America
MG334553	*Bean golden mosaic virus*	Brazil	*Phaseolus vulgaris*	Latin America
MH925107	*Bean golden mosaic virus*	Brazil	*Phaseolus lunatus*	Latin America
AF173556	*Bean golden yellow mosaic virus*	Mexico	-	Latin America
D00200	*Bean golden yellow mosaic virus*	Puerto Rico	-	Latin America
DQ119825	*Bean golden yellow mosaic virus*	USA	*Phaseolus vulgaris*	Latin America
KU145406	*Bean golden yellow mosaic virus*	Cuba	*Phaseolus vulgaris*	Latin America
L01636	*Bean golden yellow mosaic virus*	Dominican Republic	*Phaseolus vulgaris*	Latin America
M10080	*Bean golden yellow mosaic virus*	Puerto Rico	-	Latin America
M91605	*Bean golden yellow mosaic virus*	Guatemala	-	Latin America
KX857726	*Bean leaf crumple virus*	Colombia	*Phaseolus vulgaris*	Latin America
HQ542082	Bhendi yellow vein Delhi virus	India	*Abelmoschus esculentus*	India – China
HQ586006	*Bhendi yellow vein mosaic virus*	India	*Abelmoschus esculentus*	India – China
HQ586007	*Bhendi yellow vein mosaic virus*	India	*Abelmoschus esculentus*	India – China
HQ586005	*Bhendi yellow vein mosiac virus*	India	*Abelmoschus esculentus*	India – China
KJ862842	Bitter gourd yellow vein virus	Bangladesh	*Momordica charantia*	India – China

KM190928	Bitter gourd yellow vein virus	-	*Lens culinaris*	India – China
EU710757	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
JF694467	*Blainvillea yellow spot virus*	Brazil	*Cleome affinis*	Latin America
JF694469	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
JF694470	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
JF694477	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
JF694478	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706523	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706524	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706525	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706526	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706527	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706528	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
KC706529	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*	Latin America
JX827488	*Blechum interveinal chlorosis virus*	Mexico	*Blechum pyramidatum*	Latin America
KY971534	Boerhavia golden mosaic virus	Dominican Republic	*Boerhavia* sp.	Latin America
KY971536	Boerhavia golden mosaic virus	Dominican Republic	*Boerhavia* sp.	Latin America

KY971538	Boerhavia golden mosaic virus	Dominican Republic	*Boerhavia* sp.	Latin America
KY971540	Boerhavia golden mosaic virus	Dominican Republic	*Boerhavia* sp.	Latin America
DQ178609	*Cabbage leaf curl Jamaica virus*	Jamaica	*Brassica oleracea*	Latin America
DQ178611	*Cabbage leaf curl Jamaica virus*	Jamaica	*Brassica oleracea*	Latin America
DQ178613	*Cabbage leaf curl Jamaica virus*	Jamaica	-	Latin America
MH248137	*Cabbage leaf curl virus*	Ecuador	*Cucumis melo*	Latin America
MH359391	*Cabbage leaf curl virus*	Ecuador	*Phaseolus vulgaris*	Latin America
MH359393	*Cabbage leaf curl virus*	Ecuador	*Rhynchosia minima*	Latin America
MH359395	*Cabbage leaf curl virus*	Ecuador	*Rhynchosia minima*	Latin America
MH359397	*Cabbage leaf curl virus*	Ecuador	*Glycine max*	Latin America
U65530	*Cabbage leaf curl virus*	-	-	Latin America
KC426928	Capraria yellow spot Yucatan virus	Mexico	*Capraria biflora*	Latin America
HE617300	*Cassava mosaic Madagascar virus*	Madagascar	*Manihot esculenta*	EACM-like viruses
KX259340	Chayote enation yellow mosaic virus	India	*Sechium edule*	India – China
KX259341	Chayote enation yellow mosaic virus	India	*Sechium edule*	India – China
KX259342	Chayote enation yellow mosaic virus	India	*Sechium edule*	India – China
KJ826528	*Chenopodium leaf curl virus*	USA	*Chenopodium ambrosioides*	Latin America
AF007823	*Chino del tomate virus*	-	-	Latin America

AF101478	*Chino del tomate virus*	-	-	Latin America
AF226666	*Chino del tomate virus*	Mexico	*Solanum lycopersicum*	Latin America
U57458	*Chino del tomate virus*	-	-	Latin America
FN436000	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*	Latin America
JF694460	*Cleome leaf crumple virus*	Brazil	*Phaseolus* sp.	Latin America
JF694462	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*	Latin America
JF694463	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*	Latin America
JF694464	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*	Latin America
JF694465	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*	Latin America
JF694466	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*	Latin America
MF072687	*Cleome leaf crumple virus*	Brazil	*Cleome* sp.	Latin America
DQ641693	*Clerodendron golden mosaic virus*	Viet Nam	*Clerodendrum thomsoniae*	Asia
HQ317135	*Clerodendron golden mosaic virus*	China	*Clerodendrum* sp.	Asia
KT001508	*Clerodendron golden mosaic virus*	India	*Duranta erecta*	Asia
FJ011669	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*	Asia
FJ011671	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*	Asia
FJ011673	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*	
FN396963	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*	Asia
JQ305798	*Clerodendrum golden mosaic China virus*	USA	*Salvia splendens*	Asia

KY427013	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*	Asia
KY427015	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*	Asia
KT966772	*Cnidoscolus mosaic leaf deformation virus*	Brazil	*Cnidoscolus urens*	Latin America
KM244718	*Coccinia mosaic Tamil Nadu virus*	India	*Coccinia grandis*	Asia
KM887129	*Coccinia mosaic Tamil Nadu virus*	India	*Coccinia grandis*	Asia
KX011474	*Common bean mottle virus*	Cuba	*Phaseolus vulgaris*	Latin America
KX096981	*Common bean severe mosaic virus*	Cuba	*Phaseolus vulgaris*	Latin America
KX096982	*Common bean severe mosaic virus*	Cuba	*Phaseolus vulgaris*	Latin America
FJ455448	*Corchorus golden mosaic virus*	India	*Corchorus capsularis*	
AB849289	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB849291	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB849293	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971843	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971845	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971847	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971849	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971851	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971853	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971855	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America

AB971857	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971859	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971861	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
AB971863	*Corchorus golden mosaic virus*	Bangladesh	*Corchorus capsularis*	Latin America
DQ641689	*Corchorus golden mosaic virus*	Viet Nam	*Corchorus olitorius*	Latin America
FJ463901	*Corchorus golden mosaic virus*	India	*Corchorus capsularis*	
GQ183864	*Corchorus golden mosaic virus*	India	*Corchorus capsularis*	Latin America
KF962543	*Corchorus golden mosaic virus*	India	*Boehmeria nivea*	Latin America
JQ805780	Corchorus mottle virus	Brazil	*Corchorus hirtus*	Latin America
DQ875869	*Corchorus yellow spot virus*	Mexico	*Corchorus siliquosus*	Latin America
KU245931	Corchorus yellow vein Vietnam virus	China	*Corchorus olitorius*	Latin America
AY727904	*Corchorus yellow vein virus*	Viet Nam	*Corchorus capsularis*	Latin America
KX101213	*Corchorus yellow vein virus*	China	*Corchorus olitorius*	Latin America
KF358471	*Cotton chlorotic spot virus*	Brazil	*Gossypium* spp.	Latin America
AF480941	*Cotton leaf crumple virus*	Mexico	*Gossypium* sp.	Latin America
AY742221	*Cotton leaf crumple virus*	USA	-	Latin America
KY420141	*Cotton leaf curl Alabad virus*	Pakistan	*Gossypium hirsutum*	Asia
KY420150	*Cotton leaf curl Alabad virus*	Pakistan	*Gossypium hirsutum*	Asia
KT454835	*Cotton yellow mosaic virus*	Cameroon	*Gossypium* sp.	Asia – Africa

KU683749	*Cotton yellow mosaic virus*	Benin	*Gossypium raimondii*	Asia – Africa
KU683750	*Cotton yellow mosaic virus*	Benin	*Gossypium raimondii*	Asia – Africa
KX156614	Croton golden mosaic virus	Colombia	*Croton hirtus*	Latin America
AF224761	*Cucurbit leaf crumple virus*	USA	-	Latin America
AF327559	*Cucurbit leaf crumple virus*	USA	*Cucurbita* sp.	Latin America
JN848776	*Dalechampia chlorotic mosaic virus*	Venezuela	*Dalechampia* sp.	Latin America
JN848774	*Datura leaf distortion virus*	Venezuela	*Datura stramonium*	Latin America
KT878825	*Deinbollia mosaic virus*	Tanzania	*Deinbollia borbonica*	
KT878827	*Deinbollia mosaic virus*	Tanzania	*Deinbollia borbonica*	Asia – Africa
KT878828	*Deinbollia mosaic virus*	Tanzania	*Deinbollia borbonica*	Asia – Africa
KT878830	*Deinbollia mosaic virus*	Kenya	*Deinbollia borbonica*	Asia – Africa
DQ875871	*Desmodium leaf distortion virus*	Mexico	*Desmodium glabrum*	Latin America
KY294726	*Desmodium mottle virus*	Uganda	*Desmodium* sp.	Asia – Africa
KY294727	*Desmodium mottle virus*	Uganda	*Desmodium* sp.	Asia – Africa
AF170101	*Dicliptera yellow mottle virus*	-	*Dicliptera sexangularis*	Latin America
KJ481205	*Dolichos yellow mosaic virus*	India	*Dolichos purpureus*	Asia – Africa
KJ481206	*Dolichos yellow mosaic virus*	India	*Dolichos purpureus*	Asia – Africa
AF259897	*East African cassava mosaic Cameroon virus*	Cote d'Ivoire	-	EACM-like viruses
JN165087	*East African cassava mosaic Cameroon virus*	Ghana	*Manihot* sp.	EACM-like viruses

AJ704965	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704966	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704967	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704968	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704969	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704970	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704971	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704972	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*	EACM-like viruses
JF909200	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909201	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909202	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909203	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909204	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909205	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909206	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909207	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909208	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909209	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909210	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses

JF909211	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909212	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909213	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909214	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909215	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909216	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909217	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909218	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909219	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909220	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909221	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909222	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909223	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909224	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909225	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909226	*East African cassava mosaic Kenya virus*	Comoros	*Manihot esculenta*	EACM-like viruses
JF909227	*East African cassava mosaic Kenya virus*	Seychelles	*Manihot esculenta*	EACM-like viruses
JF909228	*East African cassava mosaic Kenya virus*	Seychelles	*Manihot esculenta*	EACM-like viruses
JF909229	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses

JF909230	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909231	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909232	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909233	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909234	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909235	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909236	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909237	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909238	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909239	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909240	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909241	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909242	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909243	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909244	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909245	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909246	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909247	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909248	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	

JF909249	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909250	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909251	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909252	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909253	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909254	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JF909255	*East African cassava mosaic Kenya virus*	Mayotte	*Manihot esculenta*	EACM-like viruses
JX658684	*East African cassava mosaic Malawi virus*	Malawi	*Manihot* sp.	EACM-like viruses
AF126805	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
AF126807	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
AF230375	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
AJ704934	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704935	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704936	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704937	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704938	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704939	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704949	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704950	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses

AJ704951	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704952	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704953	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704954	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704955	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704956	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704957	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704958	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704959	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704960	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704961	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704962	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704963	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704964	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	
AJ704973	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704974	*East African cassava mosaic virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AM502341	*East African cassava mosaic virus*	Uganda	*Manihot* sp.	
AM502342	*East African cassava mosaic virus*	Uganda	*Manihot* sp.	EACM-like viruses
AM502343	*East African cassava mosaic virus*	Uganda	*Manihot glaziovii*	EACM-like viruses

AM502344	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
HE979776	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
HE979777	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
HE979778	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
HE979779	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
HE979780	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*	EACM-like viruses
JX679247	*East African cassava mosaic virus*	Malawi	*Manihot* sp.	EACM-like viruses
KT780439	*East African cassava mosaic virus*	Equatorial Guinea	*Manihot esculenta*	EACM-like viruses
MH379641	*East African cassava mosaic virus*	Kenya	*Markhamia zanzibarica*	EACM-like viruses
AF422175	*East African cassava mosaic Zanzibar virus*	Tanzania	*Manihot esculenta*	EACM-like viruses
AJ628732	*East African cassava mosaic Zanzibar virus*	Kenya	-	EACM-like viruses
AJ704940	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704941	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704942	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704943	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704944	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704945	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704946	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
AJ704947	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses

AJ704948	*East African cassava mosaic Zanzibar virus*	Kenya	*Manihot esculenta*	EACM-like viruses
HE806429	*East African cassava mosaic Zanzibar virus*	Oman	*Manihot esculenta*	EACM-like viruses
HE806430	*East African cassava mosaic Zanzibar virus*	Oman	*Manihot esculenta*	EACM-like viruses
DQ318938	*Euphorbia mosaic virus*	Mexico	*Euphorbia heterophylla*	Latin America
EU740969	*Euphorbia mosaic virus*	Jamaica	*Wissadula amplissima*	Latin America
FJ807783	*Euphorbia mosaic virus*	Cuba	*Nicotiana tabacum*	Latin America
HQ185235	*Euphorbia mosaic virus*	Mexico	*Capsicum* sp.	Latin America
HQ896202	*Euphorbia mosaic virus*	Cuba	*Euphorbia heterophylla*	Latin America
JQ963888	*Euphorbia mosaic virus*	USA	*Euphorbia heterophylla*	Latin America
KJ647291	*Euphorbia mosaic virus*	USA	*Passiflora* sp.	Latin America
KU165789	*Euphorbia mosaic virus*	Cuba	*Glycine max*	Latin America
FJ619508	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
FN435996	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia* sp.	EuYMV – SqLCV
FN435998	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia* sp.	EuYMV – SqLCV
JF756677	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
JF756678	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
JN419001	*Euphorbia yellow mosaic virus*	Brazil	*Macroptilium atropurpureum*	EuYMV – SqLCV
KX348224	*Euphorbia yellow mosaic virus*	Brazil	*Leonurus sibiricus*	EuYMV – SqLCV

KY559580	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559581	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559582	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559583	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	
KY559584	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559585	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559586	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559587	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559588	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559589	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559590	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559591	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559592	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559593	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559594	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559595	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559596	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559597	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	
KY559598	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV

KY559599	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559600	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559601	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	
KY559602	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559603	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559604	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559605	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559606	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559607	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559608	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	
KY559609	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559610	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559611	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559612	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559613	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559614	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559615	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559616	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559617	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV

KY559618	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559619	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559620	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559621	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559622	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559623	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559624	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559625	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559626	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559627	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559628	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559629	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559630	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559631	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559632	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559633	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559634	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559635	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	EuYMV – SqLCV
KY559636	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*	

KY905704	*Euphorbia yellow mosaic virus*	Brazil	*Manihot esculenta*	EuYMV – SqLCV
EU384576	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium darwinii*	Asia
EU384577	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium davidsonii*	Asia
EU384578	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium punctatum*	Asia
FJ218488	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium lobatum*	Asia
FJ218489	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium mustelinum*	Asia
FJ218490	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium somalense*	Asia
FJ218491	Gossypium punctatum mild leaf curl virus	Pakistan	*Gossypium stocksii*	Asia
AJ627905	*Horsegram yellow mosaic virus*	India	*Macrotyloma uniflorum*	Asia – Africa
AM932426	*Horsegram yellow mosaic virus*	India	*Phaseolus vulgaris*	Asia – Africa
AM932428	*Horsegram yellow mosaic virus*	India	*Vigna unguiculata*	Asia – Africa
AM932430	*Horsegram yellow mosaic virus*	India	*Phaseolus lunatus*	Asia – Africa
GU323322	*Horsegram yellow mosaic virus*	Sri Lanka	*Phaseolus vulgaris*	Asia – Africa
KC019307	*Horsegram yellow mosaic virus*	India	*Phaseolus vulgaris*	Asia – Africa
KP752089	*Horsegram yellow mosaic virus*	India	*Phaseolus* sp.	Asia – Africa
AJ314740	*Indian cassava mosaic virus*	India	*Nicotiana benthamiana*	Asia
AJ575820	*Indian cassava mosaic virus*	India	*Manihot esculenta*	Asia
AM158955	*Indian cassava mosaic virus*	India	*Manihot esculanta*	Asia
AY730036	*Indian cassava mosaic virus*	India	*Nicotiana tabacum*	Asia

KU308386	*Indian cassava mosaic virus*	India	*Manihot* sp.	Asia
JQ821387	*Jacquemontia mosaic Yucatan virus*	Mexico	*Jacquemontia pentantha*	Latin America
KF661332	*Jacquemontia yellow mosaic virus*	Venezuela	*Jacquemontia* sp.	Latin America
KY617095	*Jacquemontia yellow vein virus*	Venezuela	*Jacquemontia tamnifolia*	Latin America
KY617096	*Jacquemontia yellow vein virus*	Venezuela	*Jacquemontia tamnifolia*	Latin America
GQ924761	Jatropha curcas mosaic virus	India	*Jatropha curcas*	Asia
JF496656	Jatropha curcas mosaic virus	India	*Jatropha curcas*	Asia
KR349062	*Jatropha leaf curl virus*	India	*Jatropha curcas*	Asia
KF723261	*Jatropha mosaic virus*	Jamaica	*Jatropha gossypifolia*	Latin America
KF723262	*Jatropha mosaic virus*	Jamaica	*Jatropha gossypifolia*	Latin America
KF998098	*Jatropha mosaic virus*	USA	*Jatropha multifida*	Latin America
KJ174334	*Jatropha mosaic virus*	Dominican Republic	*Jatropha* sp.	Latin America
KJ174335	*Jatropha mosaic virus*	Dominican Republic	*Jatropha* sp.	Latin America
KJ174336	*Jatropha mosaic virus*	Dominican Republic	*Jatropha* sp.	Latin America
KJ174337	*Jatropha mosaic virus*	Dominican Republic	*Jatropha* sp.	Latin America
DQ641691	*Kudzu mosaic virus*	Viet Nam	*Pueraria lobata*	Asia – Africa

FJ539015	*Kudzu mosaic virus*	China	*Pueraria lobata*	Asia – Africa
HQ162272	*Kudzu mosaic virus*	Viet Nam	*Glycine max*	Asia – Africa
AF509740	*Luffa yellow mosaic virus*	Viet Nam	*Luffa acutungula*	India – China
KT582303	*Lycianthes yellow mosaic virus*	China	*Lycianthes biflora*	Asia
KX691412	*Macroptilium common mosaic virus*	Brazil	*Macroptilium lathyroides*	Latin America
EU158097	*Macroptilium golden mosaic*	Jamaica	*Wissadula amplissima*	Latin America
FJ981727	*Macroptilium golden mosaic*	Jamaica	*Wissadula amplissima*	Latin America
KY196220	Macroptilium golden yellow mosaic virus	Dominican Republic	*Macroptilium* sp.	Latin America
AF449193	*Macroptilium mosaic Puerto Rico virus*	Puerto Rico	*Phaseolus vulgaris*	Latin America
AY044134	*Macroptilium mosaic Puerto Rico virus*	Puerto Rico	-	Latin America
KT099169	*Macroptilium mosaic Puerto Rico virus*	Puerto Rico	-	Latin America
AY044136	*Macroptilium yellow mosaic Florida virus*	USA	*Macroptilium lathyroides*	Latin America
EF582841	*Macroptilium yellow mosaic virus*	Jamaica	*Macroptilium lathyroides*	Latin America
EF585289	*Macroptilium yellow mosaic virus*	Jamaica	*Macroptilium lathyroides*	Latin America
EF585291	*Macroptilium yellow mosaic virus*	Jamaica	*Macroptilium lathyroides*	Latin America
EF585292	*Macroptilium yellow mosaic virus*	Jamaica	*Macroptilium lathyroides*	Latin America
JN418999	Macroptilium yellow net virus	Brazil	*Macroptilium lathyroides*	Latin America
KT779558	*Macroptilium yellow spot virus*	Brazil	*Desmodium glabrum*	

KT779559	*Macroptilium yellow spot virus*	Brazil	*Desmodium glabrum*	Latin America
KT779560	*Macroptilium yellow spot virus*	Brazil	*Desmodium glabrum*	Latin America
KT779563	*Macroptilium yellow spot virus*	Brazil	*Desmodium glabrum*	Latin America
KU058857	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.	Latin America
KU058858	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.	Latin America
KU058859	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.	Latin America
KU058860	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.	Latin America
KU058861	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.	Latin America
FJ600484	*Malvastrum yellow mosaic Jamaica virus*	Jamaica	*Malvastrum americanum*	Latin America
FJ600485	*Malvastrum yellow mosaic Jamaica virus*	Jamaica	*Malvastrum americanum*	Latin America
KT201152	*Melochia mosaic virus*	Brazil	*Melochia* sp.	Latin America
KT201154	*Melochia yellow mosaic virus*	Brazil	*Melochia* sp.	Latin America
AF325498	*Melon chlorotic leaf curl virus*	Guatemala	*Cucumis melo*	Latin America
AF440790	*Melon chlorotic leaf curl virus*	Costa Rica	*Curcubita* sp.	Latin America
KT099160	*Melon chlorotic leaf curl virus*	Guatemala	-	Latin America
HM163577	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*	Latin America
KF670609	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670611	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670613	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis anguria*	Latin America

KF670615	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*	Latin America
KF670617	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670619	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis dipsaceus*	Latin America
KF670621	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis anguria*	Latin America
KF670623	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670625	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670627	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis sativus*	Latin America
KF670629	*Melon chlorotic mosaic virus*	Venezuela	*Cucurbita moschata*	Latin America
KF670631	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670633	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670635	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670637	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis anguria*	Latin America
KF670639	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*	Latin America
KF670641	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*	Latin America
KF670643	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670645	*Melon chlorotic mosaic virus*	Venezuela	*Cucumis melo*	Latin America
KF670647	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*	Latin America
FJ944022	*Merremia mosaic Puerto Rico virus*	Puerto Rico	*Merremia quinquefolia*	Latin America
AY508992	*Merremia mosaic virus*	Venezuela	*Solanum lycopersicum*	Latin America

AY965899	*Merremia mosaic virus*	Puerto Rico	*Solanum lycopersicum*	Latin America
DQ644559	*Merremia mosaic virus*	Puerto Rico	-	Latin America
DQ644560	*Merremia mosaic virus*	Puerto Rico	-	Latin America
AF142440	*Mungbean yellow mosaic India virus*	India	-	Asia – Africa
AF416741	*Mungbean yellow mosaic India virus*	-	-	Asia – Africa
AF503580	*Mungbean yellow mosaic India virus*	India	Vigna unguiculata	Asia – Africa
AM992617	*Mungbean yellow mosaic India virus*	Pakistan	*Vigna radiata*	Asia – Africa
AY049771	*Mungbean yellow mosaic India virus*	India	*Glycine max*	Asia – Africa
AY271894	*Mungbean yellow mosaic India virus*	India	*Vigna radiata*	Asia – Africa
AY937196	*Mungbean yellow mosaic India virus*	India	-	Asia – Africa
AY939925	*Mungbean yellow mosaic India virus*	India	Vigna unguiculata	Asia – Africa
DQ061273	*Mungbean yellow mosaic India virus*	India	*Dolichos bean*	Asia – Africa
EU523046	*Mungbean yellow mosaic India virus*	India	*Glycine max*	Asia – Africa
FM161881	*Mungbean yellow mosaic India virus*	Pakistan	*Glycine max*	Asia – Africa
FM955603	*Mungbean yellow mosaic India virus*	Pakistan	*Vigna radiata*	Asia – Africa
FM955606	*Mungbean yellow mosaic India virus*	Pakistan	*Vigna radiata*	Asia – Africa
FM955609	*Mungbean yellow mosaic India virus*	Pakistan	*Vigna radiata*	Asia – Africa
FM958506	*Mungbean yellow mosaic India virus*	Pakistan	*Vigna radiata*	Asia – Africa
FR714861	*Mungbean yellow mosaic India virus*	India	*Phaseolus vulgaris*	Asia – Africa

JN368440	*Mungbean yellow mosaic India virus*	Indonesia	*Vigna unguiculata*	Asia – Africa
JN368441	*Mungbean yellow mosaic India virus*	Indonesia	*Vigna unguiculata*	Asia – Africa
JN368442	*Mungbean yellow mosaic India virus*	Indonesia	*Vigna unguiculata*	Asia – Africa
JN368443	*Mungbean yellow mosaic India virus*	Indonesia	*Vigna unguiculata*	Asia – Africa
JN368445	*Mungbean yellow mosaic India virus*	Indonesia	*Vigna unguiculata*	Asia – Africa
JN368446	*Mungbean yellow mosaic India virus*	Indonesia	*Glycine max*	Asia – Africa
JN368447	*Mungbean yellow mosaic India virus*	Indonesia	*Glycine max*	Asia – Africa
JN543396	*Mungbean yellow mosaic India virus*	Nepal	*Phaseolus* sp.	Asia – Africa
JQ327848	*Mungbean yellow mosaic India virus*	Nepal	*Phaseolus lunatus*	Asia – Africa
JQ327849	*Mungbean yellow mosaic India virus*	Nepal	*Phaseolus lunatus*	Asia – Africa
KC019305	*Mungbean yellow mosaic India virus*	India	*Phaseolus vulgaris*	Asia – Africa
KP779631	*Mungbean yellow mosaic India virus*	India	*Phaseolus* sp.	Asia – Africa
KP779632	*Mungbean yellow mosaic India virus*	India	*Phaseolus* sp.	Asia – Africa
KP779634	*Mungbean yellow mosaic India virus*	India	*Phaseolus* sp.	Asia – Africa
KP779636	*Mungbean yellow mosaic India virus*	India	*Phaseolus* sp.	Asia – Africa
KP828155	*Mungbean yellow mosaic India virus*	India	*Glycine max*	Asia – Africa
KU950431	*Mungbean yellow mosaic India virus*	India	*Vigna radiata*	Asia – Africa
KX363948	*Mungbean yellow mosaic India virus*	India	*Cajanus cajan*	Asia – Africa
KX452229	*Mungbean yellow mosaic India virus*	Oman	*Phaseolus vulgaris*	Asia – Africa

KX452230	*Mungbean yellow mosaic India virus*	Oman	*Phaseolus vulgaris*	Asia – Africa
KX452231	*Mungbean yellow mosaic India virus*	Oman	*Phaseolus vulgaris*	Asia – Africa
KY556680	*Mungbean yellow mosaic India virus*	India	Vigna unguiculata	Asia – Africa
LC271791	*Mungbean yellow mosaic India virus*	India	*Vegna mungo*	Asia – Africa
LC271793	*Mungbean yellow mosaic India virus*	India	*Glycine max*	Asia – Africa
LC271795	*Mungbean yellow mosaic India virus*	India	*Glycine max*	Asia – Africa
MF683073	*Mungbean yellow mosaic India virus*	India	*Solanum lycopersicum*	Asia – Africa
MF693402	*Mungbean yellow mosaic India virus*	India	*Cajanus cajan*	Asia – Africa
AF262064	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
AJ132574	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
AJ439057	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
AJ439058	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
AJ439059	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
DQ400849	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
FM242702	*Mungbean yellow mosaic virus*	Pakistan	*Rhynchosia capitata*	Asia – Africa
FM955607	*Mungbean yellow mosaic virus*	Pakistan	*Rhynchosia capitata*	Asia – Africa
JX244177	*Mungbean yellow mosaic virus*	Viet Nam	*Vigna radiata*	Asia – Africa
JX244178	*Mungbean yellow mosaic virus*	Viet Nam	*Vigna radiata*	Asia – Africa
JX244179	*Mungbean yellow mosaic virus*	Viet Nam	*Vigna radiata*	Asia – Africa

JX244180	*Mungbean yellow mosaic virus*	Viet Nam	*Vigna radiata*	Asia – Africa
JX244181	*Mungbean yellow mosaic virus*	Viet Nam	*Vigna radiata*	Asia – Africa
KC911724	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911725	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911726	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911727	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911728	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911729	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911730	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KC911731	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KF928962	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KF947526	*Mungbean yellow mosaic virus*	India	*Vigna mungo*	Asia – Africa
KP319016	*Mungbean yellow mosaic virus*	India	*Vigna radiata*	Asia – Africa
KP319017	*Mungbean yellow mosaic virus*	India	*Vigna radiata*	Asia – Africa
EU914818	*Okra mottle virus*	Brazil	*Abelmoschus esculentus*	Latin America
FJ686696	*Okra mottle virus*	Brazil	*Glycine max*	Latin America
GU972604	*Okra yellow mosaic Mexico virus*	Mexico	*Abelmoschus esculentus*	Latin America
HM035060	*Okra yellow mosaic Mexico virus*	USA	*Abelmoschus esculentus*	Latin America
JX219471	*Okra yellow mosaic Mexico virus*	Mexico	*Sida rhombifolia*	Latin America

JX219472	*Okra yellow mosaic Mexico virus*	Mexico	*Sida rhombifolia*	Latin America
JX219473	*Okra yellow mosaic Mexico virus*	Mexico	*Herissantia crispa*	Latin America
KT899303	*Passionfruit leaf distortion virus*	Colombia	*Passiflora eduli*	Latin America
FJ972768	*Passionfruit severe leaf distortion virus*	Brazil	*Passiflora edulis*	Latin America
KT948786	*Pavonia mosaic virus*	Brazil	*Pavonia* sp.	Latin America
KT948788	*Pavonia yellow mosaic virus*	Brazil	*Pavonia* sp.	Latin America
AF499442	*Pepper golden mosaic virus*	-	-	Latin America
AY928513	*Pepper golden mosaic virus*	USA	*Capsicum frutescens*	Latin America
AY928515	*Pepper golden mosaic virus*	USA	*Capsicum frutescens*	Latin America
AY928517	*Pepper golden mosaic virus*	USA	*Capsicum frutescens*	Latin America
EF210557	*Pepper golden mosaic virus*	-	-	Latin America
GU128147	*Pepper golden mosaic virus*	Mexico	*Solanum lycopersicum*	Latin America
GU564595	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
KY064019	*Pepper golden mosaic virus*	Costa Rica	*Capsicum annuum*	Latin America
KY064022	*Pepper golden mosaic virus*	Costa Rica	*Capsicum annuum*	Latin America
KY064023	*Pepper golden mosaic virus*	Costa Rica	*Capsicum annuum*	Latin America
KY064024	*Pepper golden mosaic virus*	Costa Rica	*Capsicum annuum*	Latin America
LN848798	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848799	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America

LN848800	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848801	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848802	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848803	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848804	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848805	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848806	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848807	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848808	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848809	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848810	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848811	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848812	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848813	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848814	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848815	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848816	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848817	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848818	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America

