

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create one (1) new species in the genus *Capulavirus (Geplafuvirales*: *Geminiviridae)* |
| **Code assigned:**  | 2025.011P.Ac.v3.Geminiviridae\_Capulavirus\_1nsp |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** |  | **Email address**  | **Corr. author(s)**  |
| Philippe | Roumagnac | CIRAD, UMR PHIM, Montpellier, France | philippe.roumagnac@cirad.fr | X |
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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** |
| Roumagnac, PhilippeAscencio- Ibáñez, Jose TLett, Jean-MichelLópez-Lambertini, Paola M.Martin, DarrenNavas-Castillo, JesúsRibeiro, SimoneUrbino, CicaVarsani, ArvindZerbini, F. Murilo | YYYYYYYYYY |  |  |

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| **Submission date:** |  10/06/2025 |

**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| W - Withdrawn |  |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. |

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

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| **Response of proposer:**  |
| All style-related suggestions were accepted. |

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| **Revision date:** | 22/08/2025 |

**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** |
| *“Capulavirus betae”* | Species epithet (*betae*) derived from the host plant: *Beta vulgaris* L. |
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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(s) affected*:Genus *Capulavirus* in the family *Geminiviridae* *Description of current taxonomy*:*Monodnaviria* / Shotokuvirae / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae* / *Capulavirus**Proposed* *taxonomic change(s):*We proposed to create one new species in the genus *Capulavirus*: “*Capulavirus* *betae*”*Justification*:Similar to members of the *Capulavirus* genus, members of the proposed new species “*Capulavirus* *betae*” have the virion-strand origin of replication nonanucleotide motif ‘TAATATTAC’ and show a typical capulavirus organization, with putative multiple overlapping short ORFs (V3 and V4) upstream of the CP gene that encode putative movement proteins. In addition, genome-wide pairwise analysis of the representative genomes of capulaviruses showed that beet capulavirus 1 sequence genome shared less than 78% identity with all representative genomes of capulaviruses. Since 78% nucleotide identity is the genome-wide species demarcation threshold for capulaviruses, we conclude that beet capulavirus 1 can be classified into the species “*Capulavirus* *betae”*, a new species in the genus *Capulavirus*. |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Genus *Capulavirus* in the family *Geminiviridae* *Description of current taxonomy*: *Monodnaviria* / *Shotokuvirae* / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae* / *Capulavirus*Five species are currently assigned to the genus *Capulavirus* in the family *Geminiviridae*: *Capulavirus euphorbiae, Capulavirus medicagonis*, *Capulavirus phaseoli*, *Capulavirus plantagonis*, *Capulavirus trifolii*.*Proposed* *taxonomic change(s)*: We proposed to create one new species in the genus *Capulavirus*: “*Capulavirus* *betae*”, which was isolated from sugar beet (*Beta vulgaris* L.) collected from France [1] *Demarcation criteria:*A 78% pairwise identity species demarcation threshold has been proposed and adopted for the genus *Capulavirus* [2].*Justification*: Based on the sequence analysis, beet capulavirus 1 summarized in Table 1 can be classified into one new species that shares <78% genome-wide pairwise identity with all classified capulaviruses (Figure 1). Furthermore, this is supported by phylogenetic analysis (Figure 2). |

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| **References:**  |
| [1] Zhang Z, Faure C, Marais A, Monteiro A, Candresse T, 2025. A new capulavirus infecting sugar beet (Beta vulgaris L.) in France. Arch. Virol. 170, 34.[2] Varsani, A., Roumagnac, P., Fuchs, M., Navas-Castillo, J., Moriones, E., Idris, A., Briddon, R.W., Rivera-Bustamante, R., Murilo Zerbini, F., Martin, D.P., 2017. Capulavirus and Grablovirus: two new genera in the family Geminiviridae. Arch Virol 162, 1819-1831.[3] Muhire, B.M., Varsani, A., Martin, D.P., 2014. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9, e108277.[4] Larkin, M.A., Blackshields, G., Brown, N.P., Chenna, R., McGettigan, P.A., McWilliam, H., Valentin, F., Wallace, I.M., Wilm, A., Lopez, R., Thompson, J.D., Gibson, T.J., Higgins, D.G., 2007. Clustal W and Clustal X version 2.0. Bioinformatics 23, 2947-2948. |

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| **Accompanying files** |
| **Filename** | **Description of contents** |
| 2025.011P.A.v1.Geminiviridae\_Capulavirus\_1nsp | spreadsheet |
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| **Tables, Figures:**  |

**Table 1:** Summary of the new proposed species in the *Capulavirus* genus of the *Geminiviridae* family. The new species is highlighted in red font.

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| **Genus** | **Species** | **Accession #** | **Virus name** | **Acronym** | **Isolate** | **Country** | **Host/Source** |
| *Capulavirus* | *“Capulavirus betae”* | PQ682516 | beet capulavirus 1 | BCV1 | 04-24 | France | *Beta vulgaris* L. |

**Figure 1:** Pairwise identity matrix inferred using SDT v1.2 [3].



**Figure 2:** Unrooted Neighbor-joining tree inferred from aligned full-genome nucleotide sequences of all *Capulavirus* species and “*Capulavirus* *betae”*. The genomes were aligned using Clustal W [4] and a Neighbor-joining phylogenetic tree was inferred with Jukes Cantor substitution model and 1000 bootstrap iterations.

