

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create one new species in the genus *Capulavirus (Geplafuvirales: Geminiviridae)* | |
| **Code assigned:** | 2024.007P.N.v1.Geminiviridae\_Capulavirus\_1nsp |

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| **Author(s), affiliation and email address(es):** | | | |
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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 | | | |
| **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, Philippe  Ascencio-Ibanez, Jose  Lett, Jean-Michel  López-Lambertini, Paola M.  Martin, Darren  Navas-Castillo, Jesús  Ribeiro, Simone  Urbino, Cica  Varsani, Arvind  Zerbini, F. Murilo | Y  Y  Y  Y  Y  Y  Y  Y  Y  Y |  |  |
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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 |  |
| 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| W - Withdrawn |  |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:** |
| 2024.007P.N.v1.Geminiviridae\_Capulavirus\_1nsp.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 X** |
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| **Abstract of Taxonomy Proposal:** |
| *Proposed changes:*  Add one species in the*Capulavirus* genus  *Taxonomic rank(s) affected*:  *Capulavirus* genus in the *Geminiviridae* family  *Description of current taxonomy*:  *Monodnaviria* / *Shotokuvirae* / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae* / *Capulavirus*  *Proposed* *taxonomic change(s):*  We proposed to add one new species to the *Capulavirus* genus: *Capulavirus* *trifolii*  *Justification:*  Similar to members of the *Capulavirus* genus, members of the proposed new species *Capulavirus* *trifolii* has 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 *Capulavirus* *trifolii* shares 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 *Capulavirus* *trifolii* represents a new species in the genus *Capulavirus*. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  *Capulavirus* genus in the *Geminiviridae* family (Order *Geplafuvirales*)  *Description of current taxonomy*:  *Monodnaviria* / *Shotokuvirae* / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae* / *Capulavirus*  Four species are currently assigned to the *Capulavirus* genus in the *Geminiviridae* family:   * *Capulavirus euphorbiae* * *Capulavirus medicagonis* * *Capulavirus phaseoli* * *Capulavirus plantagonis*   *Proposed* *taxonomic change(s)*:  We propose to add one new species to the *Capulavirus* genus: *Capulavirus* *trifolii*, which was isolated from white clover (*Trifolium repens*) and shrub medick (*Medicago arborea*) collected from France (Ma et al., 2021)  *Demarcation criteria:*  A 78% pairwise identity species demarcation threshold has been proposed and adopted for the genus *Capulavirus* (Varsani et al., 2017).  *Justification*:  The sequences of the viruses summarized in Table 1 can be classified into one new species that share <78% genome-wide pairwise identity with all classified capulaviruses (Figure 1). Furthermore, this is supported by phylogenetic analysis (Figure 2). |
| **References:** |
| 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.  Ma, Y., Svanella-Dumas, L., Julian, C., Galzi, S., Fernandez, E., Yvon, M., Pirolles, E., Lefebvre, M., Filloux, D., Roumagnac, P., Candresse, T., 2021. Genome characterization and diversity of trifolium virus 1: identification of a novel legume-infecting capulavirus. Arch. Virol. 166, 2573-2578.  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.  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. |

**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 trifolii* | MW698813 | Trifolium virus 1 | TrV1 | T.plasmid-1 | France | *Trifolium repens* |
|  |  | MW698814 | Trifolium virus 1 | TrV1 | T.plasmid-3 | France | *Trifolium repens* |
|  |  | MW698815 | Trifolium virus 1 | TrV1 | T.plasmid-7 | France | *Trifolium repens* |
|  |  | MW698816 | Trifolium virus 1 | TrV1 | T.plasmid-18 | France | *Trifolium repens* |
|  |  | MW698817 | Trifolium virus 1 | TrV1 | COL-2 | France | *Trifolium repens* |
|  |  | MW698818 | Trifolium virus 1 | TrV1 | COL-25 | France | *Trifolium repens* |
|  |  | MW698819 | Trifolium virus 1 | TrV1 | BG2 coro 02-2 | France | *Medicago arborea* |
|  |  | MW698820 | Trifolium virus 1 | TrV1 | BG2 coro 63-2 | France | *Medicago arborea* |
|  |  | MW698821 | Trifolium virus 1 | TrV1 | BG2 capuz 47 | France | *Medicago arborea* |

**Figure 1:** Pairwise identity matrix inferred using SDT v1.2 (Muhire et al., 2014).



**Figure 2:** Unrooted neighbor-joining tree inferred from aligned full-genome nucleotide sequences of all *Capulavirus* species and *Capulavirus* *trifolii*. The genomes were aligned using Clustal W (Larkin et al., 2007) and a Neighbor-joining phylogenetic tree was inferred with Jukes Cantor substitution model and 1000 bootstrap iterations.

A black background with a pink flower

Description automatically generated with medium confidence