

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create 19 new species in the genus *Begomovirus* (*Geplafuvirales*: *Geminiviridae*) |
| **Code assigned:**  | 2024.010P.A.v1.Begomovirus\_19nsp |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| *Geminiviridae* and *Tolecusatellitidae* Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
| *Geminiviridae* and *Tolecusatellitidae* SG |  |  |  |
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| **Submission date:** |  10/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** |  DD/MM/YYYY |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Name of accompanying Excel module:**  |
| 2024.010P.A.v1.Begomovirus\_19nsp.xlsx |

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| **Taxonomic changes proposed:**  |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:**  |  **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached**  |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank affected*: Species in the genus *Begomovirus* *Description of current taxonomy*: *Monodnaviria* -> *Shotokuvirae* -> *Cressdnaviricota* -> *Repensiviricetes* -> *Geplafuvirales* -> *Geminiviridae* -> *Begomovirus* Within the genus *Begomovirus*, viruses are classified into species based on a 91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity threshold [1].*Proposed* *taxonomic changes:* We propose the establishment of 19 new species to classify new begomoviruses that have been identified and described in the literature over the last three years.*Justification*: All 19 proposed new species have <91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity with sequences of members of currently established begomovirus species. |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Species in the genus *Begomovirus* *Description of current taxonomy*: *Begomovirus* is the largest genus in the virosphere, with 445 species. *Proposed* *taxonomic change(s)*: We propose to establish 19 new species in the genus *Begomovirus*. *Demarcation criteria:* A 91% genome-wide (or DNA-A in the case of bipartite begomoviruses) pairwise identity species demarcation threshold has been adopted [1]. *Justification*: The sequences of all 19 viruses summarized in Table 1 can be classified into new species as they share <91% genome-wide (or DNA-A in the case of bipartite begomoviruses) pairwise identity with all classified begomoviruses. This is supported by maximum likelihood phylogenetic analysis (a phylogenetic tree of all 445+19 begomoviruses is too large for a one-page format and will be provided as a pdf file to be visualized in the computer screen). We provide a brief description of each proposed new species below:***Begomovirus chuxiongense***[2]- Virus name: tomato leaf curl Chuxiong virus (TLCCxV) - Isolated from a tobacco plant with leaf curling and vein thickening symptoms collected from Liangshan and Panzhihua cities of Sichuan province of China in 2020- PCR with abutting primers, cloning and Sanger sequencing- DNA-A-like monopartite genome; no DNA-B or satellites amplified from the samples- Phylogenetic analysis grouped the new virus in the clade of the monopartite Old World begomoviruses- Construction of an infectious clone and biological assays: confirmation of Koch's postulates and monopartite nature of the virus- Highest nucleotide sequence identity of 88.65% with croton yellow vein mosaic virus (KX671964)- Species epithet based on location where the virus was isolated***Begomovirus solanumaureusreti* and *Begomovirus solanumflavusreti***[3]- Virus names: tomato golden net virus (ToGNV) and tomato yellow net virus (ToYNV) - ToGNV isolated from a tomato plant collected in 2015 in Itacarambi, state of Minas Gerais, Brazil; ToYNV was detected in two samples collected in 2003 in Leopoldo de Bulhões and Goianópolis, respectively, both