LN848819	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848820	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848821	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848822	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	
LN848823	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848824	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848825	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848826	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	
LN848827	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848828	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848829	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848830	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848831	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848832	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848833	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848834	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848835	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848836	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848837	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America

LN848838	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848839	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848840	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848841	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848842	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848843	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
LN848844	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
MF109821	*Pepper golden mosaic virus*	Mexico	*Capsicum annuum*	Latin America
AY044163	*Pepper huasteco yellow vein virus*	Sinaloa	-	Latin America
GU128146	*Pepper huasteco yellow vein virus*	Mexico	*Solanum lycopersicum*	Latin America
GU128151	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum* sp.	Latin America
GU564593	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
GU564596	*Pepper huasteco yellow vein virus*	Mexico	*Solanum rostratum*	Latin America
KP890828	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
KX440614	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
KX440615	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848887	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848888	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848889	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America

LN848890	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848891	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848892	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848893	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848894	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848895	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848896	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848897	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848898	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848899	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848900	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848901	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848902	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848903	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848904	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848905	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848906	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848907	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848908	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America

LN848909	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848910	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848911	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848912	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848913	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848914	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848915	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848916	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848917	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848918	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848919	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848920	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848921	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848922	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848923	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848924	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848925	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848926	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
LN848927	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America

LN848928	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
MG582069	*Pepper huasteco yellow vein virus*	Mexico	*Capsicum annuum*	Latin America
X70419	*Pepper huasteco yellow vein virus*	-	-	Latin America
KC769820	*Pepper leafroll virus*	Peru	*Capsicum baccatum*	Latin America
MH481902	*Pepper leafroll virus*	Ecuador	*Phaseolus vulgaris*	Latin America
AB267837	*Pepper yellow leaf curl Indonesia virus*	Indonesia	-	Asia
AB267839	*Pepper yellow leaf curl Indonesia virus*	Indonesia	*Abutilon* sp.	Asia
AB267835	*Pepper yellow leaf curl Indonesia virus*	Indonesia	-	Asia
LC314792	*Pepper yellow leaf curl Indonesia virus*	Indonesia	*Capsicum annuum*	Asia
LC314793	*Pepper yellow leaf curl Indonesia virus*	Indonesia	*Capsicum annuum*	Asia
LC314794	*Pepper yellow leaf curl Indonesia virus*	Indonesia	*Capsicum annuum*	Asia
LC314795	*Pepper yellow leaf curl Indonesia virus*	Indonesia	*Capsicum annuum*	Asia
KX885224	*Pepper yellow leaf curl Thailand virus*	Thailand	*Capsicum annuum*	Asia
KX885225	*Pepper yellow leaf curl Thailand virus*	Thailand	*Capsicum annuum*	Asia
KX943291	*Pepper yellow leaf curl Thailand virus*	Thailand	-	Asia
HE806447	Peristrophe mosaic virus	Cuba	*Peristrophe* sp.	Latin America
Y15033	*Potato yellow mosaic Panama virus*	Panama	*Solanum lycopersicum*	Latin America
AF039032	*Potato yellow mosaic virus*	Trinidad and Tobago	*Solanum lycopersicum*	Latin America

AY120883	*Potato yellow mosaic virus*	Guadeloupe	-	Latin America
AY965898	*Potato yellow mosaic virus*	Puerto Rico	*Solanum lycopersicum*	Latin America
D00941	*Potato yellow mosaic virus*	Venezuela	*Solanum tuberosum*	Latin America
FR851301	*Potato yellow mosaic virus*	Grenada	*Solanum lycopersicum*	Latin America
FR851302	*Potato yellow mosaic virus*	Grenada	*Solanum lycopersicum*	Latin America
JQ045706	*Potato yellow mosaic virus*	Colombia	*Solanum lycopersicum*	Latin America
KU665805	*Potato yellow mosaic virus*	Venezuela	*Solanum americanum*	Latin America
EU596960	Ramie mosaic virus	China	*Boehmeria nivea*	Asia
FN396970	Ramie mosaic virus	China	*Boehmeria nivea*	Asia
FN396972	Ramie mosaic virus	China	*Boehmeria nivea*	Asia
KC171651	Ramie mosaic virus	China	*Boehmeria nivea*	Asia
KC171653	Ramie mosaic virus	China	*Boehmeria nivea*	Asia
HM236369	*Rhynchosia golden mosaic Havana virus*	Cuba	*Rhynchosia minima*	Latin America
DQ406673	*Rhynchosia golden mosaic Sinaloa virus*	Mexico	*Rhynchosia minima*	Latin America
DQ356429	*Rhynchosia golden mosaic virus*	Mexico	*Glycine max*	Latin America
EU339937	*Rhynchosia golden mosaic virus*	Mexico	*Glycine max*	Latin America
FJ792608	Rhynchosia golden mosaic Yucatan virus	Mexico	*Rhynchosia minima*	Latin America
KP641348	Rhynchosia golden mosaic Yucatan virus	Jamaica	*Rhynchosia* sp.	Latin America
KP641350	Rhynchosia golden mosaic Yucatan virus	Jamaica	*Rhynchosia* sp.	Latin America

KT381194	Rhynchosia golden mosaic Yucatan virus	Cuba	*Glycine max*	Latin America
FJ944020	*Rhynchosia mild mosaic virus*	Puerto Rico	*Rhynchosia minima*	Latin America
HM236371	*Rhynchosia rugose golden mosaic virus*	Cuba	*Rhynchosia minima*	Latin America
HM777510	*Rhynchosia yellow mosaic India virus*	India	*Rhynchosia* sp.	Asia – Africa
HM777511	*Rhynchosia yellow mosaic India virus*	India	*Rhynchosia* sp.	Asia – Africa
HM777512	*Rhynchosia yellow mosaic India virus*	India	*Rhynchosia* sp.	Asia – Africa
HQ141675	*Rhynchosia yellow mosaic India virus*	India	*Rhynchosia* sp.	Asia – Africa
AM999982	*Rhynchosia yellow mosaic virus*	Pakistan	*Rhynchosia minima*	Asia – Africa
FM208848	*Rhynchosia yellow mosaic virus*	Pakistan	*Rhynchosia minima*	Asia – Africa
KP752091	*Rhynchosia yellow mosaic virus*	India	*Phaseolus* sp.	Asia – Africa
KX691415	*Sida angular mosaic virus*	Brazil	*Sida acuta*	Latin America
FN436002	Sida Brazil virus	Brazil	*Sida* sp.	Latin America
KY555799	Sida Brazil virus	Argentina	*Phaseolus vulgaris*	Latin America
KX348225	*Sida bright yellow mosaic virus*	Brazil	*Sida* sp.	Latin America
KX691413	*Sida chlorotic vein virus*	Brazil	*Sida urens*	Latin America
KX691414	*Sida chlorotic vein virus*	Brazil	*Sida urens*	Latin America
JX857692	*Sida ciliaris golden mosaic virus*	Venezuela	*Sida ciliaris*	Latin America
HQ009518	*Sida golden mosaic Buckup virus*	Jamaica	*Sida* sp.	Latin America
JX162592	*Sida golden mosaic Buckup virus*	Jamaica	*Sida* sp.	Latin America

X99551	*Sida golden mosaic Costa Rica virus*	Costa Rica	*Sida rhombifolia*	Latin America
HE806443	*Sida golden mosaic Florida virus*	Cuba	*Sida* sp.	Latin America
HM003778	*Sida golden mosaic Florida virus*	Cuba	*Malvastrum coromandelianum*	Latin America
HM359016	*Sida golden mosaic Florida virus*	Cuba	*Malvastrum coromandelianum*	Latin America
KT099161	Sida golden mosaic Honduras virus	Guatemala	-	Latin America
Y11098	Sida golden mosaic Honduras virus	Honduras	*Sida* sp.	Latin America
HE806445	Sida golden mosaic Liguanea virus	Cuba	*Sida* sp.	Latin America
AF039841	*Sida golden mosaic virus*	USA	*Sida santaremnensis*	Latin America
AJ250731	*Sida golden mosaic virus*	Honduras	-	Latin America
EF537046	*Sida golden mosaic virus*	USA	*Sida acuta*	Latin America
HM626517	*Sida golden mosaic virus*	USA	-	Latin America
GU997692	*Sida golden mottle virus*	USA	*Sida santaremensis*	Latin America
HQ009520	*Sida golden yellow vein*	Jamaica	*Sida* sp.	Latin America
JX162593	*Sida golden yellow vein*	Jamaica	*Sida* sp.	Latin America
JF907582	*Sida golden yellow vein virus*	Cuba	*Malvastrum coromandelianum*	Latin America
JN411690	*Sida golden yellow vein virus*	Cuba	*Malvastrum coromandelianum*	Latin America

KT879815	*Sida golden yellow vein virus*	USA	*Sida acuta*	Latin America
KT879818	*Sida golden yellow vein virus*	USA	*Sida acuta*	Latin America
KT879821	*Sida golden yellow vein virus*	USA	*Sida acuta*	Latin America
KT879824	*Sida golden yellow vein virus*	USA	*Sida acuta*	Latin America
KT879827	*Sida golden yellow vein virus*	USA	*Sida acuta*	Latin America
KT879829	*Sida golden yellow vein virus*	USA	*Sida acuta*	Latin America
AJ557452	*Sida micrantha mosaic virus*	Brazil	-	Latin America
AJ557453	*Sida micrantha mosaic virus*	Brazil	-	Latin America
AJ557454	*Sida micrantha mosaic virus*	Brazil	-	Latin America
EU908734	*Sida micrantha mosaic virus*	Brazil	*Abelmoschus esculentus*	Latin America
FJ686694	*Sida micrantha mosaic virus*	Brazil	*Glycine max*	Latin America
FN436004	*Sida micrantha mosaic virus*	Brazil	*Sida rhombifolia*	Latin America
FN436006	*Sida micrantha mosaic virus*	Brazil	*Sida micrantha*	Latin America
FN557523	*Sida micrantha mosaic virus*	Brazil	*Sida micrantha*	Latin America
HM585432	*Sida micrantha mosaic virus*	Bolivia	*Sida rhombifolia*	Latin America
HM585434	*Sida micrantha mosaic virus*	Bolivia	*Sidastrum micranthum*	Latin America
HM585438	*Sida micrantha mosaic virus*	Bolivia	*Sida rhombifolia*	Latin America
HM585440	*Sida micrantha mosaic virus*	Bolivia	*Sida rhombifolia*	Latin America
KC706532	*Sida micrantha mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America

KC706533	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KC706534	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KU852504	*Sida micrantha mosaic virus*	Brazil	*Glycine max*	Latin America
KX348186	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348187	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348188	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348189	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348190	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348191	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348192	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348193	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348194	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348195	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348196	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348197	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348198	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348199	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348200	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348201	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America

KX348202	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348203	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX348204	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KX691416	*Sida micrantha mosaic virus*	Brazil	*Sida* sp.	Latin America
KY650716	*Sida micrantha mosaic virus*	Brazil	*Oxalis* sp.	Latin America
KY650718	*Sida micrantha mosaic virus*	Brazil	*Oxalis* sp.	Latin America
KY650719	*Sida micrantha mosaic virus*	Brazil	*Oxalis* sp.	Latin America
KY650720	*Sida micrantha mosaic virus*	Brazil	*Oxalis* sp.	Latin America
KY650721	*Sida micrantha mosaic virus*	Brazil	*Oxalis* sp.	Latin America
KY650723	*Sida micrantha mosaic virus*	Brazil	*Oxalis* sp.	Latin America
JF694473	*Sida mosaic Alagoas virus*	Brazil	*Sida* sp.	Latin America
JF694474	*Sida mosaic Alagoas virus*	Brazil	*Sida* sp.	Latin America
JF694475	*Sida mosaic Alagoas virus*	Brazil	*Sida* sp.	Latin America
HM585442	*Sida mosaic Bolivia virus*	Bolivia	*Sida micrantha*	Latin America
HM585444	*Sida mosaic Bolivia virus*	Bolivia	*Sida micrantha*	Latin America
KJ742422	*Sida mosaic Bolivia virus*	Argentina	*Salvia hispanica*	Latin America
DQ356428	*Sida mosaic Sinaloa virus*	Mexico	-	Latin America
KX640992	*Sida yellow blotch virus*	Brazil	*Phaseolus lunatus*	Latin America
MF163259	Sida yellow golden mosaic virus	Brazil	*Sida* sp.	Latin America

DQ875873	*Sida yellow mosaic Yucatan virus*	Mexico	*Sida acuta*	Latin America
HQ822124	*Sida yellow mottle virus*	Cuba	*Sida rhombifolia*	Latin America
JN411688	*Sida yellow mottle virus*	Cuba	*Sida rhombifolia*	Latin America
HE806449	*Sida yellow vein virus*	Cuba	*Sida* sp.	Latin America
Y11100	*Sida yellow vein virus*	Honduras	*Sida* sp.	Latin America
Y11101	*Sida yellow vein virus*	Honduras	*Sida* sp.	Latin America
HM585436	*Solanum mosaic Bolivia virus*	Bolivia	*Solanum* sp.	Latin America
GQ472986	*Soybean chlorotic blotch virus*	Nigeria	*Glycine max*	Asia – Africa
GQ472988	*Soybean chlorotic blotch virus*	Nigeria	*Centrosema pubescens*	Asia – Africa
KT444612	*Soybean chlorotic blotch virus*	Nigeria	*Sida acuta*	Asia – Africa
KT444614	*Soybean chlorotic blotch virus*	Cameroon	*Manihot* sp.	Asia – Africa
KT444616	*Soybean chlorotic blotch virus*	Cameroon	*Abelmoschus esculentus*	Asia – Africa
KT444618	*Soybean chlorotic blotch virus*	Cameroon	*Centrosema pubescens*	Asia – Africa
KT454810	*Soybean chlorotic blotch virus*	Nigeria	*Centrosema pubescens*	Asia – Africa
KT454812	*Soybean chlorotic blotch virus*	Togo	*Sida cordifolia*	Asia – Africa
KT454814	*Soybean chlorotic blotch virus*	Togo	*Manihot* sp.	Asia – Africa
KT454816	*Soybean chlorotic blotch virus*	Togo	*Solanum lycopersicum*	Asia – Africa
KT454818	*Soybean chlorotic blotch virus*	Benin	*Asystasia* sp.	Asia – Africa
JX122966	Soybean chlorotic spot virus	Brazil	*Glycine max*	Latin America

AJ582267	Soybean yellow mosaic virus	India	*Glycine max*	Asia – Africa
GU967382	*Squash leaf curl China virus*	India	*Cucurbita pepo*	India – China
AF509742	*Squash leaf curl China virus*	Viet Nam	-	India – China
AM260207	*Squash leaf curl China virus*	-	-	India – China
AM260208	*Squash leaf curl China virus*	China	*Curcubita* sp.	India – China
AM709505	*Squash leaf curl China virus*	Pakistan	*Momordica charantia*	India – China
AM778959	*Squash leaf curl China virus*	Pakistan	*Cucurbita pepo*	India – China
AY184488	*Squash leaf curl China virus*	India	*Cucurbita pepo*	India – China
FJ859881	*Squash leaf curl China virus*	India	*Cucurbita pepo*	India – China
HM566113	*Squash leaf curl China virus*	China	*Cucumis melo*	India – China
JN624306	*Squash leaf curl China virus*	India	*Cucurbita pepo*	India – China
KC171649	*Squash leaf curl China virus*	China	*Cucurbita moschata*	India – China
KC857510	*Squash leaf curl China virus*	Viet Nam	*Cucurbita moschata*	India – China
KF999984	*Squash leaf curl China virus*	China	*Curcubita* sp.	India – China
KJ004521	*Squash leaf curl China virus*	India	*Benincasa hispida*	India – China
MF377397	*Squash leaf curl China virus*	India	*Jasminum* sp.	India – China
MG525552	*Squash leaf curl China virus*	China	*Cucurbita moschata*	India – China
JF746196	*Squash leaf curl Philippines virus*	Taiwan	*Sechium edule*	India – China
DQ285017	*Squash leaf curl virus*	USA	-	EuYMV – SqLCV

DQ285018	*Squash leaf curl virus*	USA	-	EuYMV – SqLCV
EF532621	*Squash leaf curl virus*	Jordan	*Malva parviflora*	
EU479711	*Squash leaf curl virus*	Taiwan	-	India – China
HG941652	*Squash leaf curl virus*	Oman	*Curcubita* sp.	EuYMV – SqLCV
HG941653	*Squash leaf curl virus*	Oman	*Curcubita* sp.	EuYMV – SqLCV
HG941654	*Squash leaf curl virus*	Oman	*Curcubita* sp.	EuYMV – SqLCV
HG941656	*Squash leaf curl virus*	Oman	*Curcubita* sp.	EuYMV – SqLCV
HM368374	*Squash leaf curl virus*	Lebanon	*Cucurbita pepo*	EuYMV – SqLCV
HQ184437	*Squash leaf curl virus*	Israel	*Curcubita* sp.	EuYMV – SqLCV
JX131282	*Squash leaf curl virus*	Jordan	-	EuYMV – SqLCV
JX444574	*Squash leaf curl virus*	Jordan	*Solanum lycopersicum*	EuYMV – SqLCV
KC441466	*Squash leaf curl virus*	Palestine	*Curcubita* sp.	EuYMV – SqLCV
KF030954	*Squash leaf curl virus*	Egypt	*Curcubita* sp.	EuYMV – SqLCV
KJ579954	*Squash leaf curl virus*	Egypt	*Phaseolus vulgaris*	EuYMV – SqLCV
KT099159	*Squash leaf curl virus*	USA	-	EuYMV – SqLCV
KT099165	*Squash leaf curl virus*	Israel	-	EuYMV – SqLCV
M38182	*Squash leaf curl virus*	-	*Curcubita pepo*	EuYMV – SqLCV
MF504012	*Squash leaf curl virus*	Pakistan	*Gossypium hirsutum*	EuYMV – SqLCV
MF504013	*Squash leaf curl virus*	Pakistan	*Gossypium hirsutum*	EuYMV – SqLCV

MG763921	*Squash leaf curl virus*	Egypt	*Solanum lycopersicum*	EuYMV – SqLCV
MH346455	*Squash leaf curl virus*	Egypt	*Capsicum* sp.	EuYMV – SqLCV
AF421553	*Squash mild leaf curl virus*	USA	-	Latin America
DQ285015	*Squash mild leaf curl virus*	USA	-	Latin America
KC153491	Squash yellow mild mottle virus	Costa Rica	*Cucurbita* sp.	Latin America
AJ314738	*Sri Lankan cassava mosaic virus*	Sri Lanka	*Nicotiana benthamiana*	Asia
KF898350	*Sri Lankan cassava mosaic virus*	India	*Manihot* sp.	Asia
KP455485	*Sri Lankan cassava mosaic virus*	India	*Manihot* sp.	Asia
KP455487	*Sri Lankan cassava mosaic virus*	India	*Manihot* sp.	Asia
KR611578	*Sri Lankan cassava mosaic virus*	India	*Manihot* sp.	Asia
KR611580	*Sri Lankan cassava mosaic virus*	India	*Manihot* sp.	Asia
KT861469	*Sri Lankan cassava mosaic virus*	Cambodia	*Manihot* sp.	Asia
KU550962	*Sri Lankan cassava mosaic virus*	India	*Manihot esculenta*	Asia
KT454833	Telfairia mosaic virus	Cameroon	*Telfairia occidentalis*	Asia – Africa
KU683745	Telfairia mosaic virus	Cameroon	*Telfairia occidentalis*	Asia – Africa
KU683746	Telfairia mosaic virus	Cameroon	*Telfairia occidentalis*	Asia – Africa
KX011472	*Tobacco leaf curl Cuba virus*	Cuba	*Phaseolus vulgaris*	Latin America
HQ896204	*Tobacco yellow crinkle virus*	Cuba	*Nicotiana tabacum*	Latin America
KP641346	*Tobacco yellow crinkle virus*	Jamaica	*Rhynchosia* sp.	Latin America

KY449278	Tomato chlorotic leaf curl virus	Venezuela	*Solanum lycopersicum*	Latin America
HQ201953	*Tomato chlorotic leaf distortion virus*	Venezuela	*Solanum lycopersicum*	Latin America
JN241633	*Tomato chlorotic leaf distortion virus*	Venezuela	*Capsicum* sp.	Latin America
KR263172	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	Latin America
KR263173	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	Latin America
KR263174	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	Latin America
KR263175	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	Latin America
KR263176	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	Latin America
KR263177	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	
KR263178	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*	
AF491306	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	Latin America
DQ336354	*Tomato chlorotic mottle virus*	Brazil	*Sida* sp.	Latin America
KC706562	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	
KC706563	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706564	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706565	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706566	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706567	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*	Latin America
EU710755	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America

KC706590	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706591	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706592	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706593	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706594	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706595	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706596	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706597	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706598	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706599	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	
KC706600	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706601	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706602	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706603	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706604	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	
KT203559	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
JN419010	Tomato crinkle leaf yellows virus	Brazil	*Macroptilium atropurpureum*	Latin America
JN419011	Tomato crinkle leaf yellows virus	Brazil	*Macroptilium atropurpureum*	Latin America

AY090556	Tomato crinkle yellow leaf virus	Brazil	*Solanum lycopersicum*	Latin America
JN564750	*Tomato dwarf leaf virus*	Argentina	*Solanum lycopersicum*	Latin America
JF694489	*Tomato golden mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
JF694491	*Tomato golden mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
K02030	*Tomato golden mosaic virus*	-	-	Latin America
M73794	*Tomato golden mosaic virus*	-	-	Latin America
DQ406674	*Tomato golden mottle virus*	Mexico	*Solanum lycopersicum*	Latin America
JF803265	*Tomato golden vein virus*	Brazil	*Solanum lycopersicum*	Latin America
KP235538	*Tomato leaf curl Gujarat virus*	India	*Capsicum* sp.	India – China
KU196751	*Tomato leaf curl Gujarat virus*	India	*Capsicum* sp.	India – China
AJ875158	*Tomato leaf curl New Delhi virus*	Bangladesh	*Solanum lycopersicum*	India – China
KF515623	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
AM286435	*Tomato leaf curl New Delhi virus*	India	*Cucurbita pepo*	India – China
AM778833	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum esculentum*	India – China
AM849547	*Tomato leaf curl New Delhi virus*	Pakistan	*Momordica charantia*	India – China
AY150304	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
AY150305	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
AY158080	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
AY438563	*Tomato leaf curl New Delhi virus*	India	-	India – China

AY939924	*Tomato leaf curl New Delhi virus*	India	*Luffa cylindrica*	India – China
DQ020490	*Tomato leaf curl New Delhi virus*	India	*Momordica charantia*	India – China
DQ169057	*Tomato leaf curl New Delhi virus*	India	-	India – China
EF043232	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
EF043233	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
EF408038	*Tomato leaf curl New Delhi virus*	-	*Solanum lycopersicum*	India – China
EF620535	*Tomato leaf curl New Delhi virus*	Pakistan	*Luffa acutangula*	India – China
FN356024	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
FN432357	*Tomato leaf curl New Delhi virus*	Pakistan	*Sonchus arvensis*	India – China
FN435311	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
FN435312	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
GU112083	*Tomato leaf curl New Delhi virus*	India	*Abelmoschus esculentus*	India – China
GU112085	*Tomato leaf curl New Delhi virus*	India	*Abelmoschus esculentus*	India – China
GU112087	*Tomato leaf curl New Delhi virus*	India	*Abelmoschus esculentus*	India – China
GU112089	*Tomato leaf curl New Delhi virus*	India	*Abelmoschus esculentus*	India – China
HG316126	*Tomato leaf curl New Delhi virus*	Pakistan	*Rumex dentatus*	India – China
HG932560	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
HG983285	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	India – China
HM159455	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China

HM803117	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
HM989846	*Tomato leaf curl New Delhi virus*	India	*Luffa acutangula*	India – China
HQ141674	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
HQ264186	*Tomato leaf curl New Delhi virus*	India	*Solanum melongena*	India – China
JN208137	*Tomato leaf curl New Delhi virus*	India	*Benincasa hispida*	India – China
JN663848	*Tomato leaf curl New Delhi virus*	India	*Capsicum* sp.	India – China
JN663867	*Tomato leaf curl New Delhi virus*	India	*Capsicum* sp.	India – China
JN663871	*Tomato leaf curl New Delhi virus*	India	*Capsicum* sp.	India – China
KC545813	*Tomato leaf curl New Delhi virus*	India	*Cucumis sativus*	India – China
KC874494	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874495	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874496	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874497	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874498	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874499	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874500	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KC874501	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KF571462	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
KF577601	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	

KF577602	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
KF577603	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
KF577604	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
KF577605	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
KF749226	*Tomato leaf curl New Delhi virus*	Spain	*Cucurbita pepo*	India – China
KF749227	*Tomato leaf curl New Delhi virus*	Spain	*Cucurbita pepo*	India – China
KF749228	*Tomato leaf curl New Delhi virus*	Spain	*Cucurbita pepo*	India – China
KF891467	*Tomato leaf curl New Delhi virus*	Spain	*Cucurbita pepo*	India – China
KJ778693	*Tomato leaf curl New Delhi virus*	Iran	*Solanum melongena*	India – China
KJ778695	*Tomato leaf curl New Delhi virus*	Iran	*Capsicum* sp.	India – China
KM921670	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*	India – China
KM977734	*Tomato leaf curl New Delhi virus*	Spain	*Solanum lycopersicum*	India – China
KP235543	*Tomato leaf curl New Delhi virus*	India	*Capsicum* sp.	India – China
KP641674	*Tomato leaf curl New Delhi virus*	Iran	*Cucumis melo*	India – China
KP641676	*Tomato leaf curl New Delhi virus*	Iran	*Cucumis sativus*	India – China
KP641678	*Tomato leaf curl New Delhi virus*	Iran	*Solanum lycopersicum*	India – China
KP709056	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KT175407	*Tomato leaf curl New Delhi virus*	Spain	*Solanum lycopersicum*	India – China
KT948071	*Tomato leaf curl New Delhi virus*	Pakistan	*Duranta repens*	India – China

KT948073	*Tomato leaf curl New Delhi virus*	Pakistan	*Cucurbita pepo*	India – China
KX827600	*Tomato leaf curl New Delhi virus*	Pakistan	*Glycine max*	India – China
KX951456	*Tomato leaf curl New Delhi virus*	India	*Solanum tuberosum*	India – China
KY420144	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	India – China
KY780200	*Tomato leaf curl New Delhi virus*	India	*Trichosanthes cucumerina*	India – China
KY780203	*Tomato leaf curl New Delhi virus*	India	*Coccinia grandis*	India – China
KY780204	*Tomato leaf curl New Delhi virus*	India	*Coccinia grandis*	India – China
KY780206	*Tomato leaf curl New Delhi virus*	India	*Cucumis sativus*	India – China
KY780208	*Tomato leaf curl New Delhi virus*	India	*Momordica charantia*	India – China
KY780211	*Tomato leaf curl New Delhi virus*	India	*Daucus carota*	India – China
KY780212	*Tomato leaf curl New Delhi virus*	India	*Daucus carota*	India – China
KY780214	*Tomato leaf curl New Delhi virus*	India	*Momordica dioica*	India – China
KY933710	*Tomato leaf curl New Delhi virus*	Pakistan	*Luffa cylindrica*	India – China
KY933711	*Tomato leaf curl New Delhi virus*	Pakistan	*Luffa cylindrica*	India – China
KY933712	*Tomato leaf curl New Delhi virus*	Pakistan	*Luffa cylindrica*	India – China
LN845934	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	India – China
LN845935	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845936	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845937	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China

LN845938	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845939	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845940	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845941	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845942	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845943	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845945	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845946	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845947	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845948	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845949	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845950	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845951	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845952	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845953	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845954	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845955	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	India – China
LN845956	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	India – China
LN845959	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China

LN845960	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845961	*Tomato leaf curl New Delhi virus*	Pakistan	*Abelmoschus esculentus*	India – China
LN845963	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	India – China
LN849711	*Tomato leaf curl New Delhi virus*	Pakistan	*Lens culinaris*	India – China
LN854628	*Tomato leaf curl New Delhi virus*	Pakistan	*Gossypium hirsutum*	
LN878124	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LN878126	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LN886526	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168849	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168850	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	
LT168851	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168852	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168853	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168854	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168855	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168856	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168857	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168858	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168859	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China

LT168860	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168861	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168862	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168863	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168864	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168865	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168866	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168867	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	
LT168868	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168869	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	
LT168870	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168871	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168872	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168873	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168874	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168875	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168876	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168877	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168878	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China

LT168879	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168880	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168881	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168882	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168883	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	Latin America
LT168884	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168885	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168886	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
LT168887	*Tomato leaf curl New Delhi virus*	Pakistan	*Solanum lycopersicum*	India – China
MF688671	*Tomato leaf curl New Delhi virus*	Italy	*Cucurbita moschata*	India – China
MG098231	*Tomato leaf curl New Delhi virus*	Morocco	*Cucurbita pepo*	India – China
MG406983	*Tomato leaf curl New Delhi virus*	Bangladesh	*Solanum lycopersicum*	India – China
MG597207	*Tomato leaf curl New Delhi virus*	India	*Capsicum annuum*	India – China
MG597208	*Tomato leaf curl New Delhi virus*	India	*Capsicum annuum*	India – China
MG597210	*Tomato leaf curl New Delhi virus*	India	*Capsicum annuum*	India – China
MG597211	*Tomato leaf curl New Delhi virus*	India	*Capsicum annuum*	India – China
MG686554	*Tomato leaf curl New Delhi virus*	India	*Calyptocarpus vialis*	India – China
MH465600	*Tomato leaf curl New Delhi virus*	India	*Solanum nigrum*	India – China
MH511990	*Tomato leaf curl New Delhi virus*	Seychelles	*Solanum lycopersicum*	India – China

FJ668379	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
EU547681	*Tomato leaf curl Palampur virus*	Iran	*Cucumis melo*	India – China
FJ660423	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	
FJ660424	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660425	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660426	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660427	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660428	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660429	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660430	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660435	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FJ660442	*Tomato leaf curl Palampur virus*	Iran	*Solanum lycopersicum*	India – China
FJ660443	*Tomato leaf curl Palampur virus*	Iran	*Cucumis sativus*	India – China
FR851930	*Tomato leaf curl Palampur virus*	Pakistan	*Cucumis melo*	India – China
FR856888	*Tomato leaf curl Palampur virus*	Pakistan	*Cucumis melo*	India – China
KC456162	*Tomato leaf curl Palampur virus*	India	*Solanum lycopersicum*	India – China
KT895906	*Tomato leaf curl Palampur virus*	India	*Rumex nepalensis*	India – China
KX778475	*Tomato leaf curl Palampur virus*	India	*Solanum melongena*	India – China
KY564206	*Tomato leaf curl Palampur virus*	India	*Cucumis melo*	India – China

