

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create three (3) new species in the genus *Begomovirus* (family *Geminiviridae*) |
| **Code assigned:** | 2025.010P.Ac.v4.Geminiviridae\_Begomovirus\_3nsp |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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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* |

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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* |  |  |  |

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| **Submission date:** | 05/06/2025 |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **X** |
| 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| W - Withdrawn |  |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:** |
| The EC voted Ac for this proposal (see the table above for explanation), to allow very minor revisions mainly concerning style issues and the replacement of the figures by original ones. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| All style-related suggestions were accepted. All three figures were replaced, and are now original to avoid copyright issues. |

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| **Revision date:** | 28/8/2025 |

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

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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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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *"Begomovirus clitoriae"* | From the host, *Clitoria ternatea* |
| *"Begomovirus melochiasecundi"* | The second species named after the host, *Melochia tomentosa* |
| *"Begomovirus citharexyli"* | From the host, *Citharexylum* *spinosum* |

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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank affected*:  Genus *Begomovirus* in the family *Geminiviridae*  *Description of current taxonomy*:  *Monodnaviria* -> *Shotokuvirae* -> *Cressdnaviricota* -> *Repensiviricetes* -> *Geplafuvirales* -> *Geminiviridae* -> *Begomovirus*  *Begomovirus* is one of the largest genera in the virosphere, with 464 species. 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:*  Creation of 3 new species to classify new begomoviruses that have been identified and described in the literature over the past two years.  *Justification*:  Members of all 3 proposed new species share <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 affected*:  Genus *Begomovirus* in the family *Geminiviridae*  *Description of current taxonomy*:  *Monodnaviria* -> *Shotokuvirae* -> *Cressdnaviricota* -> *Repensiviricetes* -> *Geplafuvirales* -> *Geminiviridae* -> *Begomovirus*  *Begomovirus* is one of the largest genera in the virosphere, with 464 species.  *Proposed* *taxonomic changes*:  Create 3 new species in the genus *Begomovirus*.  *Demarcation criteria:* 91% genome-wide (or DNA-A in the case of bipartite begomoviruses) pairwise identity threshold [1].  *Justification*: The 3 begomoviruses summarized in Table 1 can be classified into new species that 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.  We provide a brief description of each proposed new species below:    ***"Begomovirus clitoriae"*** [2]  - Leaf samples from two *Clitoria ternatea* plants exhibiting yellow mosaic symptoms were collected in Kanpur, Uttar Pradesh, India, in August 2023  - Total DNA was extracted and used as a template for rolling circle amplification (RCA); RCA products were digested with restriction enzymes and a band with ~2.7 kb was cloned and Sanger sequenced  - The clone corresponded to a begomovirus, and sequence demarcation tool SDT analysis indicated a maximum nucleotide sequence identity of 82.6% with the DNA-A of Cajanus scarabaeoides yellow mosaic virus (CsYMV, OM397101) (Figure 1)  - A cognate DNA-B was also cloned and sequence, displaying a maximum nt sequence identity of 72.2% with the DNA-B of Rhincosia yellow mosaic virus (RhYMV, AM999982)  - The authors propose to classify the new begomovirus isolate, named butterfly pea yellow mosaic virus (BpYMV), into a new species, for which they propose the name "*Begomovirus clitoriae"*  ***"Begomovirus melochiasecundi"*** [3]  - The virus was isolated from a non-symptomatic *Melochia tomentosa* (family Malvaceae) plant; the plant species was confirmed by sequencing of *matK* and *rbcL* genes  - The sequence was obtained using standard procedures (RFLP-RCA, cloning) and used for percentage nucleotide identity comparisons (SDT)  - The DNA-A-like sequence shared the highest nucleotide sequence similarity with African monopartite begomoviruses, including tomato curly stunt virus (TCSV) [MT878426] (71.7% identity) (Figure 2)  - No evidence of recombination events, no DNA-B or satellite DNA sequences were detected in the sample  - The authors propose to classify the new begomovirus isolate, named Melochia associated virus (MeAV), into a new species, for which they initially proposed the name "*Begomovirus melochiae*". However, this species name already exists, and therefore the SG proposes the name "*Begomovirus melochiasecundi*"  ***"Begomovirus citharexyli"*** [4]  - The sequence was obtained using standard procedures (RCA, cloning) and used for percentage nucleotide identity comparisons (SDT)  - The DNA-A-like sequence shares 88.7% nucleotide sequence identity with papaya leaf crumple virus (PaLCrV) isolate (KR071789) and 88.5% with rose leaf curl virus (OQ411588) (Figure 3)  - A putative recombination event was identified in CitLCuV genome at nt position 70-2106, with tomato leaf curl Kerala virus (KF551575) as major parent and Chenopodium leaf distortion virus (MN423112) as minor parent (RDP4, 7 detection methods with significant *p* values)  - Phylogenetic tree placed CitLCuV in a sister clade to PaLCrV  - No satellite DNA sequences were detected in the sample by PCR methods with universal primers  - The authors propose to classify the new begomovirus isolate, named Citharexylum leaf curl virus (CitLCuV), into a new species, but do not propose a species name  - The SG proposes the species name "*Begomovirus* *citharexyli*" |