in the state of Goiás, Brazil- RCA products digested with restriction enzymes, cloning and Sanger sequencing- Both new viruses appear to be monopartite (no DNA-B amplified from the samples); no attempts to detect DNA satellites- Phylogenetic analysis grouped the new viruses with other begomoviruses isolates in Brazil; the most closely related viruses have bipartite (not monopartite) genomes- ToGNV has the highest nucleotide sequence identity of 85% with tomato bright yellow mosaic virus (ToBYMoV, KC791691) and tomato golden leaf spot virus (ToGLSV, KC626021); ToYNV has the highest nucleotide sequence identity of 89% with tomato chlorotic leaf curl virus (ToCLCV, MK558058)- Species epithets based on host genus name plus genitive forms for golden net and yellow net***Begomovirus whitaniae***[4]- Virus name: Withania leaf curl virus (WLCV) - Isolated from a *Withania somnifera* (Indian ginseng) plant collected from an experimental field of CSIR-CIMAP, Lucknow, India, in 2019- RCA products digested with restriction enzymes, cloning and Sanger sequencing- DNA-A-like monopartite genome, with a betasatellite- Phylogenetic analysis grouped the new virus with other monopartite OW begomoviruses- Transmission electron microscopy, with image of geminate particles- Highest nucleotide sequence identity of 88% with cherry tomato leaf curl virus (CToLCV, LN906594)- Sequence is highly divergent in the 5'-region of the Rep gene (nt 2458-2758); N-terminus of Rep protein (aa 1-55) is also highly divergent- Species epithet based on host genus name***Begomovirus sidaflavusfolii***[5]- Virus name: Sida chlorotic leaf virus (SiChLV)- Isolated from *Sida* sp. and *Malvastrum* sp. plants collected from Colima, Mexico, in August 2018- Positive plants identified by RCA-RFLP; RCA products sequence in the Illumina platform; PCR products obtained with specific primers cloned and Sanger sequenced- Bipartite New World begomovirus- Phylogenetic analysis grouped the new virus in the AbMV clade of New World begomoviruses- Construction of an infectious clone and biological assays: Koch's postulates confirmed- Highest nucleotide sequence identity of 86.4% with cucumber chlorotic leaf virus (CuChLV, MN013786)- Species epithet based on host genus name plus genitive form for yellow leaf***Begomovirus cajani*** [6]- Virus name: Cajanus scarabaeoides yellow mosaic virus (CsYMV)- Isolated from a *Cajanus scarabaeoides* plant collected in Chhattisgarh State, India, in 2021- Positive plants identified by RCA-RFLP; RCA products cloned and Sanger sequenced- Bipartite Old World begomovirus- Phylogenetic analysis grouped the new virus with other Old World begomoviruses from the Indian Subcontinent- Construction of an infectious clone and biological assays: Koch's postulates confirmed- Highest nucleotide sequence identity of 81.1% and 74% (DNA-A and DNA-B, respectively) with Rhynchosia yellow mosaic virus (RhYMV, AM999981 and AM999982)- Species epithet based on host genus name***Begomovirus* *hortuscrotoni*** [7]- Virus name: garden croton enation leaf vurl virus (CroELCuV)- Isolated from *Codiaeum variegatum* plants found in several gardens in Varanasi, Uttar Pradesh state, India- Partial sequences were amplified by PCR from 10 plants, and two samples were chosen for complete genome amplification (DNA-A and DNA-B) using RCA- Sanger sequencing was employed to obtain the complete sequence after RCA and cloning.