KY564207	*Tomato leaf curl Palampur virus*	India	*Cucumis sativus*	India – China
LN864818	*Tomato leaf curl Palampur virus*	Pakistan	*Carica papaya*	India – China
AJ508782	*Tomato leaf curl Sinaloa virus*	Nicaragua	*Lycopersicon esculentum*	Latin America
AJ508783	*Tomato leaf curl Sinaloa virus*	Nicaragua	*Lycopersicon esculentum*	Latin America
KY064020	*Tomato leaf curl Sinaloa virus*	Costa Rica	*Solanum lycopersicum*	Latin America
KY064025	*Tomato leaf curl Sinaloa virus*	Costa Rica	*Solanum lycopersicum*	Latin America
MH019226	*Tomato leaf curl Sinaloa virus*	Costa Rica	*Solanum lycopersicum*	Latin America
DQ336352	Tomato mild leaf curl virus	Brazil	*Solanum lycopersicum*	Latin America
EU710753	*Tomato mild mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706609	*Tomato mild mosaic virus*	Brazil	*Sida urens*	Latin America
KC706612	*Tomato mild mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706613	*Tomato mild mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706614	*Tomato mild mosaic virus*	Brazil	*Solanum lycopersicum*	
EF547938	*Tomato mild yellow leaf curl Aragua virus*	Venezuela	*Lycopersicon esculentum*	Latin America
JN368146	*Tomato mild yellow leaf curl Aragua virus*	Venezuela	*Euphorbia heterophylla*	Latin America
KY353798	*Tomato mild yellow leaf curl Aragua virus*	Venezuela	*Solanum lycopersicum*	Latin America
KT099164	*Tomato mosaic Havana virus*	Guatemala	-	Latin America
Y14875	*Tomato mosaic Havana virus*	Cuba	*Solanum lycopersicum*	Latin America
KY449276	Tomato mosaic Trujillo virus	Venezuela	*Solanum lycopersicum*	Latin America

JF803264	*Tomato mottle leaf curl virus*	Brazil	*Solanum lycopersicum*	Latin America
AF012301	*Tomato mottle Taino virus*	Cuba	-	Latin America
AY965901	*Tomato mottle virus*	Puerto Rico	*Solanum lycopersicum*	Latin America
L14461	*Tomato mottle virus*	USA	*Solanum lycopersicum*	Latin America
JQ714138	*Tomato mottle wrinkle virus*	Argentina	*Solanum lycopersicum*	Latin America
KM243017	*Tomato mottle wrinkle virus*	Argentina	*Solanum lycopersicum*	Latin America
AF291706	*Tomato rugose mosaic virus*	Brazil	*Solanum lycopersicum*	Latin America
JN381814	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381816	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381817	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381818	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	
JN381820	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381822	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381824	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381826	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381828	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
JN381829	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*	ToRYLCV
EF534708	*Tomato severe rugose virus*	Brazil	*Capsicum baccatum*	Latin America
GU358449	*Tomato severe rugose virus*	Brazil	*Nicandra physaloides*	Latin America

HQ606468	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706621	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706622	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706623	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706624	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706625	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706626	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706627	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
KY964449	*Tomato severe rugose virus*	Brazil	*Solanum betaceum*	Latin America
MG837739	*Tomato severe rugose virus*	Brazil	*Solanum lycopersicum*	Latin America
HE806439	Tomato yellow distortion leaf virus	Cuba	*Sida* sp.	Latin America
HE806441	Tomato yellow distortion leaf virus	Cuba	*Sida* sp.	Latin America
AF511527	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	-	Asia
AF511528	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	-	Asia
DQ169055	*Tomato yellow leaf curl Kanchanaburi virus*	Viet Nam	*Solanum lycopersicum*	Asia
KF218821	*Tomato yellow leaf curl Kanchanaburi virus*	Laos	*Solanum melongena*	Asia
KF446662	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Solanum melongena*	Asia
KF446664	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Solanum melongena*	Asia
KF446666	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Solanum melongena*	Asia

KF446668	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Solanum melongena*	Asia
KF446670	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Capsicum* sp.	Asia
KF446672	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Capsicum* sp.	Asia
KF446674	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Capsicum* sp.	Asia
KF446676	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Capsicum* sp.	Asia
KU569585	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569587	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569589	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569591	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569593	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569595	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569597	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569599	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569602	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum melongena*	Asia
KU569605	*Tomato yellow leaf curl Kanchanaburi virus*	Laos	*Solanum melongena*	Asia
KU569607	*Tomato yellow leaf curl Kanchanaburi virus*	Viet Nam	*Solanum melongena*	Asia
KU569609	*Tomato yellow leaf curl Kanchanaburi virus*	Viet Nam	*Solanum melongena*	Asia
LC177332	*Tomato yellow leaf curl Kanchanaburi virus*	Indonesia	*Capsicum annuum*	Asia
MF327261	*Tomato yellow leaf curl Kanchanaburi virus*	China	*Solanum melongena*	Asia

EF577265	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
EF577267	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
EU249458	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Capsicum annuum*	Asia
GU208519	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Capsicum* sp.	Asia
GU208520	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Capsicum* sp.	Asia
GU208521	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Capsicum* sp.	Asia
GU208522	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Capsicum* sp.	Asia
GU723751	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
GU723752	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
GU723753	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
GU723754	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
GU723755	*Tomato yellow leaf curl Thailand virus*	Taiwan	*Solanum lycopersicum*	Asia
FJ999999	*Tomato yellow leaf distortion virus*	Cuba	*Solanum lycopersicum*	Latin America
KU232892	*Tomato yellow leaf distortion virus*	Cuba	*Sidastrum micranthum*	Latin America
AY508994	*Tomato yellow margin leaf curl virus*	Venezuela	*Solanum lycopersicum*	Latin America
KC176781	*Tomato yellow mottle virus*	Costa Rica	*Solanum lycopersicum*	Latin America
KY064021	*Tomato yellow mottle virus*	Costa Rica	*Solanum lycopersicum*	Latin America
DQ336351	*Tomato yellow spot virus*	Brazil	*Solanum lycopersicum*	Latin America
JX513953	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America

KJ742420	*Tomato yellow spot virus*	Argentina	*Salvia hispanica*	Latin America
KX348205	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348206	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348207	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348208	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348209	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348210	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348211	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348212	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348213	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348214	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348215	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348216	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348217	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348218	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348219	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348220	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348221	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348222	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America

KX348223	*Tomato yellow spot virus*	Brazil	*Leonurus sibiricus*	Latin America
KX348226	*Tomato yellow spot virus*	Brazil	*Sida* sp.	Latin America
EF417916	*Tomato yellow vein streak virus*	Brazil	*Solanum tuberosum*	Latin America
KC136338	*Tomato yellow vein streak virus*	Chile	*Solanum lycopersicum*	Latin America
KC136340	*Tomato yellow vein streak virus*	Chile	*Solanum lycopersicum*	Latin America
KC706655	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706656	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706657	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	
KC706658	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706659	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706660	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706661	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706662	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706663	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706664	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706665	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706666	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KC706667	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*	Latin America
KR024027	*Tomato yellow vein streak virus*	Uruguay	*Solanum lycopersicum*	Latin America

KU131589	*Triumfetta yellow mosaic virus*	Brazil	*Triumfetta* sp.	Latin America
KU131590	*Triumfetta yellow mosaic virus*	Brazil	*Triumfetta* sp.	
FN543426	*Velvet bean severe mosaic virus*	India	*Macuna* sp.	Asia – Africa
KC430937	*Vigna yellow mosaic virus*	Mexico	*Vigna elegans*	Latin America
AJ012082	*Watermelon chlorotic stunt virus*	-	*Citrullus lanatus*	Asia – Africa
EF201810	*Watermelon chlorotic stunt virus*	Israel	-	Asia – Africa
EU561236	*Watermelon chlorotic stunt virus*	Jordan	*Citrullus lanatus*	Asia – Africa
HG969288	*Watermelon chlorotic stunt virus*	Oman	-	Asia – Africa
HM368372	*Watermelon chlorotic stunt virus*	Lebanon	*Cucumis melo*	Asia – Africa
JX131284	*Watermelon chlorotic stunt virus*	Jordan	*Sinapis arvensis*	Asia – Africa
KC462553	*Watermelon chlorotic stunt virus*	Palestine	*Citrullus lanatus*	Asia – Africa
KJ939447	*Watermelon chlorotic stunt virus*	Saudi Arabia	*Citrullus lanatus*	Asia – Africa
KT272766	*Watermelon chlorotic stunt virus*	Iran	*Citrullus lanatus*	Asia – Africa
KT272768	*Watermelon chlorotic stunt virus*	Iran	*Citrullus lanatus*	Asia – Africa
KT272770	*Watermelon chlorotic stunt virus*	Iran	*Citrullus lanatus*	Asia – Africa
KT272772	*Watermelon chlorotic stunt virus*	Iran	*Citrullus lanatus*	Asia – Africa
KY124281	*Watermelon chlorotic stunt virus*	Mexico	*Citrullus lanatus*	Asia – Africa
KY488569	*Watermelon chlorotic stunt virus*	Sudan	*Datura innoxia*	Asia – Africa
KY825716	*Watermelon chlorotic stunt virus*	Iran	*Brassica rapa*	Asia – Africa

JF694485	*West African Asystasia virus*	West Africa	*Asystasia gangetica*	Asia – Africa
KT444602	*West African Asystasia virus*	Nigeria	*Asystasia* sp.	Asia – Africa
KT444604	*West African Asystasia virus*	Cameroon	*Manihot* sp.	Asia – Africa
KT444606	*West African Asystasia virus*	Cameroon	*Manihot* sp.	Asia – Africa
KT444608	*West African Asystasia virus*	Cameroon	*Asystasia* sp.	Asia – Africa
KT444610	*West African Asystasia virus*	Benin	*Asystasia* sp.	Asia – Africa
HM859903	*Whitefly-associated begomovirus 2*	USA	-	Latin America
KT099162	*Whitefly-associated begomovirus 3*	Guatemala	-	Latin America
KT099163	*Whitefly-associated begomovirus 3*	Guatemala	-	Latin America
KT099166	Whitefly-associated begomovirus 5	Puerto Rico	-	Latin America
KT099167	*Whitefly-associated begomovirus 6*	Puerto Rico	-	Latin America
KT099168	*Whitefly-associated begomovirus 6*	Puerto Rico	-	Latin America
EU158095	Wissadula golden mosaic St Thomas virus	Jamaica	*Wissadula amplissima*	Latin America
GQ355487	Wissadula golden mosaic St Thomas virus	Jamaica	*Wissadula amplissima*	Latin America

$^{-}$ Not specified

Supplementary Table S2. Recombination events detected by RDP in begomovirus subpopulations based on DNA-B sequences retrieved from GenBank.

Event	**Recombinant**[i]	**Recombination breakpoints**[ii]		**Parents**		**Methods**[iii]	**P-value**[iv]
		Initial	**Final**	**Major**	**Minor**		
'ToRYLCV' subpopulation							
1	JN381820	600 (596)	1600 (1595)	JN381814	Unknown (JN381822)	RGBMC**S**3	8.72E-25
2	^JN381820	1749* (1744*)	2585 (2547)	Unknown (JN381824)	JN381814	RBMC**S**3	9.70E-16
3	JN381820	32 (32)	320 (317)	JN381822	Unknown (JN381814)	RB**M**C3	3.33E-04
'Latin America' subpopulation							
1	LN848815	3748 (1683)	4302 (2120)	LN848832	LN848919	R**G**BMCS3	2.15E-66
2	LN848819	3730 (1665)	4280 (2109)	LN848833	LN848919	RGBMCS**3**	2.25E-54
2	LN848811			AY928517	LN848903		
2	LN848816			KY064024	LN848897		
3	^LN848835	3732 (1665)	5164 (2463)	LN848836	Unknown (LN848837)	RGBMCS**3**	4.06E-53
4	^LN848912	1586 (435)	5404 (2521)	Unknown (LN848919)	KP890828	R**G**BMCS3	2.50E-50
4	MG582069			Unknown (LN848910)	LN848924		
5	LN848814	2373 (906)	3700 (1647)	LN848820	LN848833	RGBMCS**3**	7.73E-48

6	^LN848920	1852 (628)	5532 (2566)	Unknown (LN848903)	LN848921	RGBMS**3**	1.71E-47
6	LN848910			Unknown (LN848917)			
6	LN848924						
6	KX440615						
6	KX440614						
6	KP890828						
6	LN848915						
6	LN848923						
6	LN848922						
6	LN848919						
6	LN848902						
7	^LN848835	344 (99)	2368 (898)	GU128147	LN848837	RGBMCS**3**	1.51E-45
7	LN848836						
8	^JF694459	622 (189)	3750 (1733)	JF694455	JF694457	**R**GMCS3	5.21E-43
9	LN848816	2426 (948)	3402 (1416)	LN848840	LN848918		
10	FJ686696	384 (112)	1800 (718)	AJ557454	KU852504	**R**GBMCS3	1.27E-41
10	EU914818			FN557523	EU908734		
11	^LN848908	1483 (382)	4322 (2168)	LN848893	GU564593	RGMCS**3**	1.89E-40
11	LN848898				LN848900		

12	^LN848833	2876 (1183)	5370 (2478)	LN848805	LN848838	RGMCS**3**	5.00E-39
12	LN848819			LN848807	LN848842		
13	^HE806449	1792 (552)	5228 (2421)	JX162593	KT879815	RGBMCS**3**	1.22E-38
14	^LN848836	3728 (1661)	343* (98*)	GU128147	Unknown (LN848837)	RGMCS**3**	1.25E-36
14	LN848835				Unknown (LN848838)		
15	^LN848823	1610 (414)	4454 (2156)	LN848801	Unknown (LN848813)	RGBMCS**3**	2.02E-36
15	AY928513			LN848798	Unknown (LN848830)		
15	LN848809			LN848799			
16	^LN848903	1765 (566)	5016 (2415)	LN848917	Unknown (LN848897)	RBMCS**3**	1.38E-31
17	^KC706525	141 (25)	4576 (2273)	KC706526	Unknown (KC706524)	RGBMC**S**3	4.55E-37
18	^AJ557453	5473 (2625)	4614 (2388)	Unknown (KX348195)	AJ557452	MCS**3**	4.38E-29
19	^KX348205	730 (188)	3172 (1335)	KX348212	Unknown (KX348211)	RGMCS**3**	4.57E-29
20	^EU740969	1428 (403)	5232 (2459)	FJ807783	KJ647291	RGMCS**3**	6.48E-29
21	^DQ641689	1414 (284)	4938 (2319)	AB849291	Unknown (AB971857)	RGBMCS**3**	8.12E-29
22	^JF694479	1299 (420)	5627 (2619)	Unknown (JF694469)	JF694477	RGMCS**3**	8.22E-29
23	^JQ963888	1572 (502)	5340 (2487)	FJ807783	KJ647291	RGMCS**3**	1.04E-28
24	KC706564	970 (249)	4352 (2221)	Unknown (JF803264)	KC706567	RGBMC**S**3	1.16E-35
24	DQ336354				KC706565		
25	^AB971857	1244 (239)	5431 (2485)	AB971861	Unknown (AB971853)	RGBMCS**3**	2.03E-26

26	^LN848807	5617 (2582)	3178 (1232)	LN848810	LN848843	RGBMCS**3**	2.20E-26
26	LN848804				LN848838		
27	^JF694463	5415 (2604)	3968 (2072)	Unknown (JF694465)	JF694464	GBMCS**3**	7.67E-26
28	^LN848840	1448 (344)	2796 (1177)	AF499442	LN848832	RGMCS**3**	1.29E-25
29	LN848840	3519 (1506)	5365 (2505)	LN848832	AF499442	RGMS**3**	8.79E-26
29	LN848834			LN848839	AY928515		
29	LN848827						
30	^DQ178611	5208 (2376)	5635 (2488)	U65530	AY965898	R**G**BMCS3	4.03E-25
30	DQ178609						
31	^LN848901	519 (83)	4594 (2250)	Unknown (LN848927)	LN848900	RGBMC**S**3	5.02E-27
32	^LN848892	1040 (242)	3951 (1916)	Unknown (LN848905)	GU564596	RGMCS**3**	6.07E-25
33	^LN848914	1256 (310)	5414 (2521)	LN848890	LN848893	RGMCS**3**	7.09E-24
34	^AB971847	4372 (2086)	5356 (2463)	AB971855	Unknown (AB849293)	RGBMCS**3**	8.28E-24
35	^JF694478	1482 (425)	4686 (2300)	JF694469	Unknown (JF694470)	RGBMC**S**3	2.50E-31
35	JF694477						
36	^LN848833	1605 (409)	2875* (1183*)	Unknown (LN848839)	LN848832	**R**GBMCS3	6.33E-23
36	LN848819				LN848834		
37	^JX219472	1784 (595)	3268 (1331)	GU997692	AF480941	R**G**BMCS3	2.54E-21
37	HM035060			KU232892	AY742221		

37	GU972604			JX162592			
37	JX219471			HQ009518			
37	JX219473			DQ875869			
38	KX348188	5083 (2528)	5434 (2615)	KX348186	MG837739	R**G**BMCS3	2.34E-21
38	KX348191			KX691416	GU358449		
38	KC706534			KX348201	EF534708		
38	KX348193			HM585434	KC706621		
38	AJ557452			KX348200	KC706626		
38	KX348189			KX348199	KC706627		
38	KX348194			KX348192	KC706624		
38	KX348195			KX348202	KC706622		
38	KX348203			FN436006	KC706625		
39	^LN848839	1605 (409)	2788 (1176)	LN848832	LN848838	RGMCS**3**	1.71E-38
40	LN848830	5617 (2585)	2522 (1030)	GU564595	Unknown (LN848824)	**R**GMCS3	6.98E-21
41	^KT879827	688 (118)	1198 (229)	KT879821	HE806445	**R**GBMCS3	1.33E-20
42	^LN848831	3621 (1595)	4517 (2199)	LN848812	GU128147	**R**GBCS3	1.37E-20
43	^AY120883	5230 (2443)	5591 (2551)	AF039032	KY449278	RGBMCS**3**	7.05E-20
43	AY965898			FR851301	D00941		
44	^KX348211	1028 (298)	4676 (2322)	KX348206	KX348208	RGMC**3**	1.11E-18

44	KX348205			KX348216			
44	KX348212			KX348214			
44	KX348215			KX348207			
44	KX348209						
44	KX348217						
44	KX348221						
45	^GU128146	116 (25)	4520 (2233)	Unknown (LN848913)	LN848907	GBMC**S**3	7.21E-38
45	LN848926			Unknown (LN848909)			
45	LN848925			Unknown (LN848904)			
45	LN848927			Unknown (LN848893)			
45	GU128151						
45	LN848928						
45	LN848900						
45	LN848899						
46	^FJ807783	5535 (2547)	4638 (2318)	Unknown (KJ647291)	HQ896202	R**G**BMC3	4.38E-19
47	^JF694456	1559 (375)	4474 (2208)	Unknown (JF694455)	JF694458	RGMCS**3**	4.42E-18
48	^JF694464	791 (308)	1466 (507)	JF694466	JF694467	R**G**B3	1.80E-21
49	^JN411688	331 (39)	584 (79)	HQ822124	Unknown (AM886130)	RGMS**3**	6.75E-18
50	^LN848811	1126 (271)	2876 (1182)	LN848842	Unknown (AF499442)	RGBMCS**3**	7.16E-18

50	LN848831			LN848843	Unknown (AY928515)		
51	^X15984	1426 (317)	4290 (2115)	Unknown (AM886130)	LN611624	RGMC**S**	1.89E-25
52	JF694456	4815 (2357)	178 (29)	Unknown (AB971863)	JF694455	GMCS**3**	3.10E-17
53	^LN848904	1034 (218)	4540 (2247)	Unknown (LN848894)	LN848905	**R**GBMCS3	7.41E-17
54	^HM626517	4442 (2159)	5043 (2428)	AF039841	Unknown (KT879815)	RGMCS**3**	8.01E-17
55	^AB971847	5570 (2587)	3127 (1144)	Unknown (AB971853)	AB849291	RM**S**3	2.16E-17
55	AB971855						
56	^AY965898	490 (92)	4590 (2217)	Unknown (FR851301)	AY120883	RGMCS**3**	2.88E-16
57	^AB971853	1455 (289)	5287 (2421)	Unknown (AB971863)	AB971861	RGMCS**3**	2.88E-16
57	AB971845				AB971843		
58	^AF499442	1125 (271)	3884 (1816)	LN848800	LN848843	RGBMC**S**3	6.64E-20
58	LN848806			LN848829	MF109821		
58	LN848816			LN848799	LN848844		
58	LN848818			LN848801	LN848842		
58	LN848821			LN848802	LN848841		
58	LN848820			LN848803			
58	LN848840						
58	LN848808						
58	LN848834						

58	LN848827						
58	AY928515						
58	LN848824						
58	LN848825						
58	LN848805						
58	GU564595						
59	^LN848808	4356* (2125*)	5183 (2470)	LN848825	LN848811	RGMS**3**	9.24E-17
60	^AB971859	1328 (270)	5426 (2469)	AB971863	AB971849	RGMCS**3**	2.09E-15
61	^LN848894	3554* (1580*)	4080 (2031)	LN848895	X70419	**R**GMCS3	3.85E-15
61	LN848911			GU564596			
62	^HM003778	454 (70)	3198 (1235)	HM859903	DQ875869	RBM**C**S	1.23E-14
62	HM359016						
63	^KT099167	5616 (2558)	4880 (2357)	Unknown (KT099166)	KT099168	MC**S**3	6.08E-14
64	^LN848810	2366 (897)	2657 (1159)	LN848813	Unknown (LN848844)	R**G**MCS3	2.26E-14
65	^KU058858	1010 (248)	4313 (2172)	LN611624	KU058860	RGBMC**S**3	2.38E-31
66	^KX348214	1150 (374)	3244 (1394)	KX348206	KX348213	RGBMC**S**3	9.75E-15
66	KX348216						
67	^EF210557	5396 (2517)	1164 (261)	GU564596	LN848913	**R**GMCS3	4.56E-14
68	^LN848896	3283 (1350)	4230* (2124*)	Unknown (LN848909)	LN848895	**R**GMCS3	5.68E-14

68	GU564596			Unknown (LN848913)			
69	^D00941	320 (85)	4440 (2150)	Unknown (KT879815)	FR851302	BMC**S**3	1.34E-41
70	LN848888	4745 (2326)	5452 (2534)	LN848896	Unknown (LN848889)	RGMCS**3**	3.94E-13
71	LN848891	796 (115)	3442 (1473)	LN848888	LN848913	RGMCS**3**	2.48E-15
72	^KX348202	646 (158)	4032 (2110)	KX348195	KX348199	RBM**S**3	5.70E-16
73	^KC706527	273 (123)	5300 (2498)	KC706526	KC706524	MC**S**3	1.23E-14
74	JX219473	4682 (2285)	5628* (2572*)	JX219472	JX857692	**R**GMCS3	8.96E-13
74	JX219471						
75	KX348196	1714 (632)	4922 (2477)	Unknown (KY650716)	KX348192	RGM**C**S	1.29E-12
76	KX348188	1211 (400)	5082* (2528*)	KC706533	KX348198	GMC**S**3	3.64E-15
77	^DQ875869	5382* (2507*)	1314 (272)	Unknown (HQ009518)	GU997692	RGBMC**S**3	8.84E-17
78	^JF694455	3228 (1273)	4332 (2154)	Unknown (MH925107)	JF694458	RG**B**MCS3	4.45E-17
79	^KX348189	4115* (2211*)	4815 (2460)	KX348202	KX348200	RGMCS**3**	3.66E-12
80	^LN848837	318 (66)	868 (218)	LN848811	LN848833	RGMCS**3**	4.59E-12
80	LN848801				LN848819		
81	^LN848844	1126 (271)	4634 (2238)	Unknown (LN848803)	LN848843	MC**S**3	9.96E-24
82	^KX348226	978 (276)	2845 (1256)	KX348222	KX348219	RGBMC**S**3	1.57E-18
82	KX348210						
83	^LN848838	1480 (352)	3721* (1654*)	LN848842	Unknown (LN848815)	GMCS**3**	1.41E-11

84	KY449278	5234 (2517)	5592 (2612)	HQ201953	JN848774	**R**GS3	1.95E-11
85	^KX348213	520 (141)	2755 (1244)	KX348223	KX348208	RGM**S**3	2.28E-18
86	KX348213	3016 (1297)	4715 (2335)	KX348207	Unknown (JX513953)	RGMCS**3**	2.93E-15
87	^JF694462	1523 (515)	4429 (2329)	JF694466	Unknown (JF694467)	R**G**BMCS3	1.20E-12
87	JF694464			JF694465			
88	^LN848891	4541* (2241*)	5414 (2520)	Unknown (LN848896)	LN848904	GMS**3**	2.65E-11
89	KT099166	3770 (1699)	4703 (2278)	KT099168	KT879824	**R**MCS	2.25E-13
90	LN848901	5020 (2417)	306* (48*)	Unknown (LN848898)	AB849293	GMC**S**	5.78E-11
91	LN848893	300 (49)	1256* (310*)	LN848907	Unknown (GU564593)	RGMC**S**3	7.09E-14
92	^FR851302	592 (111)	5119 (2394)	Unknown (AF039032)	FR851301	RGMC**S**3	4.32E-17
93	^KF962543	1631 (373)	1791 (504)	AB971863	Unknown (GQ183864)	R**G**BMCS3	5.99E-15
94	LN848798	2596 (1101)	3268 (1310)	LN848802	LN848832	R**G**MCS3	2.72E-11
95	^FN557523	255* (69*)	4678 (2324)	EU914818	AJ557454	GM**S**3	1.31E-11
96	JN419010	4865 (2410)	71 (17)	KC706528	KT779563	R**G**MS	4.31E-10
97	^HM585440	975 (276)	4590 (2368)	KX348193	Unknown (KX691416)	GMS**3**	4.50E-10
97	HM585432			EU908734			
98	^LN848811	617 (113)	1012* (255*)	LN848817	Unknown (LN848843)	**R**GB3	7.41E-10
99	^LN848837	4576 (2218)	4842 (2359)	Unknown (LN848843)	LN848815	RGBMC**S**3	5.46E-16
99	LN848832			Unknown (LN848841)	LN848832		

100	DQ875869	1560 (368)	3508 (1500)	Unknown (JN236209)	JX162592	RGBMC**S**3	3.62E-50
101	^KY555799	1592 (531)	4574 (2349)	KX348200	FN436002	RM**C**S3	9.85E-10
102	JF694483	2202 (855)	4388 (2251)	Unknown (KX348193)	AJ557454	G**B**MC	3.31E-09
102	FN434439			Unknown (KC706532)			
103	^KT381194	1338* (279*)	2844 (1149)	HQ896204	DQ178613	R**G**BMCS3	2.63E-17
103	FJ792608				DQ178611		
103	HM236371				DQ178609		
104	^JF694459	3751* (1734*)	4372 (2193)	GQ183864	M88687	RMCS**3**	5.57E-09
105	^JF694459	5044 (2478)	72 (17)	Unknown (AB971861)	JN419017	R**G**BMCS3	2.63E-17
105	MH925107			Unknown (KF962543)			
105	JF694455			Unknown (AB849293)			
106	^KX348191	1568 (526)	3473 (1639)	KC706533	KX348199	RMCS**3**	5.57E-09
107	HQ009518	5431* (2518*)	1562 (368)	DQ875873	Unknown (KT099166)	**M**CS3	6.09E-09
107	JX162592						
108	EF210557	3866 (1848)	1174* (271*)	LN848890	Unknown (LN848917)	RMC**3**	8.36E-09
109	^FN557523	5040 (2497)	218* (57*)	Unknown (AB971861)	AJ557454	GB**M**S	4.13E-08
109	EU914818			Unknown (KF962543)			
109	FJ686696			Unknown (GQ183864)			
110	^LN848888	3722 (1697)	4642 (2265)	LN848907	LN848905	RGMCS**3**	1.23E-06

111	^KX691416	1604 (550)	3156 (1389)	KC706533	KX348199	RMCS**3**	7.80E-08
112	KX691416	4478 (2353)	975 (283)	KU852504	Unknown (HM585438)	RMC**S**3	2.57E-16
112	EU908734						
112	KY650718						
112	KY650719						
112	KC706533						
113	^EF417916	3827 (1851)	5145 (2439)	Unknown (KC136340)	KC136338	RGMC**S**3	2.77E-14
114	^GU564596	5246 (2482)	1628 (459)	LN848896	Unknown (LN848907)	RMCS**3**	2.37E-07
115	^GU564593	5453 (2529)	2296 (861)	Unknown (LN848909)	LN848916	RGMCS**3**	3.43E-07
115	LN848890			Unknown (LN848895)	LN848917		
116	^AY044134	5139 (2429)	4285 (2065)	AF449193	KT099169	G**M**C3	5.70E-07
117	^LN848904	4730 (2329)	1033 (217)	Unknown (KY064022)	LN848887	GBM**S**	3.70E-65
117	LN848917			Unknown (AY928517)	LN848918		
117	LN848907			Unknown (KY064024)	AY044163		
117	GU564596			Unknown (KY064019)	LN848889		
117	LN848906			Unknown (KY064023)			
117	LN848905			Unknown (AY928513)			
117	LN848911			Unknown (LN848810)			
117	LN848894			Unknown (LN848817)			

118	^LN848917	1147* (254*)	3730 (1703)	Unknown (LN848887)	LN848921	RGM**S**3	3.21E-13
119	^KX348202	5320 (2558)	645* (158*)	Unknown (KU852504)	KX348200	**R**MC3	7.88E-07
120	^LN848897	1496* (382*)	3752 (1724)	Unknown (LN848887)	LN848921	GM**S**3	5.34E-14
121	^LN848839	3519 (1505)	3758 (1691)	LN848832	GU128147	**R**GB3	8.06E-07
122	KX348205	4999 (2444)	5184 (2508)	KX348215	Unknown (KX348222)	**G**MCS3	1.62E-06
122	KX348212			KX348206			
123	^FJ600484	5078 (2408)	116 (19)	Unknown (KX101213)	FJ600485	GMC**S**	2.71E-18
124	^JF694455	693 (180)	2631 (1122)	Unknown (AY727904)	MH925107	GBM**S**	4.09E-46
125	^EF582841	1810 (535)	3220 (1236)	EF585292	EF585289	RGBMC**S**3	9.03E-07
126	^FJ981727	4444* (2167*)	84 (21)	M88180	JQ045706	RGBC**S**3	1.09E-07
126	EU158097						
127	^KY650721	2057 (839)	2506 (1161)	KC706533	FN436004	RGBM**S**3	2.49E-06
127	KY650723						
128	^KX011474	2645 (1090)	4442* (2118*)	Unknown (LN848832)	DQ178609	MC**S**3	1.26E-09
129	^KX348226	4939* (2446*)	5568* (2578*)	KX348222	Unknown (KX348210)	RGMC**S**	1.77E-07
130	^KX348222	5202 (2498)	893 (233)	KX348206	Unknown (DQ336351)	RM**C**S3	1.11E-05
131	^AF170101	1749 (509)	4382* (2154*)	Unknown (U51138)	HE806447	MC**S**3	1.90E-12
132	^JF694466	1609 (558)	4144 (2205)	Unknown (HM585438)	FN436000	MC**S**3	2.42E-38
132	JF694464			Unknown (KU852504)			