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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]   Akram M, Kumar D, Kamaal N. Complete genome sequence of a novel bipartite begomovirus infecting butterfly pea (*Clitoria ternatea* L.) in India. Arch Virol. 2024;170:7.  [3]   Ouattara A, Kéré D, Hoareau M, Koïta K, Lefeuvre P, Lett JM. A new monopartite begomovirus infecting *Melochia tomentosa* in Burkina Faso. Arch Virol. 2024;169:240.  [4]   Diksha D, Sidharthan VK, Baranwal VK. Identification of a novel monopartite begomovirus associated with leaf curl disease of *Citharexylum spinosum* in India. Virus Genes 2024;60:568-571.  [5]   Muhire BM, Varsani A, Martin DP. SDT: A virus classification tool based on pairwise sequence alignment and identity calculation. PLOS One 2014;9:e108277.  [6]   Katoh K, Standley DM. MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Mol Biol Evol. 2013;30:772.  [7]   Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. Mol Biol Evol. 2015;32:268.  [8]   Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS. ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods. 2017;14:587.  [9]   Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS. UFBoot2: Improving the ultrafast bootstrap approximation. Mol Biol Evol. 2018;35:518. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.010P.A.v1.Geminiviridae\_Begomovirus\_3nsp | spreadsheet |
| **Tables, Figures:** | |

**Table 1.** Summary of the 3 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 clitoriae"* | PQ298353 (DNA-A), PQ298354 (DNA-B) | butterfly pea yellow mosaic virus (BpYMV) | India:Kanpur:2024 | India | *Clitoria ternatea* | 2 |
| *"Begomovirus melochiasecundi"* | PP897773 | melochia associated virus (MeAV) | Burkina Faso:Goue:Melochia:856BB:2016 | Burkina Faso | *Melochia tomentosa* | 3 |
| *"Begomovirus citharexyli"* | OR437368 | Citharexylum leaf curl virus (CitLCuV) | Hyderabad | India | *Citharexylum spinosum* | 4 |

A diagram of dna and dna

AI-generated content may be incorrect.

**Figure 1.** Pairwise nucleotide sequence identities (%) for the full-length DNA-A and DNA-B sequences of butterfly pea yellow mosaic virus (BpYMV; "*Begomovirus clitoriae*") and the most closely related begomoviruses.

A diagram of a number of different colored squares

AI-generated content may be incorrect.

**Figure 2. (A)** Pairwise nucleotide sequence identity matrix of the complete DNA-A sequence of Melochia associated virus (MeAV; "*Begomovirus melochiasecundi*") and the most closely related begomoviruses. Identities were calculated with SDT [5] v. 2 (https://github.com/SDT-org/SDT2/releases/tag/v2.0.0. pre.20250723). **(B)** Midpoint-rooted, maximum-likelihood phylogenetic tree based on the same data set as in (A). Filled circles at the branches indicate bootstrap values >85%, open circles indicate values between 50 and 84%. The scale bar indicates nucleotide substitutions per site. Sequences were aligned with MAFFT [6] and the tree was constructed with IQ-TREE [7] using the TIM3+F+I+G4 nucleotide substitution model (determined by ModelFinder [8]) and the ultrafast bootstrap option [9]. The tree was edited in FigTree (tree.bio.ed.ac.uk/software/figtree).

A diagram of a variety of colors

AI-generated content may be incorrect.

**Figure 3.** (A) Pairwise nucleotide sequence identiy matrix of the complete genome of Citharexylum leaf curl virus (CitLCuV; "*Begomovirus citharexyli*") and the most closely related begomoviruses. Identities were calculated with SDT [5] v. 2 (https://github.com/SDT-org/SDT2/releases/tag/v2.0.0. pre.20250723).(B) Maximum-likelihood phylogenetic tree based on the same data set as in (A). **(B)** Midpoint-rooted, maximum-likelihood phylogenetic tree based on the same data set as in (A). Filled circles at the branches indicate bootstrap values >85%, open circles indicate values between 50 and 84%. The scale bar indicates nucleotide substitutions per site. Sequences were aligned with MAFFT [6] and the tree was constructed with IQ-TREE [7] using the TIM3+F+I+G4 nucleotide substitution model (determined by ModelFinder [8]) and the ultrafast bootstrap option [9]. The tree was edited in FigTree (tree.bio.ed.ac.uk/software/figtree).