- A typical bipartite Old World begomovirus- Highest nucleotide sequence identity of 85.7% with tomato leaf curl Karnataka virus (MG758148)- Species epithet based on genitive form of host common name (garden croton)**Begomovirus** ***jatrophagunturense*** [8]- Virus name: Jatropha leaf curl Guntur virus- Isolated from a *Jatropha gossypiifolia* plant collected in Guntur, Andhra Pradesh state, India- Sanger sequencing was used to obtain the complete sequence after RCA amplification and cloning- A typical monopartite Old World begomovirus- Highest nucleotide sequence identity of 80.6% with croton yellow vein virus (FN645902)- Species epithet based on host genus name plus location where the virus was isolated***Begomovirus hyptidis*** [9]- Virus name: Hyptis golden mosaic virus (HpGMV)- Isolates from a single *Hyptis pectinata* plant collected at Prosperina, Guayas province, Ecuador, in 2019- HTS-Illumina, starting from total RNA, was used to initially identify contigs (DNA-A, DNA-B). Then, Nanopore technology was used to sequence PCR amplicons obtained with back-to-back primers. Finally, Sanger sequencing confirmed the consensus obtained by Nanopore sequencing.- A typical bipartite New World begomovirus- Highest nucleotide sequence identity (DNA-A) of 84.3% with tomato vein clearing leaf deformation virus (MK423208)- Species epithet based on host genus name***Begomovirus galii*** [10]- Virus name: Galium leaf distortion virus (GLDV) - Isolated from a *Galium mexicanum* plant in Mexico- Complete genome cloned using RCA, and Sanger-sequenced- DNA-A-like monopartite genome- Phylogenetic analysis grouped the new virus in the clade of the monopartite New World begomoviruses- Construction of an infectious clone and biological assays: confirmation of Koch's postulates and monopartite nature of the virus- Highest nucleotide sequence identity of 79.88% with tomato leaf deformation virus (ToLDeV), isolate PA10-S9 (JX501506)- Species epithet based on host genus name***Begomovirus myanmarense*** [11]- Virus name: tobacco curly shoot Myanmar virus - Isolates from a pepper plant in Myanmar- Complete genome cloned and Sanger-sequenced after RCA- Highest nucleotide sequence identity of 85–86% with tobacco curly shoot virus (TbCSV) isolate Y35 from China (AJ420318)- Phylogeny: Overlapping complex group at less than 90% nucleotide identities with tobacco curly shoot virus (TbCSV) and ChiLCV/PK isolates- It was shown to be a recombinant between TbCSV and ChiLCV- Species epithet based on location where the virus was isolated***Begomovirus caboniensis*** [12]- Virus name: Cnidoscolus mild mosaic virus - Isolated from a *Cnidoscolus urens* (Euphorbiaceae) plant in Cabo de Santo Agostinho, Pernambuco state, Brazil- Typical New World bipartite begomovirus- Complete viral genome amplified by RCA, cloned and Sanger sequenced - Highest nucleotide identity sequence of 88.9% with Cnidoscolus mosaic leaf deformation virus (CnMLDV) (KT966771)- Species epithet based on location where the virus was isolated ***Begomovirus pyrenacanthae*** [13]- Virus name: Pyrenacantha yellow mosaic virus (PyYMV)- Isolated from a *Pyrenacantha* sp. plant in Mozambique- Bipartite Old World begomovirus- RCA-based cloning of the complete DNA-A and -B followed by Sanger sequencing- Highest nucleotide sequence identity of 78.5% with the DNA-A of tomato leaf curl Namakely virus (TLCNaV, AM701764)- Phylogeny: distinct branch- Species epithet based on genitive form of the host genus***Begomovirus puerense*** [14]- Virus name: tobacco leaf curl Puer virus, Yunnan, China - Monopartite Old World begomovirus- RCA-based cloning of the complete genome, cloning and Sanger sequencing- Highest nucleotide sequence identity of 83.43% with tomato yellow leaf curl Vietnam virus (TYLCVV) isolate TYLCVV-DX1 (EU189150)- Recombinant nature- Species epithet based on location where virus was isolated***Begomovirus solanumdistorsionis*** [15]- Virus name: tomato mottle leaf distortion virus (ToMoLDiV) - Isolate from a tomato plant in Goiás state, Brazil, in April 2020- Bipartite New World begomovirus- Nanopore sequencing of partially digested RCA product; confirmed by Sanger sequencing of cloned RCA product- DNA-A showed highest nucleotide sequence identity