132	JF694462			Unknown (FJ686694)			
132	JF694467			Unknown (KY650720)			
132	JF694465			Unknown (KC706532)			
133	^JN848774	5210* (2432*)	5592* (2545*)	FR851301	MF163259	R**G**S3	8.69E-05
134	^KT948788	5018 (2489)	5513 (2645)	KT948786	Unknown (M88687)	RB**M**3	1.86E-04
135	^AB849291	5658* (2632*)	1463* (291*)	AB971849	GQ183864	**M**CS3	7.31E-04
136	^X70419	5532* (2561*)	846 (133)	Unknown (LN848895)	LN848896	RGMC**S**	4.83E-07
137	^HM626517	2192 (737)	3215 (1257)	KU232892	M88180	MC**S**3	7.48E-04
137	AF039841			DQ875873			
138	FJ686696	2450 (1110)	4404 (2311)	Unknown (KX348187)	AJ557454	GMC**S**	1.06E-34
138	KX348218			Unknown (KY650721)			
138	EU914818			Unknown (KY650723)			
139	^LN848818	810* (195*)	1124* (271*)	GU128147	Unknown (LN848817)	RGM**S**	7.54E-12
139	KY064024			LN848821			
139	KY064019						
139	KY064022						
139	KY064023						
139	LN848823						
139	AY928513						

139	LN848837						
139	AY928515						
139	AF499442						
139	LN848825						
139	LN848812						
139	LN848798						
139	LN848799						
139	LN848801						
139	LN848800						
139	LN848802						
139	GU564595						
140	^LN848817	3868 (1803)	5422* (2532*)	MF109821	Unknown (LN848829)	M**C**S3	9.46E-05
‘ACM-like viruses’ subpopulation							
1	^AF259895	2594 (2582)	2675 (2654)	HE616778	HG530118	RG**M**CS	6.06E-06
1	KR476374				HG530119		
1	KR476373				HG530117		
1	HE979790				HG530121		
1	HE979794				HG530120		

1	HE979793				HE979781		
1	HG530122				HE979783		
1	HE979789				HE979782		
1	HE979786				HE979784		
1	HE979792				HE979785		
1	HE979791				AF126803		
1	HE979788				AF126801		
1	HE979787						
1	HE979795						
1	HE979796						
‘India – China’ subpopulation							
1	LT168873	995 (636)	2536 (2098)	LN845961	LT168877	RGBMCS**3**	5.85E-49
2	KX778475	1412 (1036)	2547 (2103)	KY564206	AJ875158	**R**GBMCS3	1.88E-43
3	^HQ586006	102 (77)	2570 (2132)	EF620535	HQ586005	RGMS**3**	6.84E-40
4	^KF577603	152 (120)	728 (411)	KF515623	KY780206	R**G**BMCS3	1.83E-39
5	GU112089	2674 (2204)	408 (284)	HM803117	GU112087	**R**GBMCS3	4.86E-38
6	KY933712	1916 (1525)	2356 (1963)	KY933710	KY933711	**R**GMCS3	2.53E-33
7	LN845963	803 (446)	2636 (2182)	LN845961	AM286435	GBMS**3**	7.00E-33

8	^KY780208	2562 (2126)	3397 (2657)	KJ862842	KF577604	R**G**BMCS3	5.45E-30
9	^KY780203	1393 (1032)	2561* (2124*)	LT168870	KY780208	RGMCS**3**	6.35E-30
10	^KY780211	1186 (826)	2743 (2253)	Unknown (KY780206)	JN208137	GBMCS**3**	8.19E-29
11	KF577605	1232 (873)	2598* (2161*)	AY438563	JN208137	**R**GBMCS3	7.39E-28
12	LN845937	1796 (1409)	2631 (2176)	Unknown (LN845961)	LN845943	RGBMCS**3**	5.42E-27
12	LN845940				LT168874		
13	^LT168870	1809 (1423)	2592 (2156)	LN845961	LT168872	R**G**MCS3	1.71E-26
14	^KF577603	734* (416*)	1184 (825)	KF515623	HM159455	RGBMCS**3**	1.56E-25
15	JN624306	1692 (1331)	2586 (2172)	AM709505	AY184488	R**G**MCS3	3.47E-24
16	LT168854	1894 (1504)	2192 (1802)	LT168884	LT168881	**R**GMCS3	5.26E-20
17	^KY564207	964 (589)	1804 (1409)	KY564206	KC456162	**R**GBMCS3	5.19E-19
18	KY780214	958 (599)	1768 (1383)	KY780212	Unknown (KY780206)	RGMCS**3**	1.84E-19
19	DQ020490	1567 (1218)	184 (152)	KJ862842	MG597211	RGBMC**S**3	3.71E-28
20	LN845937	92 (70)	1374 (1011)	LN878126	LN845942	RGBMC**S**3	1.77E-32
20	LN845940			LT168872	KY780204		
21	MH465600	2648 (2208)	3234 (2555)	LN845936	DQ169057	**R**GBMCS3	2.27E-17
22	^KY780208	975 (617)	1382 (1022)	MH465600	KF577604	**R**GMCS3	2.54E-17
23	GU112089	1818 (1430)	2619 (2168)	HQ141674	AY158080	R**G**MCS3	3.70E-17
24	^HQ586007	2529 (2093)	3401 (2661)	KJ862842	AM778833	RGBMC**S**3	1.28E-26

25	^KT948071	3210 (2530)	444 (307)	AM778833	Unknown (LN845961)	**R**GBMCS3	8.30E-16
25	EF043233			MG597207	Unknown (KF577604)		
25	KC874501			MG597210	Unknown (LT168870)		
25	KP641674			HM159455	Unknown (KY780214)		
25	KC874500			FN435312	Unknown (KX951456)		
25	EF043232			KP235543	Unknown (KY780212)		
25	MH511990			JN663848	Unknown (KY780200)		
25	KC874495			JN663871	Unknown (KY780203)		
25	HG932560			JN663867	Unknown (KY780204)		
25	KC874499			MG597211	Unknown (KT948073)		
25	KP641676			KC545813	Unknown (KY420144)		
25	KC874494			MG597208	Unknown (KY780211)		
25	KP709056			DQ169057	Unknown (AM286435)		
25	FN356024			HM989846	Unknown (KY780206)		
25	KC874496				Unknown (JN208137)		
25	KC874497				Unknown (LT168874)		
25	AY158080				Unknown (LT168875)		
25	KC874498				Unknown (LN878124)		
25	KP641678				Unknown (LN845963)		

25	GU112085				Unknown (LN845942)		
26	KY780206	1532 (1168)	2602 (2165)	JN208137	Unknown (AM286435)	GMCS**3**	2.48E-15
27	^AM849547	3260 (2553)	3356 (2634)	KY933712	FJ660426	**R**GBMCS3	1.55E-14
28	LT168866	399 (274)	905 (545)	EF620535	LN845940	RGBMCS**3**	2.57E-11
28	KF577605			MG686554	AY150305		
28	AY438563				MG597210		
28	LT168854				HG316126		
28	LT168852				HM159455		
28	LT168851				FN435312		
28	LT168849				KP235543		
28	LN845956				JN663848		
28	LT168887				JN663871		
28	LT168868				JN663867		
28	LT168861				AY939924		
28	LT168853				KC545813		
28	LT168884				MG597208		
28	LT168860				DQ169057		
29	^KF515623	394 (273)	2886 (2313)	KX827600	HG316126	RMS**3**	6.65E-25
29	HM803117			FN432357	MG597207		

29	HQ141674			LN849711	AM778833		
30	GU112083	2504 (2066)	2688 (2213)	HQ586005	MG597211	**R**GBS3	5.05E-12
30	GU112087			KF577602	MG597207		
31	^HQ542082	910* (554*)	1186* (830*)	Unknown (KF577605)	EF620535	GBMC**S**3	4.52E-12
31	HQ586006						
31	HQ586005						
31	GU112087						
31	GU112083						
31	GU112085						
32	^HG316126	838 (482)	2982 (2382)	Unknown (MG597210)	FN435312	RGM**3**	5.46E-11
33	HQ542082	3126 (2481)	3335 (2621)	MG597210	Unknown (LN864818)	**R**GBMC3	3.03E-10
34	HQ586007	989 (631)	1596 (1232)	KT948073	DQ169057	R**G**MCS3	3.65E-10
35	^KY780203	3403 (2662)	940* (581*)	KY780206	KY780214	R**M**C3	1.86E-09
36	^LT168880	2661 (2197)	448 (301)	FN435312	FN432357	RM**C**S	3.44E-09
36	LT168855			AM778833	KX827600		
36	LT168857			MG597210	LN849711		
36	LT168856			HM159455	FN435311		
36	LT168858			KP235543			
36	LT168859			JN663848			

36	LT168879			JN663871			
36	LT168882			JN663867			
36	LT168881			MG597211			
37	^KT895906	922 (549)	1401 (1026)	KC456162	KY564206	R**G**B3	3.24E-08
38	KY780212	1769* (1384*)	2417 (2021)	KY780214	KM190928	RMC**3**	5.33E-08
39	^FJ660426	48 (31)	2695 (2214)	Unknown (FJ660425)	FJ660430	GCS**3**	6.85E-08
40	^HQ542082	247 (190)	410 (288)	AY150305	HQ586006	**R**MCS3	1.11E-05
40	GU112085			LN845934	HQ586005		
41	^KX951456	2763 (2272)	3302 (2581)	KY780204	Unknown (LN845961)	RGMC**S**3	1.33E-08
42	^LN845935	1803 (1417)	2644 (2190)	LN845961	LT168875	GBMCS**3**	3.93E-09
42	LN845936				LT168874		
43	^LT168870	1030 (671)	1340 (981)	MG597210	Unknown (LT168872)	RBMCS**3**	8.72E-07
43	KX951456			AY150305	Unknown (LT168878)		
43	KY780212			MG597207	Unknown (LT168877)		
43	LN845937			AM778833	Unknown (LN878126)		
43	LN845940			HM159455	Unknown (LN886526)		
43	KY780200			FN435312			
43	KY780203			KP235543			
43	KY780204			JN663848			

43	KT948073			JN663871			
43	KY420144			JN663867			
43	AM286435			MG597211			
43	KY780206			AY939924			
43	JN208137			KC545813			
43	LT168874			MG597208			
43	LT168875			DQ169057			
43	LN878124			HM989846			
43	LN845963						
43	LN845961						
43	LN845942						
43	LN845949						
43	LN845945						
43	LN845935						
43	LN845936						
43	LN845948						
43	LN845952						
43	LN845953						
43	LN845943						

43	LN845946						
43	LN845954						
43	LN845950						
43	LN845939						
43	LN845951						
43	LN845941						
43	LN845938						
43	LN845947						
43	LN845960						
44	KF577605	941* (582*)	1222* (863*)	AY438563	Unknown (MG686554)	RGMC**3**	1.39E-06
45	KY420144	2214 (1826)	3253* (2552*)	KT948073	AM286435	MC**S**3	4.45E-09
46	HG316126	3202* (2480*)	172 (141)	MG597207	Unknown (KY780212)	BMC**S**3	3.82E-06
46	MG597210			AM778833	Unknown (LT168870)		
47	^FN432357	3308 (2594)	3428 (2682)	FN435311	LN845948	RGB**S**3	8.48E-07
48	^FJ660424	2757 (2271)	1782 (1388)	FJ660425	Unknown (FJ660428)	RBM**C**3	2.00E-05
48	FJ660429				Unknown (FJ660435)		
49	^MG597210	2751* (2264*)	1043 (686)	MG597208	HM159455	RBMCS**3**	9.53E-07
‘EuYMV – SqLCV’ subpopulation							

1	^MG763921	1828 (1739)	2110 (2011)	MH346455	KT099159	RGMCS**3**	7.76E-12
2	^KY559604	2926 (2568)	974 (827)	KY559627	KY559598	RGBMCS**3**	2.91E-11
2	KY559603			KY559635	KY559600		
3	MG763921	616 (585)	662 (623)	MH346455	Unknown (DQ285018)	**R**GMCS3	9.54E-10
4	^KJ579954	2295 (2189)	1343 (1310)	MH346455	HQ184437	RGMCS**3**	2.35E-09
5	MH346455	1350 (1301)	1860 (1769)	Unknown (KT099165)	KF030954	R**M**CS3	8.01E-06
5	MG763921			Unknown (HG941653)			
6	KY559634	1708 (1442)	2506 (2207)	KY559627	Unknown (KY559620)	R**G**MC3	3.46E-03
6	KY559635			KY559604	Unknown (KY559612)		
7	KY559610	1006 (861)	1864 (1596)	KY559602	JF756677	RMC**S**3	5.37E-04
‘Asia’ subpopulation							
1	^KT001508	1068 (613)	2651 (2032)	DQ641693	Unknown (KY427015)	RGB**M**CS3	3.90E-32
2	^FJ218491	845 (540)	3160 (2372)	Unknown (KP455487)	EU384578	R**G**BMCS3	7.26E-27
2	EU384576			Unknown (AJ314740)	EU384576		
2	FJ218490			Unknown (AY730036)	FJ218489		
3	^KU569602	3918 (2649)	2828 (2004)	Unknown (GU723754)	KX885225	RBMCS**3**	4.12E-25
3	KU569607			Unknown (GU723752)	KX943291		
3	DQ169055			Unknown (EF577267)			

3	KU569609			Unknown (GU208521)			
3	LC177332			Unknown (GU208520)			
3	KF446674			Unknown (GU208522)			
3	KF446664			Unknown (GU723753)			
3	KF446670			Unknown (GU723751)			
3	KF446672			Unknown (EF577265)			
3	KF446676			Unknown (EU249458)			
3	KF446666			Unknown (GU208519)			
3	KF446668			Unknown (GU723755)			
3	KF446662						
3	MF327261						
3	KU569593						
3	KU569589						
3	KU569591						
3	KU569597						
3	KU569595						
3	KU569605						
3	KF218821						
3	KU569587						

3	AF511528						
3	AF511527						
3	KU569585						
4	MG969497	2986 (2229)	3725 (2598)	JF496656	Unknown (KU550962)	**R**GBMCS3	5.03E-22
5	^EU384577	579 (399)	3000 (2378)	Unknown (KR349062)	JF496656	RGBMC**S**3	2.01E-38
5	MG969497				GQ924761		
5	EU384576						
5	FJ218490						
5	FJ218489						
5	KY420141						
5	FJ218488						
5	EU384578						
5	KY420150						
6	^KY420141	3880 (2625)	196 (120)	MG969497	FJ218491	RGBMCS**3**	7.23E-25
6	EU384576						
6	FJ218490						
6	FJ218489						
6	EU384577						
6	FJ218488						

6	EU384578						
6	KY420150						
7	^KR611580	3698 (2593)	3899 (2713)	AY730036	Unknown (GQ924761)	R**G**BMCS3	2.87E-17
7	KR611578			AJ314740	Unknown (JF496656)		
7	KP455487			KU308386			
7	KF898350			AM158955			
7	KT861469			AJ575820			
7	KP455485						
7	KU550962						
7	AJ314738						
8	^FJ218491	545* (298*)	3324 (2451)	KY427013	EU384576	**G**MCS	2.09E-12
9	AY730036	279* (48*)	538 (75)	KR611578	Unknown (KR349062)	**R**GB3	7.03E-08
10	^EU384577	3075* (2397*)	3204 (2447)	FJ218488	Unknown (AM158955)	RGB**M**C3	5.27E-06
11	^MF327261	922 (313)	983 (364)	GU208520	Unknown (AJ575820)	R**G**MC3	1.68E-04
11	KX885224			GU723752	Unknown (KU308386)		
11	KX943291			EF577267	Unknown (AM158955)		
11	KX885225			GU208521	Unknown (KR611578)		
11	KU569602			GU208522	Unknown (KT861469)		
11	KU569599			GU723753	Unknown (AJ314738)		

11	LC177332			GU723751	Unknown (KR611580)		
11	KF446674			EF577265			
11	KF446664			EU249458			
11	KF446670			GU208519			
11	KF446676			GU723754			
11	KF446666			GU723755			
11	KF446668						
11	KF446662						
11	KU569593						
11	KU569589						
11	KU569591						
11	KU569597						
11	KU569595						
11	KU569605						
11	KF218821						
11	KU569587						
11	AF511528						
11	AF511527						
11	KU569585						

12	^KT001508	1852 (1304)	2390 (1792)	Unknown (FN396963)	DQ641693	RMC**S**3	6.32E-12
'EACM-like viruses' subpopulation							
1	HE617300	1654 (1573)	2764 (2576)	AJ704944	Unknown (AF259897)	RGBMC**S**3	2.75E-54
2	^JF909227	2704 (2583)	1194 (1156)	JN165087	JF909229	RGBMC**S**	4.79E-48
2	JF909228			AF259897	JX679247		
3	^HE806429	542 (504)	1612 (1535)	HE806430	AJ704947	RGBMCS**3**	3.51E-20
4	AF230375	2770 (2638)	2955 (2776)	AJ704962	Unknown (AJ704968)	R**G**BMCS3	1.02E-12
5	^AF259897	2774 (2594)	2936 (2714)	Unknown (AJ704944)	HE979780	RGBM**C**S3	6.75E-55
5	JN165087			Unknown (AJ704940)	AJ704971		
6	^JX658684	2712 (2570)	2959 (2754)	AJ704943	JF909234	RGBMC**S**3	1.07E-12
6	AJ704949			AJ704941	JX679247		
6	AJ704935			AJ704942	AJ704955		
6	AJ704950			AF422175	AJ704970		
6	AJ704936			HE806430	AJ704967		
6	AJ704937			HE806429	AJ704969		
6	AJ704952			AJ628732	AJ704966		
6	AJ704951			AJ704945	AJ704956		
6	AJ704974			AJ704946	AJ704938		

6	AJ704953			AJ704948	AJ704968		
6	AJ704954			AJ704947	AJ704971		
6	AJ704934			AJ704944	AJ704972		
6	AJ704973				MH379641		
6	JF909213				KT780439		
7	JF909223	2774 (2642)	36 (34)	AJ704944	AJ704971	R**G**BMCS3	3.58E-11
8	^AF259897	2390 (2248)	2732 (2558)	Unknown (AJ704960)	JF909200	**R**BMC3	4.65E-08
8	JN165087			Unknown (AJ704971)	JF909232		
9	AJ704956	1088 (1049)	1610 (1533)	AJ704957	AJ704951	RM**C**S3	6.86E-08
9	AJ704955			HE979780	AJ704942		
9	AJ704970			HE979776	AJ704949		
9	AJ704967			HE979777	AJ704935		
9	AJ704969			AM502343	AJ704950		
9	AJ704966			AF126805	AJ704936		
9	AJ704938			AJ704958	AJ704937		
9	AJ704968			AJ704959	AJ704952		
10	^AJ704944	2769 (2631)	36 (33)	JF909208	Unknown (AJ704967)	R**G**BMCS3	4.66E-10
10	AJ704940			JF909253	Unknown (AJ704955)		
10	AJ704941			JF909224	Unknown (AJ704970)		

10	AJ704942			JF909225	Unknown (AJ704969)		
10	AF422175			JF909203	Unknown (AJ704966)		
10	HE806430			JF909232	Unknown (AJ704956)		
10	HE806429			JF909246	Unknown (AJ704938)		
10	AJ628732			JF909247	Unknown (AJ704968)		
10	AJ704945			JF909254	Unknown (AJ704971)		
10	AJ704946			JF909250	Unknown (AJ704972)		
10	AJ704948			JF909243	Unknown (MH379641)		
10	AJ704947			JF909244	Unknown (KT780439)		
10	AJ704943			JF909219	Unknown (AJ704963)		
11	^JN165087	1526 (1396)	1632 (1500)	JF909227	Unknown (JF909244)	**R**GMC3	1.19E-06
11	AF259897			JF909228	Unknown (JX679247)		
12	^AJ704967	1684* (1607*)	148 (136)	Unknown (JX679247)	AJ704971	MC**S**3	8.03E-14
12	AJ704955				AJ704960		
12	AJ704970						
12	AJ704969						
12	AJ704966						
12	AJ704956						
12	AJ704938						

12	AJ704968						
13	^JF909227	597 (560)	695 (658)	Unknown (HE806430)	JF909223	R**G**MS3	9.66E-04
13	JF909228				JF909214		
13	JX679247				JF909213		
14	^JF909211	886 (848)	1244 (1190)	JF909202	Unknown (JF909247)	RGMS**3**	6.74E-04
'Asia – Africa' subpopulation							
1	^KT444604	836 (424)	1771 (1199)	KT444610	JF694485	RGBMCS**3**	5.36E-47
2	^KT444606	4068 (2636)	1823 (1218)	JF694485	KT444602	RGBMCS**3**	1.66E-36
3	^KT444608	836 (424)	2996 (2171)	Unknown (JF694485)	KT444602	RGBMCS**3**	5.38E-33
3	KT444610						
3	KT444604						
4	^KT454812	1760 (1157)	3426 (2309)	KT454818	KT444616	GBM**3**	2.29E-28
5	^KT454818	1760 (1157)	4037 (2618)	KT454816	GQ472988	GBMS**3**	3.12E-28
5	KT454812			KT454810	GQ472986		
6	KT454810	1875 (1263)	3426 (2308)	KT454816	GQ472988	GBMS**3**	1.04E-27
7	^KY124281	162 (87)	3891 (2656)	Unknown (HG969288)	EU561236	RGMCS**3**	7.68E-17
7	KC462553						
8	^JF694485	2997* (2171*)	4068 (2636)	KT444610	KT444602	RMS**3**	3.10E-15

9	KP828155	441 (159)	2932 (2102)	LC271793	EU523046	**R**GBMS3	2.16E-14
10	KT444616	892 (388)	1760 (1157)	KT454814	GQ472988	**R**GBMCS3	6.55E-13
11	^KT454814	1849 (1237)	2637 (1842)	KT444618	GQ472988	**R**GBMCS3	3.58E-12
12	KT444614	4037 (2622)	892 (389)	KT444618	GQ472988	R**G**BMCS3	8.55E-11
13	^KP663484	1151 (626)	3086 (2178)	FM955609	KT878828	MCS**3**	1.97E-07
14	^AJ439057	3858 (2561)	16 (13)	FR714861	AJ582267	**R**GBS3	8.66E-07
14	KC911729			LC271793	JX244179		
14	AJ132574			AM992617	AF262064		
14	KC911724			FM955609			
14	AJ439059			LC271791			
15	^KU683746	1841 (1326)	2106 (1482)	KU683749	Unknown (AJ582267)	RBMC**3**	9.39E-08
15	KU683745			KU683750	Unknown (AM932426)		
15	KT454833			KT454835	Unknown (AJ627905)		
16	^AF262064	3250 (2222)	4034 (2645)	JX244180	JX244179	G**M**CS3	1.26E-06
17	^KT444610	48 (42)	835* (424*)	KT444608	KT444602	GBMCS**3**	3.12E-17
17	KT444604						
18	^AM932426	13 (11)	697 (314)	AJ627905	AM932430	R**G**MC	1.02E-06
19	^JN368447	1094 (572)	2859 (2042)	KY825716	Unknown (KT878830)		
19	GU323322			KY488569			

19	AM932430			KJ939447			
19	AM932426			KT272768			
19	KP752089			HG969288			
19	KC019307			KT272766			
19	AJ627905			KT272770			
19	AM932428			KT272772			
19	LC271793			JX131284			
19	FR714861			AJ012082			
19	AM992617			HM368372			
19	FM955609			EF201810			
19	LC271791						
19	KP779636						
19	LC271795						
19	AY271894						
19	KP779632						
19	FM161881						
19	FM955603						
19	KP779634						
19	AF416741						

19	AF142440						
19	MF693402						
19	KX363948						
19	KP828155						
19	EU523046						
19	AF503580						
19	DQ061273						
19	FM958506						
19	FM955606						
19	JQ327849						
19	JQ327848						
19	JN543396						
19	KC019305						
19	KP779631						
19	AY939925						
19	AY049771						
19	AY937196						
19	KX452231						
19	KX452230						

19	KX452229						
19	KY556680						
19	JN368440						
19	JN368445						
19	JN368441						
19	JN368443						
19	JN368442						
19	JN368446						
19	KU950431						
19	MF683073						
19	KP319017						
19	KP319016						
19	KF928962						
19	KF947526						
19	KC911729						
19	AJ439057						
19	AJ132574						
19	KC911724						
19	KC911725						

19	DQ400849						
19	KC911731						
19	AJ439058						
19	AJ439059						
19	KC911730						
19	KC911728						
19	KC911726						
19	KC911727						
19	FM242702						
19	FM955607						
19	JX244180						
19	JX244179						
19	JX244177						
19	JX244178						
19	JX244181						
19	AF262064						

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[i] Numbering starts at the first nucleotide after the cleavage site at the origin of replication and increases clockwise.

^ = The recombinant sequence may have been misidentified (one of the identified parents might be the recombinant).

[ii] * = The actual breakpoint position is undetermined (it was most likely overprinted by a subsequente recombinant event).

[iii] R, RDP; G, GeneConv; B, Bootscan; M, MaxChi; C, CHIMAERA; S, SisScan; 3, 3SEQ.

[iv] The reported P-value is for the program in bold, underlined type and is the lowest P-value calculated for that event.

CHAPTER 2

Same facts but different histories: accuracy in multiple sequence alignments and its impacts on virus phylogenomics[4]

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[4] Santos, M.M.; Morais-Júnior, I.J.; Polveiro, R.C.; Sassaki, F.T.; Lima A.T.M. Genetic structure of the global meta-population of begomoviruses based on DNA-B sequences. PLOS ONE, *in preparation*.

Same facts but different histories: accuracy in multiple sequence alignments and its impacts on virus phylogenomics

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Abstract

Viruses are the most diverse biological entities on Earth. A number of evolutionary and comparative genomic tools for understanding the processes that shape the genotypic variation in virus populations have been designed over the last few decades. In order to compare three or more nucleotide sequences, multiple sequence alignments (MSAs) are necessary and there are no studies measuring their degree of accuracy based on "real" full-length genomes of viruses. This work evaluated the accuracy of eight programs and their settings for construction of MSAs based on full-length genomes of single-stranded (ss)DNA viruses (begomoviruses and circoviruses), a ssDNA subviral agent (beta-satellites) and ssRNA viruses (flaviviruses and potyviruses). The degree of accuracy was inferred using a likelihood score (LS)-based approach. The programs that generated the highest scoring MSAs were used as 'references' for calculating the sum of pairs and the topological congruence between maximum likelihood (ML) phylogenetic trees. Our results indicated that T-Coffee and MAFFT-[FFT-NS-2] were the most accurate MSA programs for ssDNA and ssRNA genomes, respectively. No other program was able to construct MSAs with identical degree of accuracy or that gave rise to congruent ML-based trees when compared to those of the 'reference' programs. Here, we presented the practical implications of using different MSA programs focusing on phylogenomics of viruses and a subviral agent.

Key words: Likelihood score; MSA accuracy; Sum of pairs score; Topological congruence.

Introduction

The multiple sequence alignment (MSA) construction is a critical step for most studies on evolutionary and comparative genomics [1]. Obtaining an exact MSA is an NP-complete computational problem [2,3] which limits such task to a few short sequences, a non-realistic scenario given the vast currently available genomic data sets [4]. Due to computational constraints, MSA programs are based on heuristic methods [5,6] that provide optimized MSAs.

The heuristic-based progressive alignment method is widely used in MSA programs [7–9]. The MSAs are constructed following a pre-established hierarchical order to assess a number of computationally feasible arrangements. The programs ClustalO [10,11], ClustalW [12], Kalign [13,14], MAFFT [15,16], Muscle [17], ProbCons [18] and T-Coffee [19], for example, incorporate progressive alignment algorithms.

Assuming that there is no “universal” MSA program and those available were designed focusing on protein MSAs, they profoundly differ in terms of accuracy [20,21]. Such programs are also nucleotide alignment tools and have been widely used in Virology [22–27]. The degree of accuracy of an MSA is heavily dependent on the content of genetic variation and its distribution across the sequences or genomes in a given data set. Therefore, these critical parameters should be taken into account for choosing the optimal MSA program [28] for each input sequence data set [5]. To our knowledge, no study has been conducted to guide the choice of the optimal program for data sets containing “real” (here defined as non-simulated or not artificially created) virus full-length genomes available in public databases.

Viruses are the most abundant and genetically diverse biological entities on Earth [29]. Their genomes show reduced sizes [30], high mutation rates [31] and a number of compacted and novel genes [29,32] even compared with genomes of cellular organisms. MSAs for virus phylogenomics [33–35] based on high taxonomic categories, *e.g.* genus or above, may incorporate extremely divergent sequences, which might give rise to further issues on reliability of homologous site comparisons and the presumable relationship with other virus groups (low accuracy in tree topologies).

In this work, we evaluated the accuracy of commonly used MSA programs and their impact on genus-based phylogenomics for ssDNA and ssRNA genomes. Our results indicate that MSA programs commonly used in Virology show different degrees of accuracy. Finally, the several aligned versions of the same data set led to incongruent tree topologies suggesting that the inferred evolutionary histories described in published studies might not be the most likely ones.

Material and methods

Sequence data sets

Five genus-based sequence data sets containing full-length genomes of reference isolates, one from each ICTV-approved species, were retrieved from Genbank on July 2019 (Supplementary Table 1). Only genera comprised of, at least, 35 full-length genomes of reference isolates from distinct virus species were used in this study. Two out of five data sets were based on genomes of ssDNA viruses (genus *Begomovirus*, $N = 408$ and 148 sequences of DNA-A and DNA-B, respectively; and genus *Circovirus*, $N = 39$), a ssDNA begomovirus-associated subviral agent (genus *Betasatellite*, $N = 61$ genomes) and ssRNA viruses (genera *Flavivirus* and *Potyvirus*, $N = 47$ and 125 genomes, respectively).

A number of data subsets were generated by random sampling without replacement of the genera data sets (2,000 and 1,000 for DNA-A and DNA-B, respectively; 500 and 400 for beta-satellites and circoviruses; and 500 and 1000 flaviviruses and potyviruses, respectively). Data subsets consisted of variable sample sizes each, roughly equivalent to those of the original genus-based data sets ($N = 200$ and 70 full-length sequences of DNA-A and DNA-B, respectively; $N = 25$ and 20 genomes of beta-satellites and circoviruses, respectively; and $N = 25$ and 60 genomes of flaviviruses and potyviruses, respectively).