of 81.64% with tomato golden leaf distortion virus (ToGLDV, HM357456)- DNA-B shared 82.57% nt identity with tomato interveinal chlorosis virus 2 (ToICV-2, MK087039) - Species epithet based on host genus name plus genitive form for distortion***Begomovirus alceacrispi*** [16]- Virus name: hollyhock vein yellowing virus (HoYVV)- Isolated from hollyhock plants collected in Punjab Province, Pakistan, in 2014- Two samples exhibiting different symptoms: one showed leaf crumple symptoms, the other one showed yellow vein mosaic symptoms - Monopartite Old World begomovirus alone (leaf crumple symptoms) or associated with a betasatellite (yellow vein mosaic)- PCR of full length begomovirus genome with universal primer pair BGAF/BGAR - PCR of full length betasatellite genome with universal primer pair B01-B02- Sanger-sequencing of PCR product- Two sequences of the A component, one from each sample, showed 99.9% identity to each other and displayed highest sequence identity of 90% with an isolate of pedilanthus leaf curl virus (PeLCV) from Pakistan (DQ116884). -- The virus alone infects hollyhock inducing leaf crumple symptoms - Species epithet based on host genus name plus genitive form for crumple***Begomovirus muntiflavi*** [17]- Virus name: Muntingia yellow spot virus- Isolates from a *Muntingia calabura* plant collected in Guayas province, Ecuador, in January 2017- Typical bipartite New World begomovirus- RCA and cloning of digested products, followed by Sanger sequencing by primer walking - Three sequences of the A component, 93.7-96.5% identical to each other and displaying highest nucleotide sequence identity of 87.4-88.1%to isolates of pepper leafroll virus (PepLRV, MH481901 and KC769819) - The DNA-B clone displayed highest nucleotide sequence similarity of 79.3-79.6% to PepLRV isolates (MH48190 and KC769820) - Species epithet based on host genus name plus genitive form for yellow***Begomovirus flavintervenae*** [18]- Virus name: tomato interveinal yellowing virus (ToIYV)- Isolated from tomato samples with interveinal yellowing and/or leaf curling collected in 2019 at Nyeou (Worodougou region in NW Cote d’Ivoire) - Degenerate primers were used to try to find B component or DNA beta-satellites, with no success- RCA product digested with BamHI produced single band of ~2.8 Kbp, which was cloned and Sanger-sequenced- Two clones from different samples had sequences with 98.3% nucleotide sequence identity, and a highest identity of 83% with tobacco leaf curl Zimbabwe virus (ToLCZWV)- ToIYV, TbLCZWV and tomato leaf curl Kunene virus (ToLCKunV) form a distinct branch in the phylogenetic tree (outliers of the West and Central African tomato-infecting begomoviruses- Species epithet based on genitive form for interveinal chlorosis***Begomovirus phaseoliparvi*** [19]- Virus name: bean bushy stunt virus (BBSV)- Isolated from common bean plants in Salta province, NW Argentina in 2017- Used Dot-Blot with general probe to detect viruses and then specific probes for BCMV, ToYSV, SbBMV, ToMoWrV, SiGMBRV and ToYVSV; ~ 20% of samples showed geminivirus infection, ~60% showed mixed infection- RCA was performed followed by digestion with restriction enzymes; ~2.6 bands were cloned- Cloned samples were Sanger sequenced - Sample P179 produced DNA-A and DNA-B clones (MN414067 and MN414068, respectively)- Typical of New World bipartite begomoviruses- DNA-A and -B are cognates (95.8% sequence identity in the CR)- Highest nucleotide sequence identity of 84.6% and 72.04% with pepper leafroll virus (PepLRV, KC769819) and melochia mosaic virus (MelMV, KT201152), for DNA-A and DNA-B, respectively- Clones were tested by biolistics, all inoculated plants showed leaf roll, dwarfism and stunting- Host range was tested for beans, tomato, pepper, soybean and *Leonurus sibiricus*; only beans and soybeans showed