MSAs construction

MSAs were constructed for each data subset using eight distinct programs-[and their settings], totalizing 13 distinct combinations (Table 1). In this study, all parameters for inferring the accuracy of MSA programs were retrieved from 26,000 and 13,000 DNA-A and DNA-B-based-MSAs, respectively; 6,500 and 5,200 beta-satellites- and circoviruses-based MSAs; 6,500 and 13,000 flaviviruses- and potyviruses-based MSAs; totalizing 70,200 alignments.

Comparative analyses of accuracy provided by each MSA program-[setting]

The degree of accuracy from all MSAs was indirectly inferred by the likelihood score (LS) of their associated ML-trees ($N = 70{,}200$ trees) generated in RAxML [36] (ML-trees are available from the authors upon request). The LS comparability was possible by keeping constant the nucleotide substitution model (GTR-GAMMA) for inference of the best ML-tree and the sequence composition of each of the MSAs generated from a given data subset.

The programs-[settings] that generated the highest scoring MSAs were considered as ‘references’ for the subsequent comparative analyses. Pairwise comparisons between ‘reference’ MSAs and the remaining ones were conducted by calculating the sum of pairs (SP) scores using FastSP program [37]. The SP scores indicate the degree of similarity between pairs of MSAs and vary from ‘zero’ to ‘one’ (‘one’ denotes identical MSAs).

Measuring topological congruence between ML-trees

To evaluate the practical implications of MSAs accuracy on virus phylogenomics, the topological congruence between ML-trees generated from ‘reference’ MSAs and the remaining ones were quantified by their numbers of exclusive clades (EC) using the package Ape v.5 [38] in R-project [39]. The lower is the number of EC between two ML-trees derived from MSAs with identical sequence composition, the higher is the topological congruence.

Statistical analyses

The statistical significance of all metrics used in this study (LS, SP scores and number of exclusive clades) was evaluated by estimating their 95% bootstrap confidence intervals from 15,000 nonparametric simulations using the package Simpleboot [40] in R-project [39].

Results

Distinct degrees of accuracy provided by MSA programs

We assumed the premise that the distinct features of genetic variation, intrinsic to each viral or subviral group, might impose distinct degrees of constraints for obtaining an optimized MSA. In other words, the greater content of genetic variation in a given viral data set provides a considerable wider MSA space (here defined as the set of all possible MSAs for a given sequence data set) which frequently leads to lower degrees of accuracy. In an attempt of sampling the viral diversity in a more representative manner, we conducted analysis to evaluated the accuracy of MSAs based on ssDNA genomes of begomoviruses (DNA-A and DNA-B components), beta-satellites (begomovirus-associated subviral agents), circoviruses and ssRNA genomes of flaviviruses and potyviruses. In addition, we generated data subsets by random resampling without replacement to simulate different scenarios of genetic variation in each genus data set. Using this strategy, we created a spectrum of genetic variation as broad and continuous as possible, from which the degree of accuracy of its derived MSAs (generated by eight distinct programs-[settings]) was estimated by likelihood scores.

For a preliminary description of this spectrum of genetic variation, we calculated the nucleotide diversity index (π) and its associated 95% bootstrap confidence interval for each of the 5,400 data subsets (Figures 1 and 2). It is important to note that even for those viral groups in which many data subsets showed statistically similar contents of genetic variation (such as the subsets for genomes of circoviruses, flaviviruses and potyviruses; Figures 1d, 2a-b, respectively), different types of nucleotide diversity were incorporated, which also made them qualitatively informative.

T-Coffee and MAFFT-[FFT-NS-2] generated the highest MSAs scoring for ssDNA and ssRNA viral genomes, respectively (Figures 3 and 4). It is important to emphasize that MSAs derived from widely used programs in Virology, Muscle and ClustalW, showed intermediate or low degrees of accuracy. In addition, MSAs generated by Muscle-[Refined] did not show statistically significant gains of accuracy compared to those from Muscle-[Default].

The variation in degrees of accuracy was dramatic for the ProbCons program. It was among the three most accurate programs for data subsets based on the DNA-A of begomoviruses, beta-satellites and circoviruses (Figure 3a, 3c-d). In contrast, it was among the three worst for the DNA-B of begomoviruses (Figure 3b) and, the worst one for ssRNA viruses (Figure 4a-b). The Kalign and ClustalO-[all settings] provided the lowest MSAs scoring (Figures 3 and 4). Curiously, there was a decrease in accuracy in most cases when using more iterations in ClustalO-[iter1, iter2 and iter3] (Figures 3 and 4).

Pairwise comparisons between MSAs

Taking T-Coffee and MAFFT-[FFT-NS-2] as 'references' for ssDNA and ssRNA viral genomes, respectively, we evaluated the similarity of their MSAs (also referred as 'reference' MSAs) with those generated in the remaining programs-[settings] by calculating the SP scores. This additional parameter quantifies the similarity shared between pairs of MSAs and returns values from 'zero' to 'one', in which the value "one" denote identical MSAs. The MSAs generated by T-Coffee were most similar to those of ProbCons and MAFFT-[L-INS-i] (Figure 5). In contrast, as expected from the previous results, the ProbCons program provided the most dissimilar MSAs to those of MAFFT-[FFT-NS-2] based on ssRNA genomes.

Effects of MSAs accuracy on ML-tree topologies

Differences in MSAs may be expressed in their associated ML-phylogenetic trees. The inference of accurate ML-trees is heavily dependent on the determination of the best-fit nucleotide substitution model and the provision of a highly accurate MSA. Under these conditions, the evolutionary history represented in a ML-tree is the most likely one, given the sequence data set (which should be aligned at the highest possible degree of accuracy) and the nucleotide substitution model. In this context, we investigated whether the different degrees of accuracy provided by each of the MSA programs-[settings] would affect the ML-tree topology when based on identical sequence composition.

The ML-trees derived from 'reference' MSAs were compared with the remaining ones and did not show complete topological congruence in any case (Figures 7 and 8). For ssDNA and ssRNA viral genomes, ML-trees derived from MSAs generated by Kalign and ProbCons, respectively, were the most incongruent from those derived from 'reference' MSAs. The highest degree of incongruence was observed for ML-trees based on potyvirus genomes, in which the mean number of EC between the ML-trees based on 'reference' MSAs and ProbCons was 0.82 (Figure 8b). In ML-trees based on genomes of flaviviruses, MSAs derived from MAFFT-[L-INS-i] and ClustalO [all settings] yielded ML-trees with less than a EC, but still statistically different from zero, *i.e.*, showed high topological congruence with ML-trees derived from 'reference' MSAs (Figure 8a). In summary, our results indicate that the distinct degrees of accuracy provided by each MSA program-[setting] lead to incongruent ML-trees. It is important to emphasize that T-Coffee and MAFFT programs are less frequently used in the field of Virology than Muscle and ClustalW. Therefore, it is reasonable to suppose that the inferred evolutionary histories based on MSAs derived from these latter programs might not be the most likely ones.

Discussion

In this study, MSAs constructed for genomes of viruses and a subviral agent showed different degrees of accuracy when based on a same kind of nucleic acid (ssDNA or ssRNA) and even between genome segments of the same viruses, as observed for the DNA-A and DNA-B of begomoviruses. The greater accuracy of MSAs generated by T-Coffee program is explained by the consistency strategy adopted in its algorithm. Guide trees in T-Coffee are inferred after obtaining the best pairwise sequence alignments and also considering their scores added of a third nucleotide sequence [19]. In this strategy, low similarity sequence pairs in the guide tree are avoided, which is progressively continued preserving its accuracy. The ProbCons program [18] and MAFFT-[L-INS-i] [16] are also based on variations in the consistency, but it was not enough to make them similarly accurate for the data sets analyzed in this study.

To build their guide trees, ClustalW, Kalign, Muscle and MAFFT-[FFT-NS-2] calculate the distances between sequence pairs using ‘k-mers’ [12,14,15,17]. Such approximation does not require a pairwise alignment step, which can compromise the accuracy of the final MSA [41]. However, Muscle and MAFFT-[FFT-NS-2] use iterations to improve the accuracy of their MSAs. For ClustalW and Kalign programs, the first complete MSAs are already the final MSAs, while in the other ones, the first MSAs are used to recalculate the distances among their sequences using the aligned sequence pairs, and, from them, to build a new guide tree. In MAFFT-[FFT-NS-2], the next complete MAS is its final MSA [15]. In Muscle, the second MSA is compared to the first one and the best is used to restart the iterative cycle that extends a higher number of times than that of MAFFT-[FFT-NS-2], which conducts only one iteration (the number of iterations may also be determined by the user) [17]. Muscle-[Refined] applies even more iterative cycles than Muscle-[Default]. Therefore, among these four programs-[settings], it was expected that the degree of accuracy would be higher for those which applies more iterations, a contrasting scenario compared to our results in which a higher number of iterations did not implicate in gains of accuracy.

MAFFT-[FFT-NS-2] and -[L-INS-i] show substantial differences in their algorithms [15,16]. The MAFFT-[FFT-NS-2] is computationally simpler and, therefore, recommended for large data sets (approx. 5,000 sequences). In contrast, MAFFT-[L-INS-i] [16] is significantly more accurate, since it uses the Smith-Waterman algorithm [42] to align the sequences pairs and obtain a complete distance matrix to build its guide tree. This latter setting also employs a mixed score function, which combines an iterative refinement function [43] similar to the predecessor version of T-Coffee [44]. Such complexity makes this setting recommended for data sets of up to 200 sequences (a common feature of all data subsets analyzed in this study) and it is expected that the accuracy of its MSAs is higher than those of MAFFT-[FFT-NS-2] [16]. Contrary to this premise, for the genomes analyzed in this study, the degree of accuracy of MAFFT-[L-INS-i] MSAs was not higher than those of MAFFT-[FFT-NS-2].

The ClustalO program was designed for large scale MSAs [10,11]. For data sets with more than 100 sequences (such as those subsets based on DNA-A of begomoviruses), the mBed algorithm [45] is employed in the construction of its guide trees. This algorithm uses a method of spatial incorporation that allows approximating the relationship between sequences without necessarily computing the distance between all possible sequence pairs [10,11,45]. Guided by this tree, the MSA is continued progressively. In constrast, considering that this program was especially designed for data sets with more than 10,000 sequences [10] and that such condition was not analyzed in this study, its algorithm may have been underused in our analyses. Amongst its settings, the only difference between ClustalO-[Default] and ClustalO-[Kimura] is that the latter applies Kimura correction for MSA construction; however, there was no increase in accuracy. ClustalO-[iter1, iter2 and iter3) showed reduced degree of accuracy compared with ClustalO-[Default]. Unlike Muscle, in ClustalO program the iterative cycle is always restarted by the last complete MSA. Therefore, the best MSA is the first to be generated (such as in ClustalO-[Default]) and its iterations, for the conditions analyzed in this study were not viable.

Interestingly, the MSA programs were not ranked according to the similarities in their algorithms. The highest scoring MSAs generated by T-Coffee and MAFFT-[FFT-NS-2] exemplify this scenario. Both use progressive strategies, but with drastic differences during the process of MSA construction. In fact, the similarity analyses (Figure 5 and 6) revealed that their MSAs are not the most similar ones. However, the similarity with the 'reference' MSAs did not implicate that their degrees of accuracy were similar and that their associated ML-trees were less incongruent. For ssDNA genomes, the ProbCons program yielded the most similar MSAs to those considered as 'references', but its trees were not the most congruent. For ssRNA genomes, both MAFFT settings, despite the differences in their algorithms, yielded the most similar MSAs and ML-trees. These settings and those of Muscle, which show similar strategies, generated similar MSAs, but incongruent ML-trees.

Taking into account the viral and subviral groups analyzed in this study, T-Coffee and MAFFT-[FFT-NS-2] were the most accurate MSA programs-[setting] for ssDNA and ssRNA viral genomes, respectively. No other aligner built identical MSAs or congruent ML-trees. Similar results to those obtained in this work have been shown for protein-based MSAs [46].

Our results indicate that the choice of a MSA program directly affects the results of subsequent analyses, such as those presented here for viral phylogenomics. In addition, the LS approach was a useful and informative metrics for large-scale estimate of accuracy in MSAs based on viral genomes.

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Table 1. MSA programs and settings used in this study.

Program	**Setting**	**Main algorithm**	**Reference**
Clustal Omega[1] v.1	Default Iter 1 Iter 2 Iter 3 Kimura	Progressive	[10,11]
ClustalW v.2	Default	Progressive	[12]
Kalign v.2	Default	Progressive	[14]
MAFFT[1] v.7	FFT-NS-2 L-INS-i	Iterative/Consistency	[15,16]
Muscle v.3	Default Refined	Iterative	[17]
ProbCons v.1	Default	Consistency	[18]
T-Coffee v.1	Default	Consistency	[19]

[1] Multi-core mode: 4 CPUs

Figure legends

Figure 1. Nucleotide diversity (π, 'x' axis) and their associated 95% bootstrap confidence intervals (CIs) calculated for each data subset ('y' axis) containing ssDNA genomes of begomoviruses (DNA-A and DNA-B, **a** – **b**, respectively), beta-satellites (**c**) and circoviruses (**d**). Ninety-five percent bootstrap confidence intervals (CIs) were estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40]. Overlapping CIs indicate that the difference between π values is not statistically significant.

Figure 2. Nucleotide diversity (π, 'x' axis) and their associated 95% bootstrap confidence intervals (CIs) calculated for each data subset ('y' axis) containing ssRNA genomes of flaviviruses (**a**) and potyviruses (**b**). Ninety-five percent bootstrap confidence intervals (CIs) were estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40]. Overlapping CIs indicate that the difference between π values is not statistically significant.

Figure 3. Degree of accuracy in MSAs estimated indirectly by likelihood scores (LS) of their associated ML-trees for ssDNA genomes of begomoviruses (DNA-A and DNA-B, **a** – **b**, respectively), beta-satellites (**c**) and circoviruses (**d**). Bars with identical letters denote means that do not differed statistically by their 95% bootstrap confidence intervals estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40].

Figure 4. Degree of accuracy in MSAs estimated indirectly by likelihood scores (LS) of their associated ML-trees for ssRNA genomes of flaviviruses (**a**) and potyviruses (**b**). Bars with identical letters denote means that do not differed statistically by their 95%

bootstrap confidence intervals estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40].

Figure 5. Mean sum of pairs (SP) scores calculated between ‘references’ and lower scoring MSAs for ssDNA genomes of begomoviruses (DNA-A and DNA-B, **a** – **b**, respectively), beta-satellites (**c**) and circoviruses (**d**). Ninety-five percent bootstrap confidence intervals (CIs) were estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40]. Overlapping CIs indicate that the difference between mean SP scores is not statistically significant.

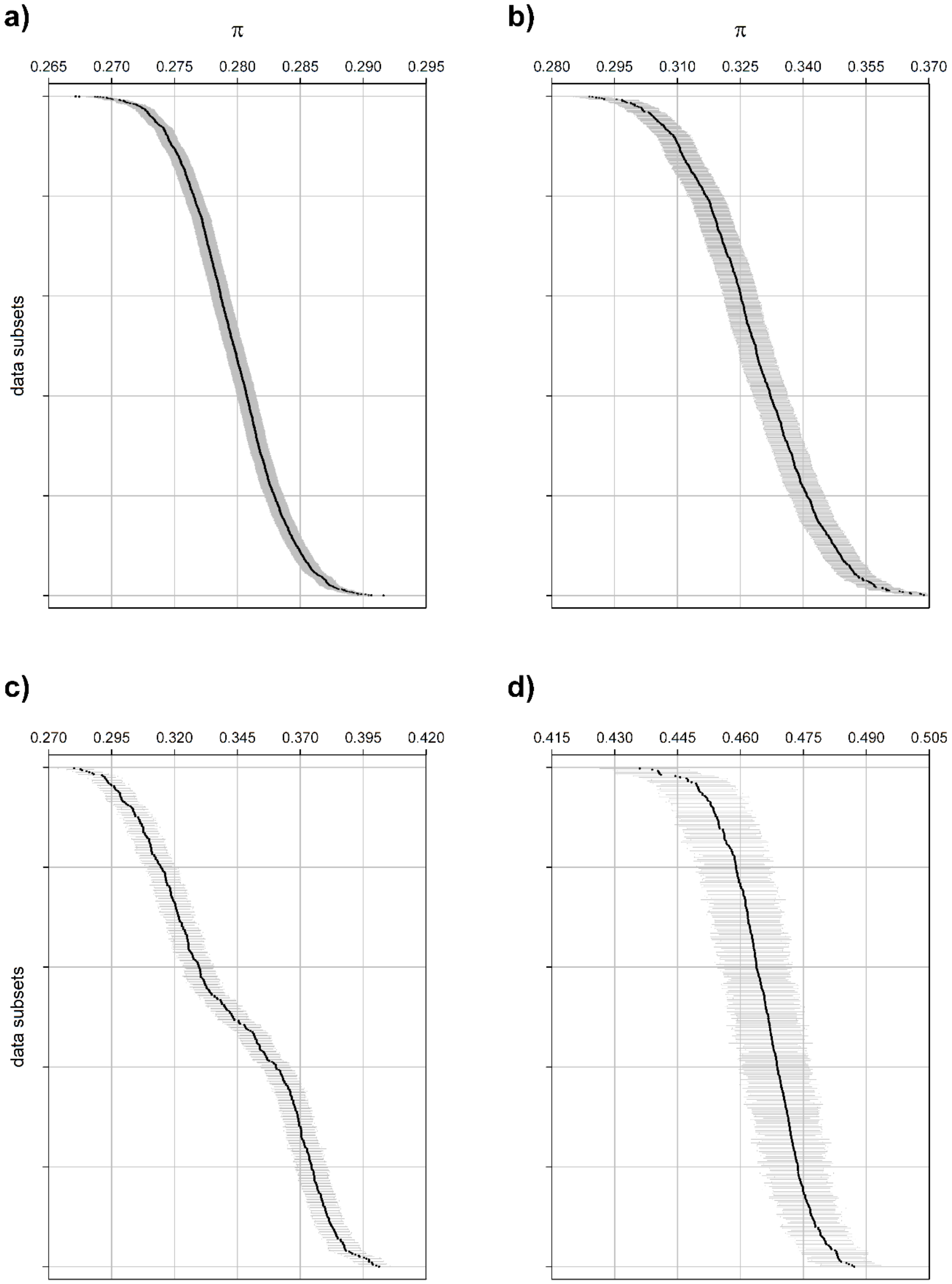
Figure 6. Mean sum of pairs (SP) scores calculated between ‘references’ and lower scoring MSAs for ssRNA genomes of flaviviruses (**a**) and potyviruses (**b**). Ninety-five percent bootstrap confidence intervals (CIs) were estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40]. Overlapping CIs indicate that the difference between mean SP scores is not statistically significant.

Figure 7. Mean fraction of exclusive clades (EC) calculated between ML-trees derived from ‘references’ and lower scoring MSAs for ssDNA genomes of begomoviruses (DNA-A and DNA-B, **a** – **b**, respectively), beta-satellites (**c**) and circoviruses (**d**). Ninety-five percent bootstrap confidence intervals (CIs) were estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot statistical package [40]. Overlapping CIs indicate that the difference between mean fractions of EC is not statistically significant. Values equal to ‘one’ denote complete topological incongruence.

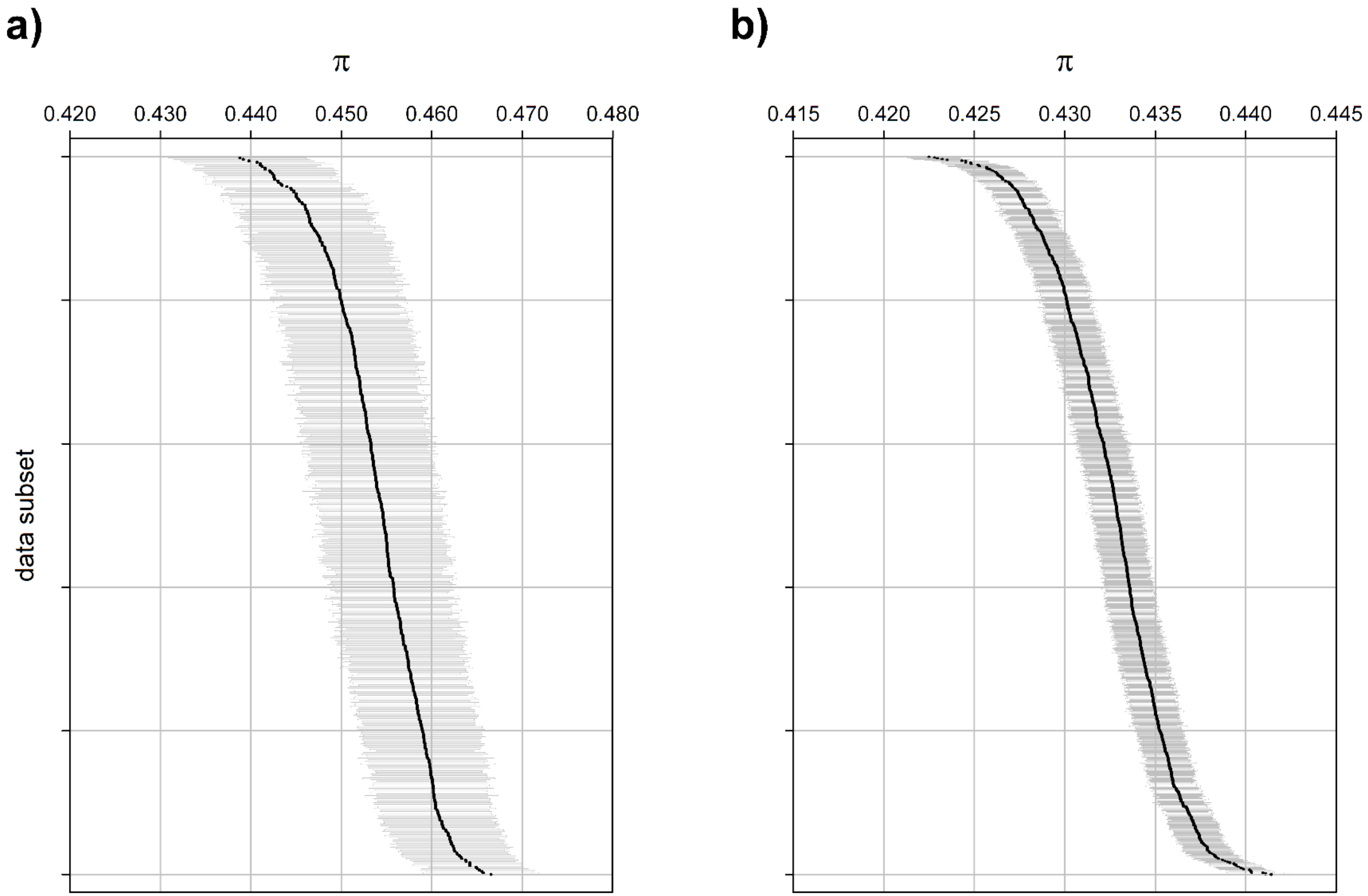
Figure 8. Mean fraction of exclusive clades (EC) calculated between ML-trees derived from ‘references’ and lower scoring MSAs for ssRNA genomes of flaviviruses (**a**) and potyviruses (**b**). Ninety-five percent bootstrap confidence intervals (CIs) were estimated from 15,000 nonparametric simulations in R software [39] using the Simpleboot

statistical package [40]. Overlapping CIs indicate that the difference between mean fractions of EC is not statistically significant. Values equal to ‘one’ denote complete topological incongruence.

Figure 1


a)
π
0.265
0.270
0.275
0.280
0.285
0.290
0.295
data subsets
b)
π
0.280
0.295
0.310
0.325
0.340
0.355
0.370
c)
0.270
0.295
0.320
0.345
0.370
0.395
0.420
data subsets
d)
0.415
0.430
0.445
0.460
0.475
0.490
0.505

464 **Figure 2**



465

Figure 3

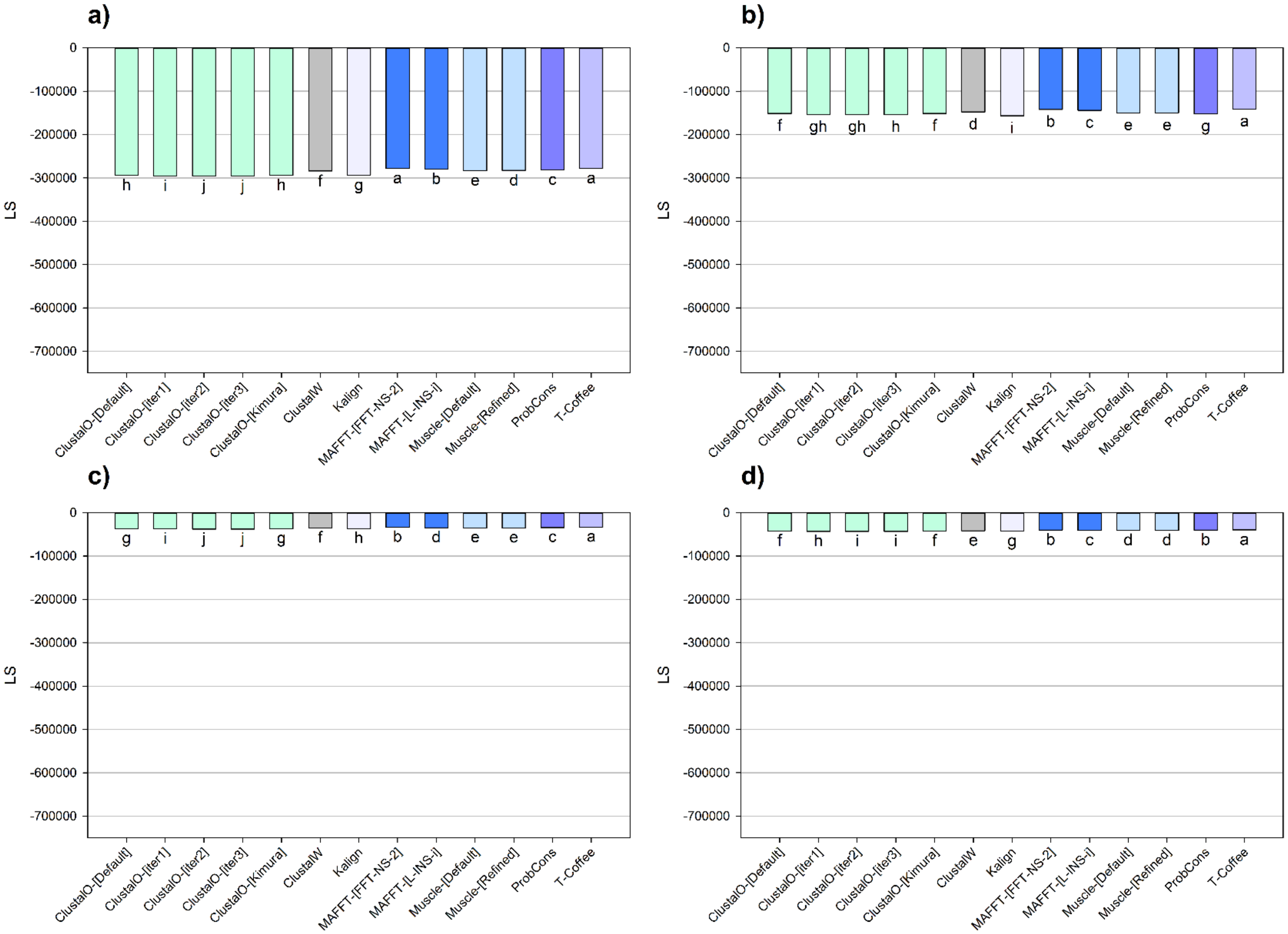
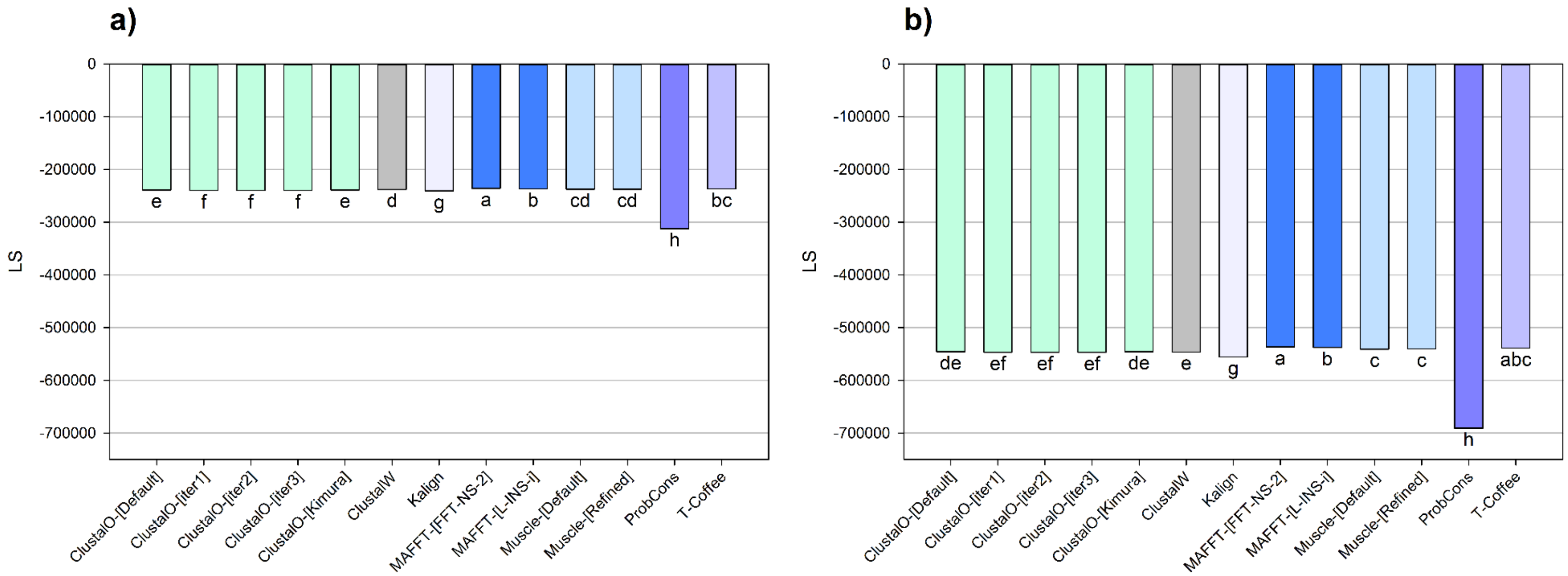

a)
b)
c)
d)
LS
0
-100000
-200000
-300000
-400000
-500000
-600000
-700000
ClustalO-[Default]
ClustalO-[iter1]
ClustalO-[iter2]
ClustalO-[iter3]
ClustalO-[Kimura]
ClustalW
Kalign
MAFFT-[FFT-NS-2]
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
T-Coffee
a) h i j j h f g a b e d c a
b) f gh gh h f d i b c e e g a
c) g i j j g f h b d e e c a
d) f h i i f e g b c d d b a

Figure 4


a)
b)
LS
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-300000
-400000
-500000
-600000
-700000
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b): de ef ef ef de e g a b c c h abc
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ClustalW
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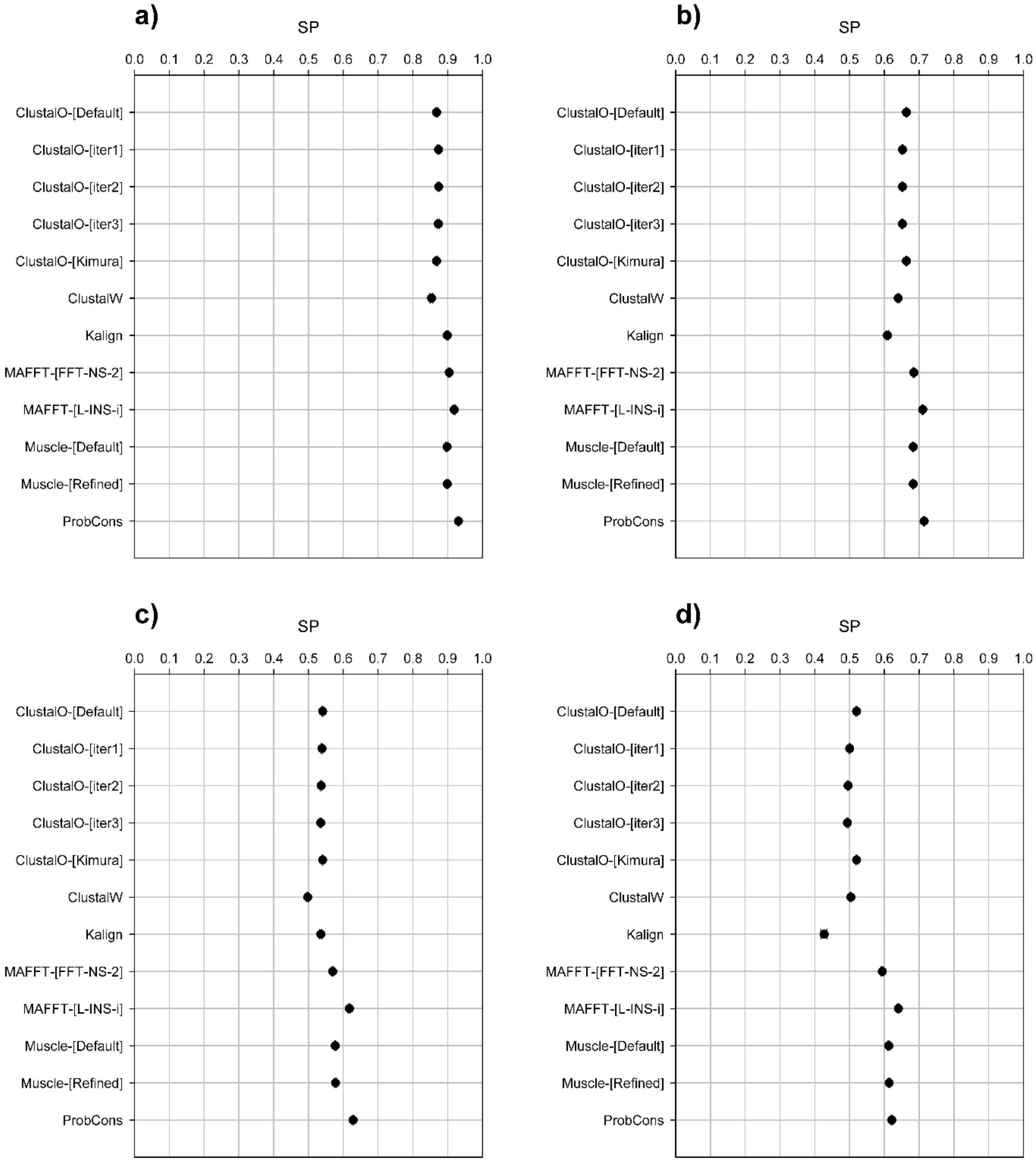
Muscle-[Default]
Muscle-[Refined]
ProbCons
T-Coffee

Figure 5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ClustalO-[iter3]
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ClustalW
Kalign
MAFFT-[FFT-NS-2]
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
b)
SP
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0.1
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0.6
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1.0
ClustalO-[Default]
ClustalO-[iter1]
ClustalO-[iter2]
ClustalO-[iter3]
ClustalO-[Kimura]
ClustalW
Kalign
MAFFT-[FFT-NS-2]
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
c)
SP
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0.3
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0.5
0.6
0.7
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0.9
1.0
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ClustalO-[iter1]
ClustalO-[iter2]
ClustalO-[iter3]
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ClustalW
Kalign
MAFFT-[FFT-NS-2]
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
d)
SP
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0.3
0.4
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0.7
0.8
0.9
1.0
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ClustalO-[iter2]
ClustalO-[iter3]
ClustalO-[Kimura]
ClustalW
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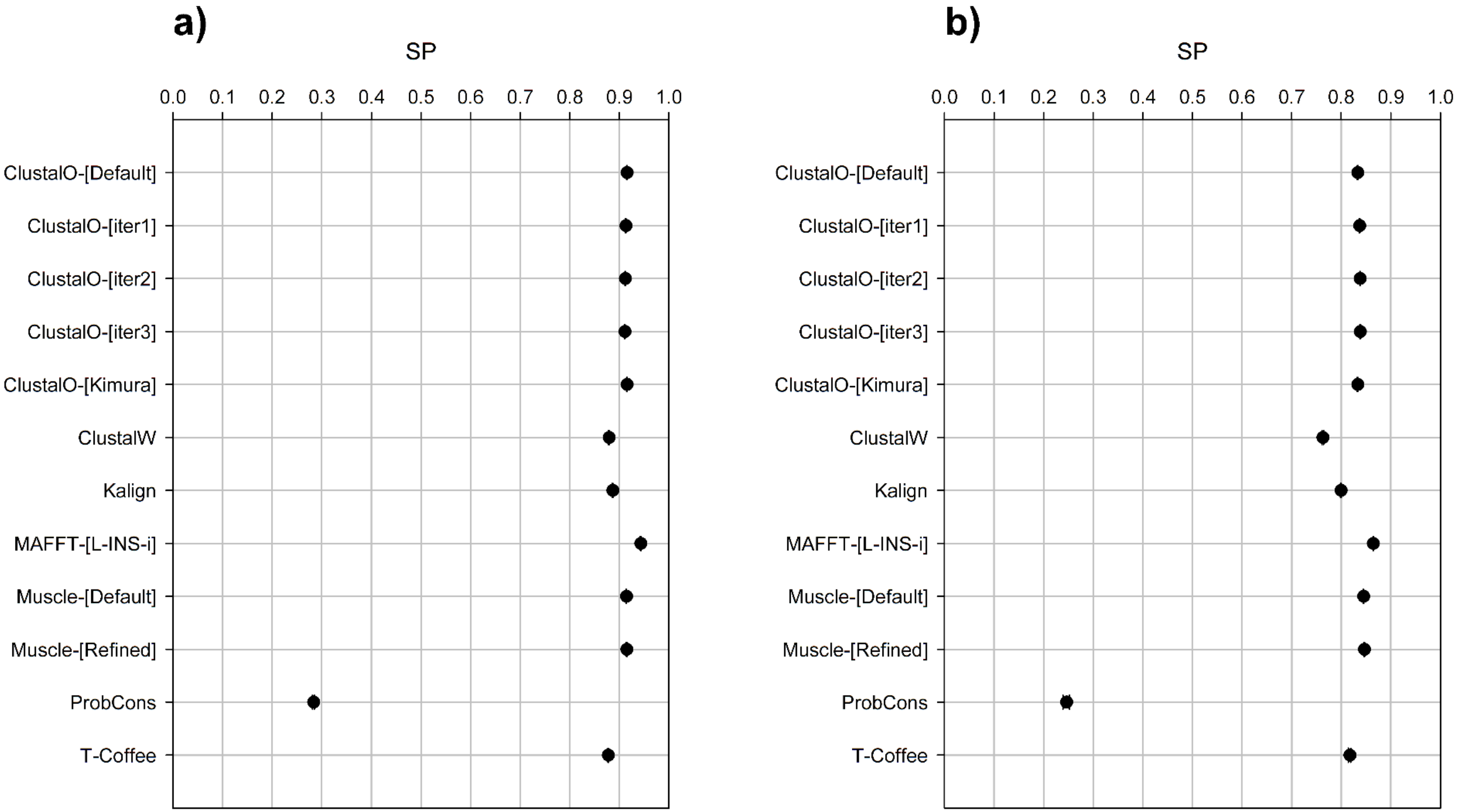
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons

Figure 6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ClustalO-[Default]
ClustalO-[iter1]
ClustalO-[iter2]
ClustalO-[iter3]
ClustalO-[Kimura]
ClustalW
Kalign
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
T-Coffee
b)
SP
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0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
ClustalO-[Default]
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Kalign
MAFFT-[L-INS-i]
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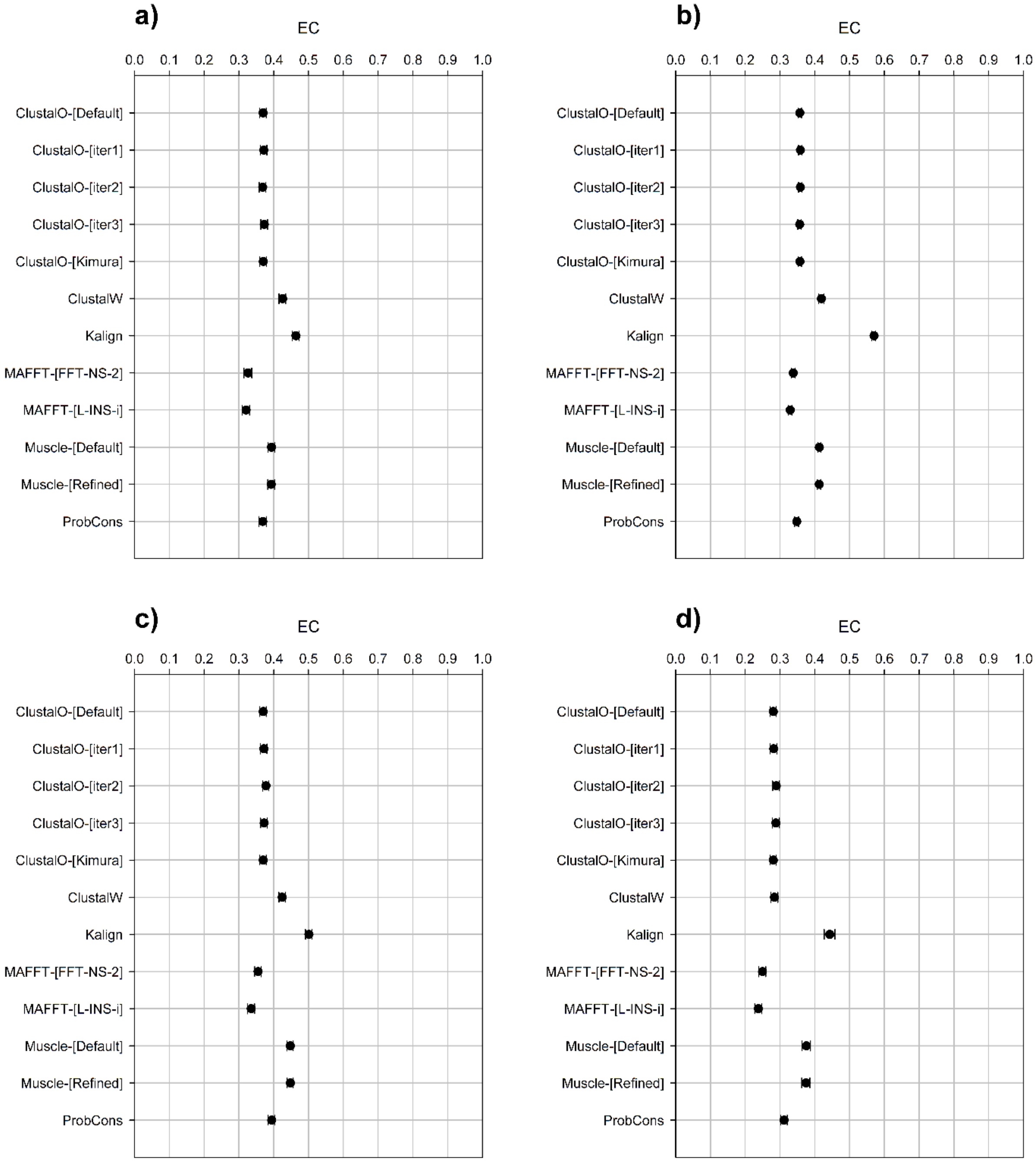
ProbCons
T-Coffee

Figure 7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ClustalO-[Kimura]
ClustalW
Kalign
MAFFT-[FFT-NS-2]
MAFFT-[L-INS-i]
Muscle-[Default]
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ProbCons
b)
EC
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ClustalO-[iter3]
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ClustalW
Kalign
MAFFT-[FFT-NS-2]
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
c)
EC
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ClustalO-[Default]
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ClustalO-[iter3]
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Muscle-[Default]
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ProbCons
d)
EC
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ClustalO-[Kimura]
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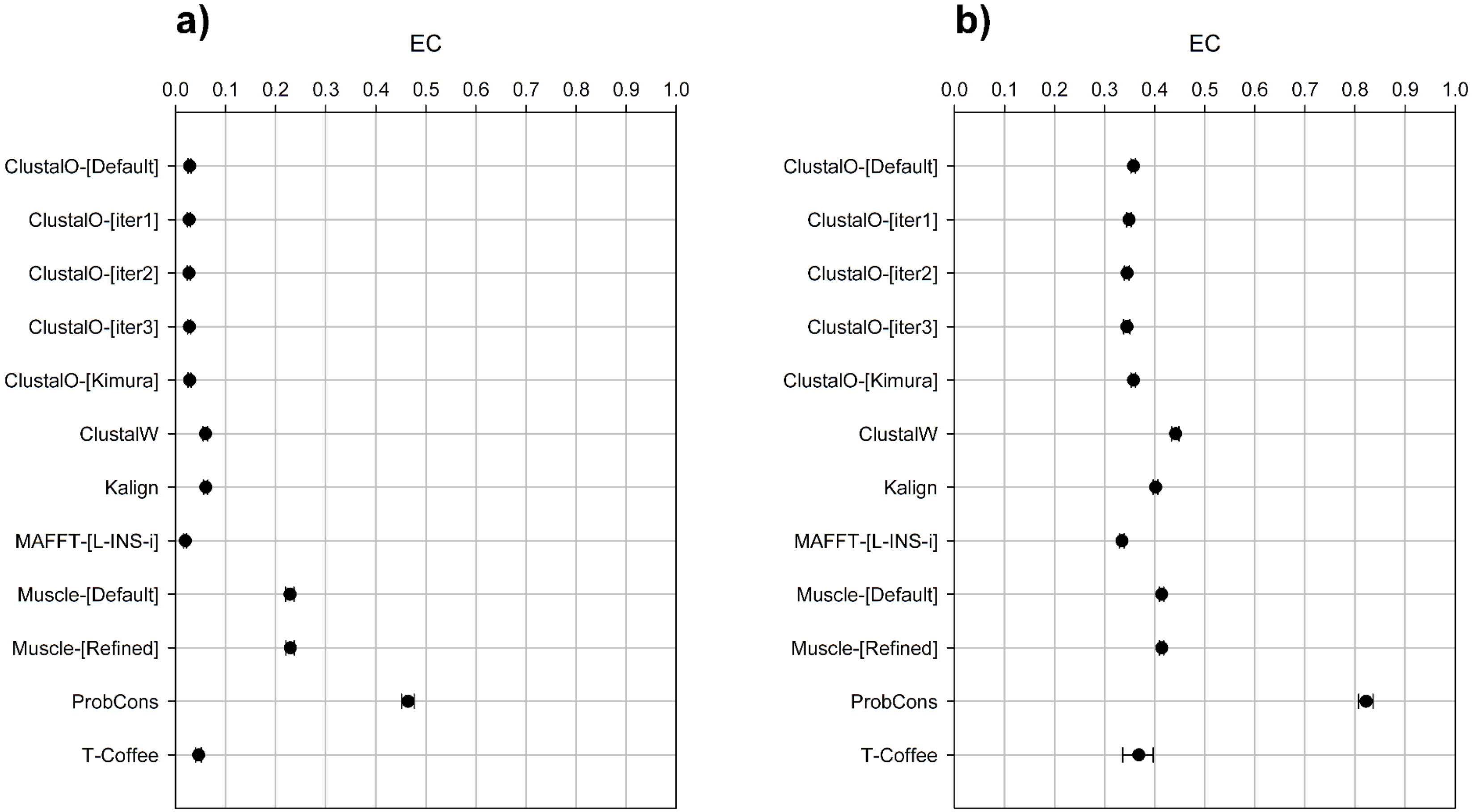
Muscle-[Refined]
ProbCons

Figure 8


a)
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0.8
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ClustalO-[Default]
ClustalO-[iter1]
ClustalO-[iter2]
ClustalO-[iter3]
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ClustalW
Kalign
MAFFT-[L-INS-i]
Muscle-[Default]
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ProbCons
T-Coffee
b)
EC
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0.5
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0.9
1.0
ClustalO-[Default]
ClustalO-[iter1]
ClustalO-[iter2]
ClustalO-[iter3]
ClustalO-[Kimura]
ClustalW
Kalign
MAFFT-[L-INS-i]
Muscle-[Default]
Muscle-[Refined]
ProbCons
T-Coffee

Supplementary Table 1. Full-length genomes used in this study

Genus	**GenBank access #**	**Species**	**Country**	**Host**
Begomovirus (DNA-A)	AB007990	*Eupatorium yellow vein virus*	Japan	*Eupatorium makinoi*
	AB050597	*Tomato leaf curl Philippines virus*	Philippines	*Solanum lycopersicum*
	AB085793	*Squash leaf curl Philippines virus*	Philippines	*Cucurbita moschata*
	AB100304	*Tomato leaf curl Java virus*	Indonesia	*Nicotiana benthamiana*
	AB236323	*Tomato leaf curl Japan virus*	Japan	*Lonicera caprifolium*
	AB267834	*Pepper yellow leaf curl Indonesia virus*	Indonesia	-
	AF012300	*Tomato mottle Taino virus*	Cuba	-
	AF029217	*Cowpea golden mosaic virus*	Nigeria	*Vigna* sp.
	AF049336	*Sida golden mosaic virus*	USA	*Sida santaremnensis*
	AF068636	*Merremia mosaic virus*	Puerto Rico	*Merremia quinquefolia*
	AF101476	*Chino del tomate virus*	Mexico	-
	AF104036	*Sweet potato leaf curl virus*	USA	*Ipomoea* sp.
	AF110189	*Bean calico mosaic virus*	Mexico	*Phaseolus vulgaris*
	AF112354	*East African cassava mosaic Cameroon virus*	Cameroon	*Manihot esculenta*
	AF126406	*Mungbean yellow mosaic India virus*	India	-
	AF126806	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*
	AF130415	*Tomato severe leaf curl virus*	Guatemala	*Solanum lycopersicum*

AF134484	*Pepper leaf curl virus*	Thailand	-
AF139168	*Dicliptera yellow mottle virus*	USA	*Dicliptera sexangularis*
AF141922	*Tomato yellow leaf curl Thailand virus*	Thailand	-
AF155806	*South African cassava mosaic virus*	South Africa	*Manihot esculenta*
AF188481	*Tomato leaf curl Bangladesh virus*	Bangladesh	-
AF189018	*Tomato yellow leaf curl Indonesia virus*	Indonesia	*Solanum lycopersicum*
AF195782	*Tomato leaf curl Laos virus*	Laos	-
AF224760	*Cucurbit leaf crumple virus*	USA	*Cucurbita* sp.
AF241479	*Bhendi yellow vein mosaic virus*	India	*Abelmoschus esculentus*
AF260241	*Cotton leaf curl Gezira virus*	Sudan	*Gossypium* sp.
AF261885	*Tomato curly stunt virus*	South Africa	-
AF264063	*Tomato leaf curl Vietnam virus*	Viet Nam	*Solanum lycopersicum*
AF271234	*Tomato yellow leaf curl Malaga virus*	Spain	-
AF274349	*Tomato leaf curl Sri Lanka virus*	Sri Lanka	*Solanum lycopersicum*
AF291705	*Tomato rugose mosaic virus*	Brazil	*Solanum lycopersicum*
AF311734	*Tomato yellow leaf curl China virus*	China	*Solanum lycopersicum*
AF314144	*Ageratum yellow vein Sri Lanka virus*	Sri Lanka	-
AF314531	*Pepper leaf curl Bangladesh virus*	Bangladesh	*Capsicum annuum*
AF326775	*Sweet potato leaf curl Georgia virus*	USA	*Ipomoea batatas*

AF327436	*Tomato leaf curl Malaysia virus*	Malaysia	*Solanum lycopersicum*
AF336806	*Chilli leaf curl virus*	Pakistan	*Capsicum annuum*
AF350330	*Tobacco leaf curl Zimbabwe virus*	Zimbabwe	*Nicotiana tabacum*
AF421552	*Squash mild leaf curl virus*	USA	-
AF422174	*East African cassava mosaic Zanzibar virus*	Tanzania	*Manihot esculenta*
AF480940	*Cotton leaf crumple virus*	Mexico	*Gossypium* sp.
AF490004	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*
AF509739	*Luffa yellow mosaic virus*	Viet Nam	*Luffa acutungula*
AF509743	*Squash leaf curl China virus*	Viet Nam	*Cucurbita* spp.
AF511529	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum lycopersicum*
AJ002449	*Cotton leaf curl Kokhran virus*	Pakistan	*Abelmoschus esculentus*
AJ002455	*Cotton leaf curl Alabad virus*	Pakistan	*Abelmoschus esculentus*
AJ006460	*East African cassava mosaic Malawi virus*	Malawi	*Manihot esculenta*
AJ012081	*Watermelon chlorotic stunt virus*	Yemen	*Citrullus lanatus*
AJ223191	*Chayote yellow mosaic virus*	Nigeria	*Sechium edule*
AJ314737	*Sri Lankan cassava mosaic virus*	Sri Lanka	*Nicotiana benthamiana*
AJ420319	*Squash leaf curl Yunnan virus*	China	*Cucurbita* sp.
AJ437618	*Ageratum enation virus*	Nepal	*Ageratum conyzoides*
AJ438937	*Eupatorium yellow vein mosaic virus*	Japan	*Eupatorium makinoi*

AJ457824	*Malvastrum yellow vein virus*	China	*Malvastrum coromandelianum*
AJ457986	*Tobacco curly shoot virus*	China	*Solanum lycopersicum*
AJ488768	*Tobacco leaf rugose virus*	Cuba	*Nicotiana tabacum*
AJ489258	*Tomato yellow leaf curl virus*	Spain	*Capsicum annuum*
AJ495813	*Ageratum yellow vein virus*	China	*Ageratum conyzoides*
AJ495814	*Stachytarpheta leaf curl virus*	China	*Stachytarpheta jamaicensis*
AJ507777	*Croton yellow vein mosaic virus*	India	*Croton bonplandianum*
AJ512761	*Tobacco leaf curl Yunnan virus*	China	*Nicotiana* sp.
AJ542540	*Honeysuckle yellow vein virus*	United Kingdom	*Lonicera japonica*
AJ549960	*Dicliptera yellow mottle Cuba virus*	Cuba	*Dicliptera vahliana*
AJ557450	*Sida mottle virus*	Brazil	*Sida micrantha*
AJ557451	*Sida micrantha mosaic virus*	Brazil	*Sida micrantha*
AJ558118	*Tomato leaf curl China virus*	China	*Solanum lycopersicum*
AJ558121	*Euphorbia leaf curl virus*	China	*Euphorbia pulcherrima*
AJ558122	*Papaya leaf curl Guandong virus*	China	*Carica papaya*
AJ558124	*Papaya leaf curl China virus*	China	*Ageratum conyzoides*
AJ608286	*Tomato leaf curl Sinaloa virus*	Nicaragua	*Solanum lycopersicum*
AJ627904	*Horsegram yellow mosaic virus*	India	*Macrotyloma uniflorum*
AJ717572	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*

AJ786711	*Malvastrum yellow vein Yunnan virus*	China	*Malvastrum coromandelianum*
AJ851005	*Ageratum leaf curl virus*	China	*Ageratum conyzoides*
AJ865338	*Tomato leaf curl Madagascar virus*	Madagascar	*Solanum lycopersicum*
AJ865340	*Tomato leaf curl Comoros virus*	Mayotte	*Solanum lycopersicum*
AJ876550	*Senecio yellow mosaic virus*	China	*Senecio scandens*
AJ965539	*Ludwigia yellow vein virus*	China	*Ludwigia hyssopifolia*
AJ965540	*Alternanthera yellow vein virus*	China	*Ludwigia hyssopifolia*
AJ971263	*Malvastrum leaf curl virus*	China	*Malvastrum coromandelianum*
AM048837	*Sida yellow mosaic China virus*	China	*Sida acuta*
AM050730	*Sida leaf curl virus*	China	*Sida cordifolia*
AM182232	*Vernonia yellow vein virus*	India	*Vernonia cinerea*
AM183224	*Siegesbeckia yellow vein virus*	China	*Siegesbeckia glabrescens*
AM236755	*Malvastrum yellow mosaic virus*	China	*Malvastrum coromandelianum*
AM236784	*Tomato leaf curl Guangxi virus*	China	*Solanum lycopersicum*
AM238692	*Siegesbeckia yellow vein Guangxi virus*	China	*Siegesbeckia glabrescens*
AM411424	*Euphorbia leaf curl Guangxi virus*	China	*Euphorbia pulcherrima*
AM491778	*Tomato leaf curl Seychelles virus*	Seychelles	*Solanum lycopersicum*
AM701758	*Tomato leaf curl Anjouan virus*	Comoros	*Solanum lycopersicum*
AM701760	*Tobacco leaf curl Comoros virus*	Comoros	*Nicotiana tabacum*

AM701763	*Tomato leaf curl Moheli virus*	Comoros	-
AM701764	*Tomato leaf curl Namakely virus*	Madagascar	-
AM701765	*Tomato leaf curl Diana virus*	Madagascar	*Solanum lycopersicum*
AM701768	*Tomato leaf curl Toliara virus*	Madagascar	-
AM712436	*Pedilanthus leaf curl virus*	Pakistan	*Pedilanthus tithymaloides*
AM884015	*Tomato leaf curl Palampur virus*	India	*Solanum lycopersicum*
AM886131	*Euphorbia mosaic Peru virus*	Peru	*Euphorbia heterophylla*
AM999981	*Rhynchosia yellow mosaic virus*	Pakistan	*Rhynchosia minima*
AY044133	*Macroptilium mosaic Puerto Rico virus*	Puerto Rico	*Macroptilium lathyroides*
AY044135	*Macroptilium yellow mosaic Florida virus*	USA	*Macroptilium lathyroides*
AY044137	*Tomato leaf curl Sudan virus*	Sudan	-
AY064391	*Melon chlorotic leaf curl virus*	Costa Rica	*Cucurbita* sp.
AY090558	*Sida yellow mosaic virus*	Brazil	*Sida* sp.
AY190290	*Tomato leaf curl Gujarat virus*	India	*Solanum lycopersicum*
AY271891	*Dolichos yellow mosaic virus*	Bangladesh	-
AY297924	*Tomato leaf curl Iran virus*	Iran	*Solanum lycopersicum*
AY339618	*Tomato chino La Paz virus*	Mexico	*Solanum lycopersicum*
AY502935	*Pepper yellow vein Mali virus*	Mali	*Capsicum annuum*
AY502936	*Tomato leaf curl Mali virus*	Mali	*Solanum lycopersicum*

AY508993	*Tomato yellow margin leaf curl virus*	Venezuela	*Solanum lycopersicum*
AY602165	*Tomato leaf curl Guangdong virus*	China	*Solanum lycopersicum*
AY602166	*Tomato yellow leaf curl Guangdong virus*	China	*Solanum lycopersicum*
AY705380	*Cotton leaf curl Bangalore virus*	India	*Gossypium barbadense*
AY727903	*Corchorus yellow vein virus*	Viet Nam	*Corchorus capsularis*
AY754814	*Tomato leaf curl Pune virus*	India	*Solanum lycopersicum*
AY927277	*Tomato mild yellow leaf curl Aragua virus*	Venezuela	*Solanum lycopersicum*
D00940	*Potato yellow mosaic virus*	Venezuela	-
D14703	*Mungbean yellow mosaic virus*	Thailand	-
DQ022611	*Okra yellow mosaic Mexico virus*	Mexico	*Abelmoschus esculentus*
DQ127170	*Tomato leaf curl Uganda virus*	Uganda	*Solanum lycopersicum*
DQ178608	*Cabbage leaf curl Jamaica virus*	Jamaica	*Brassica oleracea*
DQ207749	*Tomato severe rugose virus*	Brazil	*Capsicum annuum*
DQ318937	*Euphorbia mosaic virus*	Mexico	*Euphorbia heterophylla*
DQ336350	*Tomato yellow spot virus*	Brazil	*Solanum lycopersicum*
DQ339117	*Tomato leaf curl Rajasthan virus*	India	*Solanum lycopersicum*
DQ347950	*Rhynchosia golden mosaic virus*	Mexico	*Rhynchosia* sp.
DQ395343	*Wissadula golden mosaic virus*	Jamaica	*Wissadula amplissima*
DQ406672	*Rhynchosia golden mosaic Sinaloa virus*	Mexico	*Rhynchosia minima*