symptoms- Species epithet based on genitive form for stunted beans***Begomovirus sidaflavitessellati*** [20]- Virus name: sida yellow mosaic Gujarat virus (SiYMGV)- Isolated from a *Sida* spp. sample collected around agricultural fields in Gujarat state, India, in 2016- Degenerate primers showed presence of geminiviruses in symptomatic plants (*n*=10) but not in asymptomatic plant (*n*=1)- Amplified fragments were cloned and sequenced, 98-99% nucleotide identity with each other- One sample (S9) was RCA amplified, the product was digestions with several restriction enzymes and ~2.7 fragments were cloned; all cloned products were Sanger-sequenced- Highest nucleotide sequence identity of 90.4% with pea leaf distortion virus (PLDV, JQ327840)- Species epithet based on host genus name plus genitive form for yellow mosaic |

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| **References:**  |
| [1] Brown JK, Zerbini FM, Navas-Castillo J, Moriones E, Ramos-Sobrinho R, Silva JC, et al. Revision of Begomovirus taxonomy based on pairwise sequence comparisons. Arch Virol. 2015;160:1593-619.[2] Chen Y, Guo S, Jiang L, Yan F, Hao K, Wang Z, An M, Xia Z, Li F, Zhou X, Wu Y. Molecular characterization and pathogenicity of a novel monopartite geminivirus infecting tobacco in China. Virology. 2024;594:110061. doi: 10.1016/j.virol.2024.110061. PMID: 38518441.[3] Reis LNA, Boiteux LS, Fonseca MEN, Rojas MR, Gilbertson RL, Pereira-Carvalho RC. Tomato golden net virus and tomato yellow net virus: two novel New World begomoviruses with monopartite genomes. Arch Virol. 2023;168:235. doi: 10.1007/s00705-023-05836-0. PMID: 37642719.[4] Khan A, Saeed ST, Sinha S, Yadav SS, Samad A. Identification and characterization of a novel begomovirus, *Withania leaf curl virus* associated with leaf curl disease of *Withania somnifera*. 3 Biotech. 2023:178. doi: 10.1007/s13205-023-03606-y. PMID: 37188293.[5] García-Rodríguez DA, Partida-Palacios BL, Regla-Márquez CF, Centeno-Leija S, Serrano-Posada H, Bañuelos-Hernández B, Cárdenas-Conejo Y. *Sida chlorotic leaf virus*: a new recombinant begomovirus found in non-cultivated plants and *Cucumis sativus* L. PeerJ. 2023;11:e15047. doi: 10.7717/peerj.15047. PMID: 36974135.[6] Dokka N, Marathe A, Sahu B, Kaushal P, Ghosh PK, Sivalingam PN. Cajanus scarabaeoides yellow mosaic virus, a new bipartite begomovirus causing yellow mosaic disease in *Cajanus scarabaeoides* in India. Plant Dis. 2023;107:2924-2928. doi: 10.1094/PDIS-06-22-1473-SC. PMID: 36890129.[7] Venkataravanappa V, Vinaykumar HD, Hiremath S, Mantesh M, Shankarappa KS, Basha CRJ, Reddy MK, Reddy CNL. Molecular characterization of novel bipartite begomovirus associated with enation leaf disease of Garden croton (*Codiaeum variegatum* L.). Virusdisease. 2022;33:194-207. doi: 10.1007/s13337-022-00772-0. PMID: 35991698.[8] Gireeshbai S, Prabhudas SK, Sharma SK, Mandal B, Roy A, Geetanjali AS. Mixed infection of a new begomovirus, Jatropha leaf curl Guntur virus and recombinant/chimeric jatropha leaf curl Gujarat virus in *Jatropha gossypiifolia*. Lett Appl Microbiol. 2022;75:1000-1009. doi: 10.1111/lam.13774. PMID: 35723883.[9] Reyes-Proaño E, Alvarez-Quinto R, Delgado-Jiménez JA, Cornejo-Franco JF, Mollov D, Bejerman N, Quito-Avila DF. Genome characterization and pathogenicity of two New *Hyptis pectinata* viruses transmitted by distinct insect vectors. Phytopathology. 2022;112:2440-2448. doi: 10.1094/PHYTO-04-22-0130-R. PMID: 35694887.[10] Guevara-Rivera EA, Rodríguez-Negrete EA, Aréchiga-Carvajal ET, Leyva-López NE, Méndez-Lozano J. From metagenomics to discovery of new viral species: Galium leaf distortion virus, a monopartite begomovirus endemic in Mexico. Front Microbiol. 2022;13:843035. doi: 10.3389/fmicb.2022.843035. 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| **Tables, Figures:** |