DQ512731	*Sweet potato leaf curl China virus*	China	*Ipomoea batatas*
DQ519575	*Tomato leaf curl Tanzania virus*	Tanzania	*Solanum lycopersicum*
DQ520943	*Tomato golden mottle virus*	Mexico	*Solanum lycopersicum*
DQ520944	*Sida mosaic Sinaloa virus*	Mexico	*Sida* sp.
DQ641688	*Corchorus golden mosaic virus*	Viet Nam	*Corchorus capsularis*
DQ641690	*Kudzu mosaic virus*	Viet Nam	*Pueraria montana*
DQ641692	*Clerodendron golden mosaic virus*	Viet Nam	*Clerodendrum philippinum*
DQ641694	*Spilanthes yellow vein virus*	Viet Nam	*Spilanthes paniculata*
DQ641695	*Mimosa yellow leaf curl virus*	Viet Nam	*Mimosa* sp.
DQ641696	*Sida yellow vein Vietnam virus*	Viet Nam	*Sida rhombiforlia*
DQ641697	*Tomato yellow leaf curl Vietnam virus*	Viet Nam	*Solanum lycopersicum*
DQ641698	*Erectites yellow mosaic virus*	Viet Nam	*Erectites valerianifolia*
DQ641699	*Ludwigia yellow vein Vietnam virus*	Viet Nam	*Ludwigia octovalvis*
DQ641701	*Lindernia anagallis yellow vein virus*	Viet Nam	*Lindernia procumbens*
DQ866132	*Ageratum yellow vein Hualian virus*	Taiwan	*Ageratum* sp.
DQ871221	*Tobacco leaf curl Thailand virus*	Thailand	*Nicotiana benthamiana*
DQ875868	*Corchorus yellow spot virus*	Mexico	*Corchorus siliquosus*
DQ875870	*Desmodium leaf distortion virus*	Mexico	*Desmodium glabrum*
DQ875872	*Sida yellow mosaic Yucatan virus*	Mexico	*Sida acuta*

DQ875879	*Okra yellow crinkle virus*	Mali	*Abelmoschus esculentus*
EF016486	*Soybean blistering mosaic virus*	Argentina	*Glycine max*
EF121755	*Boerhavia yellow spot virus*	Mexico	*Boerhavia coccinea*
EF165536	*Crassocephalum yellow vein virus*	China	*Crassocephalum crepidioides*
EF175733	*Radish leaf curl virus*	India	*Raphanus sativus*
EF194760	*Tomato leaf curl Arusha virus*	Tanzania	*Solanum lycopersicum*
EF197941	*Pumpkin yellow mosaic virus*	Malaysia	*Cucurbita* sp.
EF373060	*Mesta yellow vein mosaic virus*	India	*Hibiscus cannabinus*
EF408037	*Clerodendron yellow mosaic virus*	India	*Clerodendron* sp.
EF417915	*Tomato yellow vein streak virus*	Brazil	*Solanum lycopersicum*
EF450316	*Tomato leaf curl New Delhi virus 5*	Bangladesh	*Cucumis sativus*
EF585290	*Macroptilium yellow mosaic virus*	Jamaica	*Macroptilium lathyroides*
EF602306	*Allamanda leaf curl virus*	China	*Allamanda cathartica*
EU158096	*Macroptilium golden mosaic virus*	Jamaica	*Wissadula amplissima*
EU350585	*Tomato leaf curl Ghana virus*	Ghana	*Solanum lycopersicum*
EU360303	*Mesta yellow vein mosaic Bahraich virus*	India	*Hibiscus cannabinus*
EU365613	*Cotton leaf curl Multan virus*	Pakistan	*Gossypium darwinii*
EU377539	*Emilia yellow vein virus*	China	*Emilia sonchifolia*
EU487042	*Tomato leaf curl Cebu virus*	Philippines	*Solanum lycopersicum*

EU487046	*Tomato leaf curl Mindanao virus*	Philippines	*Solanum lycopersicum*
EU585781	*Pepper leaf curl Yunnan virus*	China	*Capsicum annuum*
EU596959	*Tomato leaf curl Hsinchu virus*	China	*Boehmeria nivea*
EU710749	*Tomato leaf distortion virus*	Brazil	*Solanum lycopersicum*
EU710750	*Sida yellow leaf curl virus*	Brazil	*Sida rhombifolia*
EU710751	*Sida common mosaic virus*	Brazil	*Sida rhombifolia*
EU710752	*Tomato mild mosaic virus*	Brazil	*Solanum lycopersicum*
EU710754	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*
EU710756	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*
EU734831	*Tomato yellow leaf curl Axarquia virus*	Italy	*Solanum lycopersicum*
EU798996	*Jatropha leaf curl virus*	India	*Jatropha* sp.
EU862323	*Tomato leaf curl Patna virus*	India	*Solanum lycopersicum*
EU910141	*Tomato leaf curl Kerala virus*	India	*Solanum lycopersicum*
EU914817	*Okra mottle virus*	Brazil	*Abelmoschus esculentus*
FJ011668	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*
FJ174698	*Tomato yellow leaf distortion virus*	Cuba	*Solanum lycopersicum*
FJ177030	*Jatropha yellow mosaic virus*	India	*Jatropha gossypiifolia*
FJ213931	*Tobacco yellow crinkle virus*	Cuba	-
FJ237617	*Tomato leaf curl Sulawesi virus*	Indonesia	*Solanum lycopersicum*

FJ455449	*Sunn hemp leaf distortion virus*	India	*Crotalaria juncea*
FJ515747	*Bhendi yellow vein mosaic Delhi virus*	India	*Abelmoschus esculentus*
FJ529203	*Sweet potato leaf curl Canary virus*	Spain	*Ipomoea batatas*
FJ561298	*Bhendi yellow vein Haryana virus*	India	*Abelmoschus esculentus*
FJ589571	*Bhendi yellow vein Bhubhaneswar virus*	India	*Abelmoschus esculentus*
FJ600483	*Malvastrum yellow mosaic Helshire virus*	Jamaica	*Malvastrum americanum*
FJ601917	*Malvastrum yellow mosaic Jamaica virus*	Jamaica	*Malvastrum americanum*
FJ619507	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*
FJ685621	*Tomato leaf curl Nigeria virus*	Nigeria	*Solanum lycopersicum*
FJ944019	*Rhynchosia mild mosaic virus*	Puerto Rico	*Rhynchosia minima*
FJ944021	*Merremia mosaic Puerto Rico virus*	Puerto Rico	*Merremia quinquefolia*
FJ944023	*Bean yellow mosaic Mexico virus*	Mexico	*Phaseolus vulgaris*
FJ969831	*Sweet potato mosaic virus*	Brazil	*Ipomoea batatas*
FJ972767	*Passionfruit severe leaf distortion virus*	Brazil	*Passiflora edulis*
FM160943	*Tobacco mottle leaf curl virus*	Cuba	*Nicotiana* sp.
FM877858	*Chilli leaf curl India virus*	India	*Capsicum* sp.
FN396966	*Clerodendrum golden mosaic Jiangsu virus*	China	*Clerodendrum cyrtophyllum*
FN436001	*Sida golden mosaic Brazil virus*	Brazil	*Sida* sp.
FN543425	*Velvet bean severe mosaic virus*	India	*Mucuna* spp.

FN552749	*Malvastrum yellow vein Honghe virus*	China	*Malvastrum coromandelianum*
FR772082	*Hollyhock leaf curl virus*	Pakistan	*Alcea rosea*
GQ334472	*Tomato leaf deformation virus*	Peru	*Solanum lycopersicum*
GQ472984	*Soybean mild mottle virus*	Nigeria	*Glycine max*
GQ472985	*Soybean chlorotic blotch virus*	Nigeria	*Glycine max*
GU111998	*Okra enation leaf curl virus*	India	*Abelmoschus esculentus*
GU997691	*Sida golden mottle virus*	USA	*Sida santaremnensis*
HE616777	*African cassava mosaic Burkina Faso virus*	Burkina Faso	*Manihot esculenta*
HE617299	*Cassava mosaic Madagascar virus*	Madagascar	*Manihot esculenta*
HE862273	*Okra leaf curl Oman virus*	Oman	*Abelmoschus esculentus*
HF912280	*Tomato leaf curl Liwa virus*	Oman	*Solanum lycopersicum*
HM003779	*Sida golden mosaic Florida virus*	Cuba	*Malvastrum coromandelianum*
HM007106	*Chilli leaf curl Kanpur virus*	India	*Capsicum annuum*
HM007121	*Chilli leaf curl Vellanad virus*	India	*Capsicum annuum*
HM140367	*Papaya leaf crumple virus*	India	*Carica papaya*
HM163576	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*
HM230683	*Jatropha mosaic India virus*	India	*Jatropha curcas*
HM236368	*Rhynchosia golden mosaic Havana virus*	Cuba	*Rhynchosia minima*
HM236370	*Rhynchosia rugose golden mosaic virus*	Cuba	*Rhynchosia minima*

HM357456	*Tomato golden leaf distortion virus*	Brazil	*Solanum lycopersicum*
HM357458	*Sidastrum golden leaf spot virus*	Brazil	*Sidastrum* sp.
HM357461	*Chino del tomate Amazonas virus*	Brazil	*Solanum lycopersicum*
HM585435	*Solanum mosaic Bolivia virus*	Bolivia	*Solanum* sp.
HM585441	*Sida mosaic Bolivia virus 1*	Bolivia	*Sida micrantha*
HM585443	*Sida mosaic Bolivia virus 2*	Bolivia	*Sida micrantha*
HM585445	*Abutilon mosaic Bolivia virus*	Bolivia	*Abutilon* sp.
HM626515	*Chenopodium leaf curl virus*	USA	*Chenopodium ambrosioides*
HM777508	*Rhynchosia yellow mosaic India virus*	India	*Rhynchosia* sp.
HM991146	*Tomato leaf curl Joydebpur virus*	India	*Capsicum annuum*
HM992939	*Chilli leaf curl Bhavanisagar virus*	India	*Capsicum annuum*
HQ008338	*Sida golden mosaic Buckup virus*	Jamaica	*Sida* sp.
HQ162270	*Tomato leaf curl Hanoi virus*	Viet Nam	*Solanum lycopersicum*
HQ180391	*Tobacco leaf curl Pusa virus*	India	*Nicotiana tabacum*
HQ201952	*Tomato chlorotic leaf distortion virus*	Venezuela	*Solanum lycopersicum*
HQ333144	*Sweet potato leaf curl South Carolina virus*	USA	*Ipomoea batatas*
HQ393477	*Sweet potato leaf curl Sao Paulo virus*	Brazil	*Ipomoea batatas*
HQ396465	*Cleome golden mosaic virus*	Brazil	*Cleome* sp.
J02057	*African cassava mosaic virus*	Cameroon	*Manihot esculenta*

JF265670	*Vernonia yellow vein Fujian virus*	China	*Vernonia cinerea*
JF694461	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*
JF694471	*Sida mosaic Alagoas virus*	Brazil	*Sida* sp.
JF694480	*Abutilon mosaic Brazil virus*	Brazil	*Sida rhomboidea*
JF694484	*West African Asystasia virus 1*	West Africa	*Asystasia gangetica*
JF694486	*West African Asystasia virus 2*	West Africa	*Asystasia gangetica*
JF803252	*Tomato interveinal chlorosis virus*	Brazil	*Solanum lycopersicum*
JF803254	*Tomato golden vein virus*	Brazil	*Solanum lycopersicum*
JN135234	*Pepper leaf curl Lahore virus*	India	*Solanum lycopersicum*
JN381819	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*
JN411687	*Sida yellow mottle virus*	Cuba	*Sida rhombifolia*
JN419002	*Centrosema yellow spot virus*	Brazil	*Centrosema brasilianum*
JN419013	*Macroptilium yellow spot virus*	Brazil	*Macroptilium lathyroides*
JN419021	*Macroptilium yellow vein virus*	Brazil	*Macroptilium* sp.
JN555601	*Chilli leaf curl Sri Lanka virus*	Sri Lanka	*Capsicum annuum*
JN564749	*Tomato dwarf leaf virus*	Argentina	*Solanum lycopersicum*
JN698954	*Jatropha leaf yellow mosaic virus*	India	*Jatropha curcas*
JN809819	*Sauropus leaf curl virus*	Thailand	*Sauropus androgynus*
JN848770	*Bean chlorosis virus*	Venezuela	*Phaseolus vulgaris*

JN848772	*Bean white chlorosis mosaic virus*	Venezuela	*Phaseolus vulgaris*
JN848773	*Datura leaf distortion virus*	Venezuela	*Datura stramonium*
JN848775	*Dalechampia chlorotic mosaic virus*	Venezuela	*Dalechampia* sp.
JQ429791	*Leonurus mosaic virus*	Brazil	*Leonurus sibiricus*
JQ714137	*Tomato mottle wrinkle virus*	Argentina	*Solanum lycopersicum*
JQ793786	*Premna leaf curl virus*	Viet Nam	*Premna serratifolia*
JQ821386	*Jacquemontia mosaic Yucatan virus*	Mexico	*Jacquemontia pentantha*
JQ866297	*French bean leaf curl virus*	India	*Phaseolus vulgaris*
JQ897969	*Tomato leaf curl New Delhi virus 2*	India	*Solanum lycopersicum*
JQ911766	*Hollyhock yellow vein mosaic virus*	India	*Alcea rosea*
JX025358	*Jatropha mosaic Nigeria virus*	Nigeria	*Jatropha curcas*
JX162595	*Sida golden mosaic Braco virus*	Jamaica	*Sida* sp.
JX183732	*Pouzolzia golden mosaic virus*	China	*Pouzolzia zeylanica*
JX827487	*Blechum interveinal chlorosis virus*	Mexico	*Blechum pyramidatum*
JX857691	*Sida ciliaris golden mosaic virus*	Venezuela	*Sida ciliaris*
JX857693	*Sida golden mosaic Lara virus*	Venezuela	*Sida* sp.
JX871376	*Sida yellow net virus*	Brazil	*Sida micrantha*
JX871380	*Sida yellow blotch virus*	Brazil	*Sida urens*
JX871383	*Sida yellow mosaic Alagoas virus*	Brazil	*Sida urens*

JX871385	*Sida mottle Alagoas virus*	Brazil	*Sida urens*
K02029	*Tomato golden mosaic virus*	Brazil	-
KC149938	*Pepper yellow leaf curl virus*	China	*Capsicum* sp.
KC176780	*Tomato yellow mottle virus*	Costa Rica	*Solanum lycopersicum*
KC202818	*Allamanda leaf mottle distortion virus*	India	*Allamanda cathartica*
KC223600	*Corchorus yellow vein mosaic virus*	India	*Corchorus olitorius*
KC426927	*Capraria yellow spot virus*	Mexico	*Capraria biflora*
KC430935	*Abutilon golden mosaic virus*	Mexico	*Abutilon permolle*
KC430936	*Vigna yellow mosaic virus*	Mexico	*Vigna elegans*
KC488316	*Sweet potato leaf curl Sichuan virus 1*	China	*Ipomoea batatas*
KC577540	*Malvastrum leaf curl Philippines virus*	Philippines	*Malvastrum coromandelianum*
KC626021	*Tomato golden leaf spot virus*	Uruguay	*Solanum lycopersicum*
KC686705	*Tomato yellow leaf curl Yunnan virus*	China	*Solanum lycopersicum*
KC706615	*Tomato mottle leaf curl virus*	Brazil	*Solanum lycopersicum*
KC769819	*Pepper leafroll virus*	Peru	*Capsicum baccatum*
KC791690	*Tomato bright yellow mosaic virus*	Brazil	*Solanum lycopersicum*
KC791691	*Tomato bright yellow mottle virus*	Brazil	*Solanum lycopersicum*
KC898543	*Hemidesmus yellow mosaic virus*	India	*Hemidesmus indicus*
KC907406	*Sweet potato leaf curl Henan virus*	China	*Ipomoea batatas*

KF150142	*Tomato leaf curl Hainan virus*	China	*Solanum lycopersicum*
KF156759	*Sweet potato leaf curl Sichuan virus 2*	China	*Ipomoea batatas*
KF358470	*Cotton chlorotic spot virus*	Brazil	*Gossypium hirsutum* x *G. mustelinum*
KF414123	*Pouzolzia mosaic Guangdong virus*	China	*Pouzolzia zeylanica*
KF429251	*Hedyotis uncinella yellow mosaic virus*	Viet Nam	*Hedyotis uncinella*
KF446659	*Blechum yellow vein virus*	Philippines	*Ruellia blechum*
KF551578	*Tomato leaf curl Karnataka virus 2*	India	*Solanum lycopersicum*
KF551585	*Tomato leaf curl Karnataka virus 3*	India	*Solanum lycopersicum*
KF551592	*Tomato leaf curl New Delhi virus 4*	India	*Solanum lycopersicum*
KF660223	*Spinach yellow vein virus*	India	*Spinacia oleracea*
KF661331	*Jacquemontia yellow mosaic virus*	Venezuela	*Jacquemontia* sp.
KF723258	*Jatropha mosaic virus*	Jamaica	*Jatropha gossypifolia*
KF927128	*Pouzolzia yellow mosaic virus*	Taiwan	*Pouzolzia zeylanica*
KJ476510	*Sweet potato leaf curl Guangxi virus*	China	*Ipomoea* sp.
KJ739692	*Rose leaf curl virus*	India	*Rosa* sp.
KJ957157	*Chilli leaf curl Gonda virus*	India	*Capsicum annuum*
KM244719	*Coccinia mosaic Tamil Nadu virus*	India	*Coccinia grandis*
KM359406	*Andrographis yellow vein leaf curl virus*	India	*Andrographis paniculata*
KM411359	*Jatropha leaf curl Gujarat virus*	India	*Jatropha curcas*

KM880103	*Chilli leaf curl Ahmedabad virus*	India	*Capsicum annuum*
KM887907	*Oxalis yellow vein virus*	USA	*Oxalis debilis*
KM926624	*Tomato latent virus*	Cuba	*Solanum lycopersicum*
KP188831	*Malvastrum yellow vein Cambodia virus*	Cambodia	*Malvastrum coromandelianum*
KP195260	*Tomato enation leaf curl virus*	India	*Solanum lycopersicum*
KP195267	*Tomato severe leaf curl Kalakada virus*	India	*Solanum lycopersicum*
KP663485	*Asystasia mosaic Madagascar virus*	Madagascar	*Asystasia gangetica*
KR263181	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*
KR612272	*Vinca leaf curl virus*	India	*Vinca rosea*
KT099124	*Whitefly-associated begomovirus 1*	Guatemala	-
KT099125	*Whitefly-associated begomovirus 2*	Guatemala	-
KT099127	*Whitefly-associated begomovirus 3*	Guatemala	-
KT099128	*Whitefly-associated begomovirus 4*	Guatemala	-
KT099139	*Whitefly-associated begomovirus 6*	Puerto Rico	-
KT099156	*Whitefly-associated begomovirus 7*	Spain	-
KT159766	*Euphorbia yellow leaf curl virus*	Pakistan	*Euphorbia pulcherrima*
KT201151	*Melochia mosaic virus*	Brazil	*Melochia* sp.
KT201153	*Melochia yellow mosaic virus*	Brazil	*Melochia* sp.
KT390456	*Eclipta yellow vein virus*	India	*Hibiscus cannabinus*

KT444609	*West African Asystasia virus 3*	Benin	*Asystasia* sp.
KT454832	*Telfairia golden mosaic virus*	Cameroon	*Telfairia occidentalis*
KT582302	*Lycianthes yellow mosaic virus*	China	*Lycianthes biflora*
KT809345	*Pepper yellow leaf curl Indonesia virus 2*	Indonesia	*Capsicum annuum*
KT878829	*Deinbollia mosaic virus*	Tanzania	*Deinbollia borbonica*
KT899302	*Passionfruit leaf distortion virus*	Colombia	*Passiflora edulis*
KT948069	*Duranta leaf curl virus*	Pakistan	*Duranta repens*
KT948785	*Pavonia mosaic virus*	Brazil	*Pavonia* sp.
KT948787	*Pavonia yellow mosaic virus*	Brazil	*Pavonia* sp.
KT962229	*Tomato yellow leaf curl Shuangbai virus*	China	*Solanum lycopersicum*
KT966771	*Cnidoscolus mosaic leaf deformation virus*	Brazil	*Cnidoscolus urens*
KT992056	*Sweet potato golden vein Korea virus*	South Korea	*Ipomoea* sp.
KU058856	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.
KU131588	*Triumfetta yellow mosaic virus*	Brazil	*Triumfetta* sp.
KU323597	*Sweet potato leaf curl Shandong virus*	China	*Ipomoea batatas*
KU522485	*Ramie mosaic Yunnan virus*	China	*Boehmeria* sp.
KU569583	*Velvet bean golden mosaic virus*	Taiwan	Mucuna pruriens
KU683748	*Cotton yellow mosaic virus*	Benin	*Gossypium raimondii*
KU852742	*Senna leaf curl virus*	India	*Senna occidentalis*

KX011471	*Tobacco leaf curl Cuba virus*	Cuba	*Phaseolus vulgaris*
KX011473	*Common bean mottle virus*	Cuba	*Phaseolus vulgaris*
KX011477	*Common bean severe mosaic virus*	Cuba	*Phaseolus vulgaris*
KX348183	*Sida chlorotic mottle virus*	Brazil	*Sida* sp.
KX348184	*Sida bright yellow mosaic virus*	Brazil	*Sida* sp.
KX348185	*Sida golden yellow spot virus*	Brazil	*Sida* sp.
KX363443	*Synedrella yellow vein clearing virus*	India	*Synedrella nodiflora*
KX691396	*Macroptilium common mosaic virus*	Brazil	*Macroptilium lathyroides*
KX691400	*Macroptilium bright mosaic virus*	Brazil	*Macroptilium lathyroides*
KX691402	*Sida chlorotic vein virus*	Brazil	*Sida urens*
KX691407	*Sida angular mosaic virus*	Brazil	*Sida acuta*
KX691411	*Wissadula yellow mosaic virus*	Brazil	*Wissadula* sp.
KX831132	*Vernonia crinkle virus*	Uganda	*Vernonia amygdalina*
KX853168	*Tomato leaf curl Burkina Faso virus*	Burkina Faso	*Solanum lycopersicum*
KX857725	*Bean leaf crumple virus*	Colombia	*Phaseolus vulgaris*
KX943290	*Pepper yellow leaf curl Thailand virus*	Thailand	*Capsicum annuum*
KY001635	*Pea leaf distortion virus*	Nepal	*Pisum sativum*
KY196216	*Tomato leaf curl purple vein virus*	Brazil	*Solanum lycopersicum*
KY294725	*Desmodium mottle virus*	Uganda	*Desmodium* sp.

KY373213	*Emilia yellow vein Thailand virus*	Thailand	*Emilia sonchifolia*
KY449275	*Tomato wrinkled mosaic virus*	Venezuela	*Solanum lycopersicum*
KY617094	*Jacquemontia yellow vein virus*	Venezuela	*Jacquemontia tamnifolia*
L01635	*Bean golden yellow mosaic virus*	Dominican Republic	-
L14460	*Tomato mottle virus*	USA	*Solanum lycopersicum*
LC080677	*Cotton leaf curl Barasat virus*	India	*Malachra capitata*
LC091538	*Lisianthus enation leaf curl virus*	Taiwan	*Eustoma grandiflorum*
LK028570	*Catharanthus yellow mosaic virus*	Pakistan	*Duranta repens*
LK054801	*Mirabilis leaf curl virus*	India	*Mirabilis jalapa*
LM651400	*Tomato yellow leaf curl Mali virus*	Burkina Faso	*Solanum lycopersicum*
M38183	*Squash leaf curl virus*	USA	*Cucurbita pepo*
M88179	*Bean dwarf mosaic virus*	Colombia	-
M88686	*Bean golden mosaic virus*	Brazil	*Phaseolus vulgaris*
MF402918	*Datura leaf curl virus*	Sudan	*Datura inoxia*
S53251	*Tomato leaf curl virus*	Australia	*Solanum lycopersicum*
U15015	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*
U38239	*Tomato leaf curl Karnataka virus*	India	*Solanum lycopersicum*
U57457	*Pepper golden mosaic virus*	Mexico	-
U65529	*Cabbage leaf curl virus*	USA	*Brassica* sp.

	U77964	*Sida golden yellow vein virus*	USA	*Sida* sp.
	U88692	*Tomato leaf curl Taiwan virus*	Taiwan	*Solanum lycopersicum*
	X15983	*Abutilon mosaic virus*	Germany	*Abutilon sellovianum*
	X61153	*Tomato yellow leaf curl Sardinia virus*	Italy	*Solanum lycopersicum*
	X70418	*Pepper huasteco yellow vein virus*	Mexico	-
	X99550	*Sida golden mosaic Costa Rica virus*	Costa Rica	*Sida* sp.
	Y11099	*Sida yellow vein virus*	Honduras	*Sida* sp.
	Y14874	*Tomato mosaic Havana virus*	Cuba	*Solanum lycopersicum*
	Y15034	*Potato yellow mosaic Panama virus*	Panama	*Solanum lycopersicum*
	Y15934	*Papaya leaf curl virus*	India	-
	Z24758	*Indian cassava mosaic virus*	India	*Manihot esculenta*
Begomovirus (DNA-B)	AB085794	*Squash leaf curl Philippines virus*	Philippines	*Cucurbita moschata*
	AB267835	*Pepper yellow leaf curl Indonesia virus*	Indonesia	*Capsicum* sp.
	AF012301	*Tomato mottle Taino virus*	Cuba	-
	AF039841	*Sida golden mosaic virus*	USA	*Sida santaremnensis*
	AF101478	*Chino del tomate virus*	Mexico	-
	AF110190	*Bean calico mosaic virus*	Mexico	*Phaseolus vulgaris*
	AF112355	*East African cassava mosaic Cameroon virus*	Cameroon	*Manihot esculenta*
	AF126807	*East African cassava mosaic virus*	Uganda	*Manihot esculenta*

AF141897	*Tomato yellow leaf curl Thailand virus*	Thailand	-
AF142440	*Mungbean yellow mosaic India virus*	India	-
AF155807	*South African cassava mosaic virus*	South Africa	*Manihot esculenta*
AF170101	*Dicliptera yellow mottle virus*	USA	*Dicliptera sexangularis*
AF224761	*Cucurbit leaf crumple virus*	USA	*Cucurbita* sp.
AF291706	*Tomato rugose mosaic virus*	Brazil	*Solanum lycopersicum*
AF421553	*Squash mild leaf curl virus*	USA	-
AF422175	*East African cassava mosaic Zanzibar virus*	Tanzania	*Manihot esculenta*
AF440790	*Melon chlorotic leaf curl virus*	Costa Rica	*Cucurbita* sp.
AF480941	*Cotton leaf crumple virus*	Mexico	*Gossypium* sp.
AF491306	*Tomato chlorotic mottle virus*	Brazil	*Solanum lycopersicum*
AF499442	*Pepper golden mosaic virus*	Mexico	-
AF509740	*Luffa yellow mosaic virus*	Viet Nam	*Luffa acutungula*
AF509742	*Squash leaf curl China virus*	Viet Nam	*Cucurbita* spp.
AF511528	*Tomato yellow leaf curl Kanchanaburi virus*	Thailand	*Solanum lycopersicum*
AJ012082	*Watermelon chlorotic stunt virus*	Yemen	*Citrullus lanatus*
AJ314738	*Sri Lankan cassava mosaic virus*	Sri Lanka	*Nicotiana benthamiana*
AJ508783	*Tomato leaf curl Sinaloa virus*	Nicaragua	*Solanum lycopersicum*
AJ557453	*Sida micrantha mosaic virus*	Brazil	*Sida micrantha*

AJ557454	*Sida mottle virus*	Brazil	*Sida micrantha*
AJ627905	*Horsegram yellow mosaic virus*	India	*Macrotyloma uniflorum*
AJ704971	*East African cassava mosaic Kenya virus*	Kenya	*Manihot esculenta*
AM992534	*Tomato leaf curl Palampur virus*	India	*Solanum lycopersicum*
AM999982	*Rhynchosia yellow mosaic virus*	Pakistan	*Rhynchosia minima*
AY044134	*Macroptilium mosaic Puerto Rico virus*	Puerto Rico	*Macroptilium lathyroides*
AY044136	*Macroptilium yellow mosaic Florida virus*	USA	*Macroptilium lathyroides*
AY190291	*Tomato leaf curl Gujarat virus*	India	*Solanum lycopersicum*
AY508994	*Tomato yellow margin leaf curl virus*	Venezuela	*Solanum lycopersicum*
AY727904	*Corchorus yellow vein virus*	Viet Nam	*Corchorus capsularis*
AY965899	*Merremia mosaic virus*	Puerto Rico	*Solanum lycopersicum*
D00941	*Potato yellow mosaic virus*	Venezuela	-
D14704	*Mungbean yellow mosaic virus*	Thailand	-
DQ178609	*Cabbage leaf curl Jamaica virus*	Jamaica	*Brassica oleracea*
DQ318938	*Euphorbia mosaic virus*	Mexico	*Euphorbia heterophylla*
DQ336351	*Tomato yellow spot virus*	Brazil	*Solanum lycopersicum*
DQ356428	*Sida mosaic Sinaloa virus*	Mexico	*Sida* sp.
DQ406673	*Rhynchosia golden mosaic Sinaloa virus*	Mexico	*Rhynchosia minima*
DQ406674	*Tomato golden mottle virus*	Mexico	*Solanum lycopersicum*

DQ641689	*Corchorus golden mosaic virus*	Viet Nam	*Corchorus capsularis*
DQ641691	*Kudzu mosaic virus*	Viet Nam	*Pueraria montana*
DQ641693	*Clerodendron golden mosaic virus*	Viet Nam	*Clerodendrum philippinum*
DQ875869	*Corchorus yellow spot virus*	Mexico	*Corchorus siliquosus*
DQ875871	*Desmodium leaf distortion virus*	Mexico	*Desmodium glabrum*
DQ875873	*Sida yellow mosaic Yucatan virus*	Mexico	*Sida acuta*
EF417916	*Tomato yellow vein streak virus*	Brazil	*Solanum tuberosum*
EF534708	*Tomato severe rugose virus*	Brazil	*Capsicum baccatum*
EF547938	*Tomato mild yellow leaf curl Aragua virus*	Venezuela	*Solanum lycopersicum*
EF585291	*Macroptilium yellow mosaic virus*	Jamaica	*Macroptilium lathyroides*
EU158095	*Wissadula golden mosaic virus*	Jamaica	*Wissadula amplissima*
EU158097	*Macroptilium golden mosaic virus*	Jamaica	*Wissadula amplissima*
EU339937	*Rhynchosia golden mosaic virus*	Mexico	*Glycine max*
EU596960	*Tomato leaf curl Hsinchu virus*	China	*Boehmeria nivea*
EU710753	*Tomato mild mosaic virus*	Brazil	*Solanum lycopersicum*
EU710755	*Tomato common mosaic virus*	Brazil	*Solanum lycopersicum*
EU710757	*Blainvillea yellow spot virus*	Brazil	*Blainvillea rhomboidea*
EU914818	*Okra mottle virus*	Brazil	*Abelmoschus esculentus*
FJ011669	*Clerodendrum golden mosaic China virus*	China	*Clerodendrum cyrtophyllum*

FJ600484	*Malvastrum yellow mosaic Jamaica virus*	Jamaica	*Malvastrum americanum*
FJ619508	*Euphorbia yellow mosaic virus*	Brazil	*Euphorbia heterophylla*
FJ944020	*Rhynchosia mild mosaic virus*	Puerto Rico	*Rhynchosia minima*
FJ944022	*Merremia mosaic Puerto Rico virus*	Puerto Rico	*Merremia quinquefolia*
FJ972768	*Passionfruit severe leaf distortion virus*	Brazil	*Passiflora edulis*
FJ999999	*Tomato yellow leaf distortion virus*	Cuba	*Solanum lycopersicum*
FN543426	*Velvet bean severe mosaic virus*	India	*Mucuna* spp.
GQ472986	*Soybean chlorotic blotch virus*	Nigeria	*Glycine max*
GU972604	*Okra yellow mosaic Mexico virus*	Mexico	*Abelmoschus esculentus*
GU997692	*Sida golden mottle virus*	USA	*Sida santaremensis*
HE617300	*Cassava mosaic Madagascar virus*	Madagascar	*Manihot esculenta*
HM003778	*Sida golden mosaic Florida virus*	Cuba	*Malvastrum coromandelianum*
HM163577	*Melon chlorotic mosaic virus*	Venezuela	*Citrullus lanatus*
HM236369	*Rhynchosia golden mosaic Havana virus*	Cuba	*Rhynchosia minima*
HM236371	*Rhynchosia rugose golden mosaic virus*	Cuba	*Rhynchosia minima*
HM585436	*Solanum mosaic Bolivia virus*	Bolivia	*Solanum* sp.
HM585442	*Sida mosaic Bolivia virus 1*	Bolivia	*Sida micrantha*
HM585444	*Sida mosaic Bolivia virus 2*	Bolivia	*Sida micrantha*
HM585446	*Abutilon mosaic Bolivia virus*	Bolivia	*Abutilon* sp.

HM777510	*Rhynchosia yellow mosaic India virus*	India	*Rhynchosia* sp.
HQ009518	*Sida golden mosaic Buckup virus*	Jamaica	*Sida* sp.
HQ201953	*Tomato chlorotic leaf distortion virus*	Venezuela	*Solanum lycopersicum*
HQ896204	*Tobacco yellow crinkle virus*	Cuba	*Nicotiana tabacum*
J02058	*African cassava mosaic virus*	Cameroon	*Manihot esculenta*
JF694462	*Cleome leaf crumple virus*	Brazil	*Cleome affinis*
JF694473	*Sida mosaic Alagoas virus*	Brazil	*Sida* sp.
JF694479	*Abutilon mosaic Brazil virus*	Brazil	*Blainvillea rhomboidea*
JF694485	*West African Asystasia virus 1*	West Africa	*Asystasia gangetica*
JF803264	*Tomato mottle leaf curl virus*	Brazil	*Solanum lycopersicum*
JF803265	*Tomato golden vein virus*	Brazil	*Solanum lycopersicum*
JN381814	*Tomato rugose yellow leaf curl virus*	Uruguay	*Solanum lycopersicum*
JN411688	*Sida yellow mottle virus*	Cuba	*Sida rhombifolia*
JN564750	*Tomato dwarf leaf virus*	Argentina	*Solanum lycopersicum*
JN848771	*Bean chlorosis virus*	Venezuela	*Phaseolus vulgaris*
JN848774	*Datura leaf distortion virus*	Venezuela	*Datura stramonium*
JN848776	*Dalechampia chlorotic mosaic virus*	Venezuela	*Dalechampia* sp.
JQ283246	*Bean white chlorosis mosaic virus*	Venezuela	*Phaseolus vulgaris*
JQ714138	*Tomato mottle wrinkle virus*	Argentina	*Solanum lycopersicum*

JQ821387	*Jacquemontia mosaic Yucatan virus*	Mexico	*Jacquemontia pentantha*
JX827488	*Blechum interveinal chlorosis virus*	Mexico	*Blechum pyramidatum*
K02030	*Tomato golden mosaic virus*	Brazil	-
KC176781	*Tomato yellow mottle virus*	Costa Rica	*Solanum lycopersicum*
KC426928	*Capraria yellow spot virus*	Mexico	*Capraria biflora*
KF358471	*Cotton chlorotic spot virus*	Brazil	*Gossypium hirsutum x G. mustelinum*
KF661332	*Jacquemontia yellow mosaic virus*	Venezuela	*Jacquemontia* sp.
KF723261	*Jatropha mosaic virus*	Jamaica	*Jatropha gossypifolia*
KM244718	*Coccinia mosaic Tamil Nadu virus*	India	*Coccinia grandis*
KP663484	*Asystasia mosaic Madagascar virus*	Madagascar	*Asystasia gangetica*
KR263172	*Tomato chlorotic mottle Guyane virus*	French Guiana	*Solanum lycopersicum*
KT201152	*Melochia mosaic virus*	Brazil	*Melochia* sp.
KT201154	*Melochia yellow mosaic virus*	Brazil	*Melochia* sp.
KT582303	*Lycianthes yellow mosaic virus*	China	*Lycianthes biflora*
KT878828	*Deinbollia mosaic virus*	Tanzania	*Deinbollia borbonica*
KT899303	*Passionfruit leaf distortion virus*	Colombia	*Passiflora edulis*
KT948786	*Pavonia mosaic virus*	Brazil	*Pavonia* sp.
KT948788	*Pavonia yellow mosaic virus*	Brazil	*Pavonia* sp.
KT966772	*Cnidoscolus mosaic leaf deformation virus*	Brazil	*Cnidoscolus urens*

KU058860	*Malvastrum bright yellow mosaic virus*	USA	*Malvastrum* sp.
KU131589	*Triumfetta yellow mosaic virus*	Brazil	*Triumfetta* sp.
KU683750	*Cotton yellow mosaic virus*	Benin	*Gossypium raimondii*
KX011472	*Tobacco leaf curl Cuba virus*	Cuba	*Phaseolus vulgaris*
KX011474	*Common bean mottle virus*	Cuba	*Phaseolus vulgaris*
KX096982	*Common bean severe mosaic virus*	Cuba	*Phaseolus vulgaris*
KX348225	*Sida bright yellow mosaic virus*	Brazil	*Sida* sp.
KX691412	*Macroptilium common mosaic virus*	Brazil	*Macroptilium lathyroides*
KX691413	*Sida chlorotic vein virus*	Brazil	*Sida* sp.
KX691415	*Sida angular mosaic virus*	Brazil	*Sida acuta*
KX943291	*Pepper yellow leaf curl Thailand virus*	Thailand	*Capsicum annuum*
KY294727	*Desmodium mottle virus*	Uganda	*Desmodium* sp.
L01636	*Bean golden yellow mosaic virus*	Dominican Republic	-
L14461	*Tomato mottle virus*	USA	*Solanum lycopersicum*
M38182	*Squash leaf curl virus*	USA	-
M88180	*Bean dwarf mosaic virus*	Colombia	-
M88687	*Bean golden mosaic virus*	Brazil	*Phaseolus vulgaris*
MG969497	*Allamanda leaf mottle distortion virus*	India	*Allamanda cathartica*
U15017	*Tomato leaf curl New Delhi virus*	India	*Solanum lycopersicum*

	U65530	*Cabbage leaf curl virus*	USA	*Brassica* sp.
	X15984	*Abutilon mosaic virus*	Germany	*Abutilon sellovianum*
	X70419	*Pepper huasteco yellow vein virus*	Mexico	-
	X99551	*Sida golden mosaic Costa Rica virus*	Costa Rica	*Sida* sp.
	Y11100	*Sida yellow vein virus*	Honduras	*Sida* sp.
	Y14875	*Tomato mosaic Havana virus*	Cuba	*Solanum lycopersicum*
	Y15033	*Potato yellow mosaic Panama virus*	Panama	*Solanum lycopersicum*
Betasatellite	AB100306	*Tomato leaf curl Java betasatellite*	Indonesia	*Solanum lycopersicum*
	AB182263	*Honeysuckle yellow vein mosaic Hyogo betasatellite*	Japan	*Lonicera japonica*
	AB236324	*Honeysuckle yellow vein Japan betasatellite*	Japan	*Solanum lycopersicum*
	AB236326	*Honeysuckle yellow vein Kochi betasatellite*	Japan	*Solanum lycopersicum*
	AB287442	*Honeysuckle yellow vein mosaic betasatellite*	Japan	*Lonicera japonica*
	AB287443	*Honeysuckle yellow vein mosaic Nara betasatellite*	Japan	*Lonicera japonica*
	AB294512	*Tomato yellow dwarf betasatellite*	Japan	*Solanum lycopersicum*
	AB308071	*Tomato leaf curl Philippines betasatellite*	Philippines	*Solanum lycopersicum*
	AJ252072	*Ageratum yellow vein betasatellite*	Singapore	*Ageratum conyzoides*
	AJ292769	*Cotton leaf curl Multan betasatellite*	Pakistan	*Gossypium hirsutum*
	AJ308425	*Bhendi yellow vein betasatellite*	India	*Abelmoschus esculentus*

AJ316029	*Okra leaf curl betasatellite*	Pakistan	*Hibiscus esculentis*
AJ316032	*Chilli leaf curl betasatellite*	Pakistan	*Capsicum annuum*
AJ316033	*Tobacco leaf curl betasatellite*	Pakistan	*Nicotiana tabacum*
AJ316036	*Tomato leaf curl betasatellite*	Pakistan	*Solanum lycopersicum*
AJ316039	*Cotton leaf curl Gezira betasatellite*	Egypt	*Hibiscus esculentis*
AJ316040	*Honeysuckle yellow vein betasatellite*	United Kingdom	*Lonicera japonica*
AJ316041	*Ageratum yellow leaf curl betasatellite*	Pakistan	*Zinnia elegans*
AJ421485	*Tobacco curly shoot betasatellite*	China	-
AJ421620	*Tomato yellow leaf curl Yunnan betasatellite*	China	-
AJ438938	*Eupatorium yellow vein betasatellite*	Japan	*Eupatorium makinoi*
AJ536621	*Tomato yellow leaf curl Thailand betasatellite*	China	*Nicotiana* sp.
AJ542489	*Tomato leaf curl Bangladesh betasatellite*	Bangladesh	*Solanum lycopersicum*
AJ542491	*Tomato leaf curl Laos betasatellite*	Laos	*Solanum lycopersicum*
AJ542493	*Ageratum yellow vein Sri Lanka betasatellite*	Sri Lanka	*Solanum lycopersicum*
AJ542499	*Zinnia leaf curl betasatellite*	Thailand	*Zinnia* sp.
AJ704609	*Tomato leaf curl China betasatellite*	China	*Solanum lycopersicum*
AJ786712	*Malvastrum yellow vein Yunnan betasatellite*	China	*Malvastrum coromandelianum*
AJ965541	*Ludwigia yellow vein betasatellite*	China	*Ludwigia hyssopifolia*
AJ966244	*Tomato leaf curl Joydebpur betasatellite*	Bangladesh	*Solanum lycopersicum*

AJ967003	*Sida yellow vein betasatellite*	India	*Sida cordifolia*
AJ971459	*Malvastrum yellow vein betasatellite*	China	*Malvastrum coromandelianum*
AM048833	*Sida yellow mosaic China betasatellite*	China	*Sida acuta*
AM050732	*Sida leaf curl betasatellite*	China	*Sida cordifolia*
AM072289	*Malvastrum leaf curl betasatellite*	China	*Malvastrum coromandelianum*
AM230643	*Siegesbeckia yellow vein betasatellite*	China	*Siegesbeckia glabrescens*
AM238695	*Siegesbeckia yellow vein Guangxi betasatellite*	China	*Siegesbeckia glabrescens*
AM260730	*Bean leaf curl China betasatellite*	China	*Solanum lycopersicum*
AM410551	*Croton yellow vein mosaic betasatellite*	Pakistan	*Croton* sp.
AM933578	*Cardiospemum yellow leaf curl betasatellite*	United Kingdom	*Cardiospermum microcarpum*
AY230138	*Papaya leaf curl betasatellite*	India	*Solanum lycopersicum*
AY428768	*Tomato leaf curl Bangalore betasatellite*	India	*Solanum lycopersicum*
AY705381	*Kenaf leaf curl betasatellite*	India	*Croton* sp.
AY754813	*Tomato leaf curl Karnataka betasatellite*	India	*Solanum lycopersicum*
AY838894	*Tomato leaf curl Maharastra betasatellite*	India	*Solanum lycopersicum*
DQ641712	*Sida yellow vein Vietnam betasatellite*	Viet Nam	*Sida* sp.
DQ641713	*Erectites yellow mosaic betasatellite*	Viet Nam	*Chamaenerion angustifolium*
DQ641714	*Tomato yellow leaf curl Vietnam betasatellite*	Viet Nam	*Solanum lycopersicum*
DQ641715	*Lindernia anagallis yellow vein betasatellite*	Viet Nam	*Lindernia procumbens*

	DQ641716	*Alternanthera yellow vein betasatellite*	Viet Nam	*Zinnia elegans*
	EF175734	*Radish leaf curl betasatellite*	India	*Raphanus sativus*
	EF614160	*Mesta yellow vein mosaic betasatellite*	India	*Hibiscus cannabinus*
	EU188921	*Sida yellow vein mosaic betasatellite*	India	*Sida cordifolia*
	EU557374	*Luffa leaf distortion betasatellite*	India	*Hibiscus cannabinus*
	EU862324	*Tomato leaf curl Patna betasatellite*	India	*Solanum lycopersicum*
	FJ869906	*Emilia yellow vein betasatellite*	China	*Emilia sonchifolia*
	FM164738	*Ageratum leaf curl Cameroon betasatellite*	Cameroon	*Ageratum conyzoides*
	FN435836	*Vernonia yellow vein betasatellite*	India	*Vernonia cinerea*
	GQ421324	*Leucas zeylanica yellow vein betasatellite*	Sri Lanka	*Leucas zeylanica*
	U74627	*Tomato leaf curl virus satellite*	Australia	-
Circovirus	AF071878	*Beak and feather disease virus*	USA	-
	AF071879	*Porcine circovirus 1*	USA	*Sus* sp.
	AF252610	*Pigeon circovirus*	Germany	*Pigeon*
	AJ301633	*Canary circovirus*	Italy	*Serinus canaria*
	AJ304456	*Goose circovirus*	Germany	*Anser* sp.
	AY228555	*Duck circovirus*	Germany	*Duck*
	AY651850	*Porcine circovirus 2*	China	*Sus* sp.
	DQ146997	*Raven circovirus*	Australia	*Corvus coronoides*

DQ172906	*Starling circovirus*	Germany	*Sturnus vulgaris*
DQ845074	*Gull circovirus*	United Kingdom	*Gull*
DQ845075	*Finch circovirus*	United Kingdom	*Chloebia gouldiae*
EU056309	*Swan circovirus*	Germany	*Cygnus olor*
GQ404851	*Chimpanzee associated circovirus 1*	Rwanda	*Pan troglodytes*
GQ404856	*Human associated circovirus 1*	Nigeria	*Homo sapiens*
GU799606	*Barbel circovirus*	Hungary	*Barbus barbus*
JQ011377	*European catfish circovirus*	Hungary	*Silurus glanis*
JQ814849	*Bat associated circovirus 3*	China	*Rhinolophus ferrumequinum*
JX863737	*Bat associated circovirus 1*	Myanmar	*Rhinolophus ferrumequinum*
KC241982	*Canine circovirus*	USA	*Canis lupus familiaris*
KC339249	*Bat associated circovirus 2*	Myanmar	*Rhinolophus ferrumequinum*
KJ020099	*Mink circovirus*	China	*Neovison vison*
KJ641711	*Bat associated circovirus 8*	China	*Myotis ricketti*
KJ641723	*Bat associated circovirus 7*	China	*Rhinolophus sinicus*
KJ641724	*Bat associated circovirus 6*	China	*Rhinolophus affinis*
KJ641727	*Bat associated circovirus 5*	China	*Plecotus auritus*
KJ641741	*Bat associated circovirus 9*	China	*Rhinolophus ferrumequinum*
KP793918	*Zebra finch circovirus*	Germany	*Taeniopygia guttata*

	KT783484	*Bat associated circovirus 4*	Brazil	*Tadarida brasiliensis*
	KT869077	*Porcine circovirus 3*	USA	*Sus domesticus*
	KU230452	*Tick associated circovirus 1*	USA	*Ixodes scapularis*
	KX756986	*Bat associated circovirus 10*	China	*Vespertilio sinensis*
	KX756996	*Bat associated circovirus 11*	China	*Hipposideros armiger*
	KX987146	*Tick associated circovirus 2*	China	*Ixodes scapularis*
	KY370027	*Rodent associated circovirus 5*	China	*Niviventer eha*
	KY370029	*Rodent associated circovirus 4*	China	*Allactaga sibirica*
	KY370034	*Rodent associated circovirus 1*	China	*Neodon clarkei*
	KY370037	*Rodent associated circovirus 6*	China	*Apodemus draco*
	KY370039	*Rodent associated circovirus 3*	China	*Neodon clarkei*
	KY370042	*Rodent associated circovirus 2*	China	*Apodemus chevrieri*
Flavivirus	AB114858	*Yokose virus*	Japan	*Miniopterus fuliginosus*
	AF160193	*Apoi virus*	-	*Apodemus* spp.
	AF161266	*Murray Valley encephalitis virus*	-	*Homo sapiens*
	AF253419	*Langat virus*	USA	*Ixodes granulatus*
	AJ242984	*Modoc virus*	USA	*Peromyscus maniculatus*
	AJ299445	*Montana myotis leukoencephalitis virus*	USA	*Myotis lucifugus*
	AY193805	*Omsk hemorrhagic fever virus*	-	-

AY323490	*Kyasanur Forest disease virus*	-	-
AY453411	*Usutu virus*	Austria	*Blackbird*
AY632535	*Zika virus*	Uganda	*Sentinel monkey*
AY632536	*Aroa virus*	USA	-
AY632539	*Ilheus virus*	USA	-
AY632540	*Kedougou virus*	Senegal	*Aedes minutus*
AY632541	*Kokobera virus*	USA	-
AY632545	*Bagaza virus*	Central African Republic	*Culex* spp.
DQ235144	*Meaban virus*	France	*Ornithodoros maritimus*
DQ235145	*Gadgets Gully virus*	Australia	*Ixodes uriae*
DQ235146	*Kadam virus*	Uganda	*Rhipicephalus pravus*
DQ235149	*Royal Farm virus*	Afghanistan	*Argas hermanni*
DQ235150	*Saumarez Reef virus*	Australia	*Ornithodoros capensis*
DQ525916	*Saint Louis encephalitis virus*	USA	-
DQ837641	*Entebbe bat virus*	Uganda	*Tadarida limbata*
DQ837642	*Sepik virus*	Papua New Guinea	*Mosquito*
DQ859056	*Banzi virus*	South Africa	-
DQ859057	*Bouboui virus*	Central African Republic	*Anopheles paludis*

DQ859060	*Edge Hill virus*	Australia	*Aedes vigilax*
DQ859062	*Saboya virus*	Senegal	*Tatera kempi*
DQ859065	*Uganda S virus*	Uganda	*Aedes* spp.
DQ859066	*Jugra virus*	Malaysia	*Aedes* spp.
EU082199	*Yaounde virus*	Cameroon	*Culex nebulosis*
EU082200	*Koutango virus*	Senegal	*Tatera kempi*
EU707555	*Wesselsbron virus*	South Africa	-
JF895923	*Tembusu virus*	China	*Goose*
JQ582840	*Rio Bravo virus*	USA	*Tadarida brasiliensis mexicana*
JX236040	*Ntaya virus*	Germany	*Mosquitoes*
KC734549	*Israel turkey meningoencephalomyelitis virus*	Israel	*Meleagris gallopavo*
KF815939	*Tyuleniy virus*	Russia	*Ixodes uriae*
KF917536	*Cacipacore virus*	Brazil	*Formicarius analis*
KJ469371	*Jutiapa virus*	Guatemala	*Sigmodon hispidus*
KJ469372	*Phnom Penh bat virus*	Cambodia	*Cynopterus brachyotis angulatus*
L06436	*Powassan virus*	Canada	*Homo sapiens*
M12294	*West Nile virus*	Germany	-
M18370	*Japanese encephalitis virus*	Japan	*Aedes albopictus*
U27495	*Tick-borne encephalitis virus*	Austria	*Ixodes ricinus*

	U87411	*Dengue virus*	Thailand	*Homo sapiens*
	X03700	*Yellow fever virus*	USA	*Homo sapiens*
	Y07863	*Louping ill virus*	United Kingdom	-
Potyvirus	AB011819	*Clover yellow vein virus*	Japan	-
	AB027007	*Japanese yam mosaic virus*	Japan	*Dioscorea japonica*
	AB219545	*Konjac mosaic virus*	Japan	*Amorphophallus konjac*
	AB246773	*East Asian Passiflora virus*	Japan	*Passiflora* sp.
	AB541985	*Pepper yellow mosaic virus*	Brazil	*Capsicum annuum*
	AB551370	*Brugmansia suaveolens mottle virus*	Brazil	-
	AB818538	*Habenaria mosaic virus*	Japan	*Habenaria radiata*
	AF023848	*Peanut mottle virus*	USA	*Arachis hypogaea*
	AF127929	*Zucchini yellow mosaic virus*	Taiwan	*Luffa cylindrica*
	AF169561	*Turnip mosaic virus*	Spain	*Brassica napus*
	AF348210	*Cowpea aphid-borne mosaic virus*	Zimbabwe	*Vigna* sp.
	AF499738	*Cocksfoot streak virus*	Germany	*Dactylis* sp.
	AF538686	*Bidens mottle virus*	Taiwan	*Helianthus annuus*
	AJ001691	*Maize dwarf mosaic virus*	Bulgaria	*Zea mays*
	AJ237843	*Chilli veinal mottle virus*	India	*Capsicum annuum*
	AJ243766	*Potato virus V*	United Kingdom	*Solanum* sp.

AJ243957	*Plum pox virus*	Serbia and Montenegro	*Prunus* sp.
AJ296311	*Potato virus A*	Hungary	*Solanum tuberosum*
AJ297628	*Sugarcane mosaic virus*	China	*Zea mays*
AJ298033	*Dasheen mosaic virus*	China	*Zantedeschia aethiopica*
AJ307057	*Leek yellow stripe virus*	China	*Allium sativum*
AJ310197	*Sorghum mosaic virus*	China	*Saccharum* sp.
AJ312437	*Bean common mosaic virus*	China	*Vigna* sp.
AJ316084	*Scallion mosaic virus*	China	*Allium chinense*
AJ437279	*Wild potato mosaic virus*	Peru	*Solanum chancayense*
AJ437280	*Peru tomato mosaic virus*	Peru	-
AJ510223	*Onion yellow dwarf virus*	China	*Allium sativum*
AJ564636	*Lily mottle virus*	China	*Lilium* sp.
AJ851866	*Thunberg fritillary mosaic virus*	China	*Fritillaria thunbergii*
AJ865076	*Shallot yellow stripe virus*	China	*Allium fistulosum*
AM039800	*Fritillary virus Y*	China	*Fritillaria thunbergii*
AM158908	*Narcissus yellow stripe virus*	China	*Narcissus tazetta*
AM181350	*Pepper severe mosaic virus*	South Korea	*Capsicum annuum*
AM182028	*Narcissus degeneration virus*	China	*Narcissus tazetta*
AY206394	*Beet mosaic virus*	USA	*Beta vulgaris*

AY437609	*Watermelon mosaic virus*	France	-
AY626825	*Zantedeschia mild mosaic virus*	Taiwan	*Zantedeschia* sp.
AY642590	*Pennisetum mosaic virus*	China	-
AY656816	*Wisteria vein mosaic virus*	China	*Wisteria* sp.
BD171712	*Papaya leaf distortion mosaic virus*	Japan	-
D00507	*Soybean mosaic virus*	USA	*Glycine max*
D10930	*Pea seed-borne mosaic virus*	Denmark	*Pisum sativum*
D83749	*Bean yellow mosaic virus*	Australia	*Vicia faba*
D86371	*Sweet potato feathery mottle virus*	Japan	*Ipomoea* sp.
DQ299908	*Daphne mosaic virus*	Czech Republic	*Daphne mezereum*
DQ645484	*Pepper veinal mottle virus*	Germany	*Capsicum frutescens*
DQ821938	*Basella rugose mosaic virus*	Taiwan	*Anredera cordifolia*
DQ851493	*Telosma mosaic virus*	Viet Nam	*Telosma cordata*
DQ851495	*Wild tomato mosaic virus*	Viet Nam	*Solanum torvum*
DQ851496	*Banana bract mosaic virus*	Philippines	*Musa* sp.
DQ925486	*Arracacha mottle virus*	Brazil	*Arracacia xanthorrhiza*
EF219408	*Tobacco vein banding mosaic virus*	China	*Nicotiana* sp.
EF427894	*Gloriosa stripe mosaic virus*	Taiwan	*Sandersonia aurantiaca*
EF579955	*Moroccan watermelon mosaic virus*	Tunisia	*Cucurbita pepo*

EU410442	*Algerian watermelon mosaic virus*	Algeria	*Cucurbita* sp.
EU564817	*Verbena virus Y*	USA	*Verbena* sp.
EU847625	*Lupinus mosaic virus*	Czech Republic	*Lupinus polyphyllus*
FM206346	*Freesia mosaic virus*	South Korea	*Freesia* sp.
GQ421689	*Canna yellow streak virus*	United Kingdom	*Canna* sp.
GQ916624	*Panax virus Y*	China	*Panax notoginseng*
GU181199	*Sunflower chlorotic mottle virus*	Argentina	*Helianthus annuus*
GU207957	*Sweet potato virus C*	Peru	*Ipomoea* sp.
HM363516	*Apium virus Y*	USA	*Apium graveolens*
HQ122652	*Passion fruit woodiness virus*	Australia	*Passiflora caerulea*
HQ161081	*Hardenbergia mosaic virus*	Australia	*Hardenbergia comptoniana*
HQ676607	*Celery mosaic virus*	USA	*Apium graveolens*
JF838187	*Keunjorong mosaic virus*	South Korea	*Cynanchum wilfordii*
JN008909	*Chilli ringspot virus*	China	*Capsicum* sp.
JN190431	*Yambean mosaic virus*	Peru	*Pachyrhizus erosus*
JN613807	*Sweet potato virus 2*	USA	*Ipomoea batatas*
JQ314463	*Tomato necrotic stunt virus*	Mexico	*Solanum lycopersicum*
JQ350738	*Sunflower mild mosaic virus*	Argentina	*Helianthus annuus*
JQ395040	*Hippeastrum mosaic virus*	Australia	*Hippeastrum* sp.

JQ692088	*Zea mosaic virus*	Iran	*Sorghum halepense*
JQ723475	*Cyrtanthus elatus virus A*	Australia	*Cyrtanthus elatus*
JQ801448	*Colombian datura virus*	United Kingdom	*Nicotiana tabacum*
JQ807997	*Ornithogalum mosaic virus*	Australia	*Diuris magnifica*
JQ807999	*Blue squill virus A*	Australia	*Diuris corymbosa*
JQ824374	*Sweet potato virus G*	Argentina	*Ipomoea batatas*
JX156422	*Donkey orchid virus A*	Australia	*Diuris corymbosa*
JX156434	*Carrot thin leaf virus*	USA	*Coriandrum sativum*
JX291161	*Pokeweed mosaic virus*	USA	*Phytolacca americana*
JX470965	*Yam mild mosaic virus*	Brazil	*Dioscorea trifida*
JX867236	*Brugmansia mosaic virus*	South Korea	*Brugmansia suaveolens*
KC345607	*Zucchini tigre mosaic virus*	France	*Momordica charantia*
KC443039	*Sweet potato latent virus*	Taiwan	*Ipomoea batatas*
KC691259	*Narcissus late season yellows virus*	Australia	*Narcissus* sp.
KF649336	*Bidens mosaic virus*	Brazil	*Bidens pilosa*
KF906523	*Vanilla distortion mosaic virus*	India	*Coriandrum sativum*
KJ830760	*Asparagus virus 1*	Germany	-
KM523548	*Tamarillo leaf malformation virus*	Colombia	*Solanum betaceum*
KP343681	*Catharanthus mosaic virus*	USA	*Mandevilla* sp.

KP769852	*Lettuce Italian necrotic virus*	Italy	*Lactuca sativa*
KT222674	*Jasmine virus T*	China	*Jasminum* sp.
KT633868	*Pecan mosaic-associated virus*	China	*Carya illinoensis*
KT692938	*Iris severe mosaic virus*	China	*Iris* sp.
KT834407	*Tobacco mosqueado virus*	Brazil	*Nicotiana tabacum*
KU355553	*Zucchini shoestring virus*	South Africa	*Cucurbita pepo*
KU556609	*Daphne virus Y*	South Korea	*Daphne odora*
KU685505	*Barbacena virus Y*	Brazil	-
KU941946	*Endive necrotic mosaic virus*	France	*Lactuca sativa*
KU981084	*Impatiens flower break virus*	South Korea	*Impatiens walleriana*
KX013584	*Callistephus mottle virus*	South Korea	*Callistephus chinensis*
KX355613	*Euphorbia ringspot virus*	Germany	*Euphorbia milii x lophogona*
KX856009	*Sunflower ring blotch virus*	Argentina	*Helianthus annuus*
KY562565	*Saffron latent virus*	Iran	*Crocus sativus*
KY623505	*Sudan watermelon mosaic virus*	Sudan	*Cucumis melo*
KY623506	*Wild melon banding virus*	Sudan	*Cucumis melo*
KY657266	*Cucurbit vein banding virus*	Argentina	*Cucurbita maxima*
KY828925	*Hyacinth mosaic virus*	Australia	*Muscari neglectum*
LC159494	*Wild onion symptomless virus*	Turkey	*Allium* sp.

M11458	*Tobacco etch virus*	USA	*Nicotiana tabacum*
M96425	*Pepper mottle virus*	USA	*Capsicum* sp.
MF509898	*Paris mosaic necrosis virus*	China	*Daiswa polyphylla*
MF953305	*Mediterranean ruda virus*	Spain	*Ruta montana*
MF997470	*African eggplant mosaic virus*	Tanzania	*Solanum aethiopicum*
MH779475	*Henbane mosaic virus*	USA	*Hyoscamus niger*
MK440140	*Alstroemeria mosaic virus*	Ecuador	*Alstroemeria* sp.
U09509	*Potato virus Y*	Canada	*Solanum tuberosum*
U19287	*Bean common mosaic necrosis virus*	USA	*Phaseolus vulgaris*
U42596	*Yam mosaic virus*	Ivory Coast	*Dioscorea* sp.
X04083	*Tobacco vein mottling virus*	USA	-
X67673	*Papaya ringspot virus*	Taiwan	-
X97705	*Lettuce mosaic virus*	France	*Lactuca sativa*
Z26920	*Johnsongrass mosaic virus*	Australia	-

[-] Not Specified