**Table 1.** Summary of the 19 new species in the genus *Begomovirus* and their members.

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| Species name | Accession no. | Virus name | Isolate name | Country | Host/source | Ref. |
| *Begomovirus chuxiongense* | OR543988 | tomato leaf curl Chuxiong virus | SC-1 | China | *Nicotiana tabacum* | 2 |
| *Begomovirus solanumaureusreti* | MT214095 | tomato golden net virus | MG-378 LR\_LVV 15 | Brazil | *Solanum lycopersicon* | 3 |
| *Begomovirus solanumflavusreti* | MT214096 | tomato yellow net virus | GO-169 LR\_LVV 14 | Brazil | *Solanum lycopersicon* | 3 |
| *Begomovirus whitaniae* | OP617239 | Withania leaf curl virus  | Ws | India | *Withania sonifera* | 4 |
| *Begomovirus sidaflavusfolii* | MN013784, MN013785 | sida chlorotic leaf virus  | Colima | Mexico | *Sida sp.* | 5 |
| *Begomovirus cajani* | OM397101, OM397102 | Cajanus scarabaeoides yellow mosaic virus | Baronda Raipur | India | *Cajanus scarabaeoides* | 6 |
| *Begomovirus hortuscrotoni* | MW816855, MW816857 | garden croton enation leaf curl virus | CR1A | India | *Codiaeum variegatum* | 7 |
| *Begomovirus jatrophagunturense* | MZ217773 | Jatropha leaf curl Guntur virus | GuWC10 | India | *Jatropha gossypiifolia* | 8 |
| *Begomovirus hyptidis* | ON073795, ON073796 | Hyptis golden mosaic virus | Prosperina | Ecuador | *Hyptis pectinata* | 9 |
| *Begomovirus galii* | OL689630 | Galium leaf distortion virus  | GMV-1 | Mexico | *Galium mexicanum*  | 10 |
| *Begomovirus myanmarense* | MK920410 | tobacco curly shoot Myanmar virus | MM16P1 | Myanmar | Pepper | 11 |
| *Begomovirus caboniensis* | MZ465527, MZ465585 | Cnidoscolus mild mosaic virus | BR\_CA96\_19A | Brazil | *Cnidoscolus urens*  | 12 |
| *Begomovirus pyrenacanthae* | MZ390982, MZ390984 | Pyrenacantha yellow mosaic virus  | MZ:Mal170.2:19 | Mozambique | *Pyrenacantha sp.* | 13 |
| *Begomovirus puerense* | MZ465370 | tobacco leaf curl Puer virus | TbLCPeV | China | *Nicotiana tabacum* | 14 |
| *Begomovirus solanumdistorsionis* | MW561191, MW650837 | tomato mottle leaf distortion virus | 22682 | Brazil | *Solanum lycopersicum* | 15 |
| *Begomovirus alceacrispi*  | LK028571 | hollyhock vein yellowing virus | 3AK | Pakistan | *Alcea rosea* | 16 |
| *Begomovirus muntiflavi* | MW032664, MW032665 | Muntingia yellow spot virus | E56P11A | Ecuador | *Muntingia calabura*  | 17 |
| *Begomovirus flavintervenae* | MW057360 | tomato interveinal yellowing virus | CI-Nyeou-CI359-BamD-2019 | Cote d’Ivoire | *Solanum lycopersicum* | 18 |
| *Begomovirus sidaflavitessellati* | KX513859 | sida yellow mosaic Gujarat virus | India-Gandhinagar-2016 | India | *Sida* spp | 19 |