

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create 31 new species in the genera *Ampelovirus, Closterovirus, Crinivirus*, *Olivavirus* and *Velarivirus* and abolish one species in the genus *Closterovirus* |
| **Code assigned:** | 2025.019P.Ac.v3.Closteroviridae\_31nsp\_abolish\_1sp | |

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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:** |
| *Closteroviridae* SG |

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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** |
| *Closteroviridae* | 10 | 0 | 1 |
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| **Submission date:** | 25/06/2025 |

**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| W - Withdrawn |  |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 the minor style issues have been addressed. |

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| **Revision date:** | 28/08/2025 |

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

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon | **X** | 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** |
| *“Ampelovirus allamandae”* | From host species name *Allamanda cathartica* |
| *“Ampelovirus alpiniae”* | From host species name *Alpinia purpurata* |
| *“Ampelovirus unesculentae”* | From Latin for number one and host species name *Manihot esculenta* |
| *“Ampelovirus duesculentae”* | From Latin for number two and host species *name Manihot esculenta* |
| *“Ampelovirus unocitri”* | From Latin for number one and common host name “citrus” |
| *“Ampelovirus duocitri”* | From Latin for number one and common host name “citrus” |
| *“Ampelovirus odontonemae”* | From host species name *Odontonema strictum* |
| *“Ampelovirus pentananas”* | From Latin for number five and the host species *Ananas comosus* |
| *“Ampelovirus hexananas”* | From Latin for number six and the host species *Ananas comosus* |
| *“Ampelovirus septananas”* | From Latin for number seven and the host species *Ananas comosus* |
| *“Ampelovirus sacchari”* | From host species name *Saccharum officinarum* |
| *“Ampelovirus croton”* | From common host name “Croton” |
| *“Ampelovirus alphaolivae”* | From the first letter of Greek alphabet and common host name “olive” |
| *“Ampelovirus kaki”* | From host species name *Diospyros kaki* |
| *“Ampelovirus perseae”* | From host species name *Persea lingue* |
| *“Closterovirus alphafici”* | From the first letter of Greek alphabet and genus of the host *Ficus* |
| *“Closterovirus betafici”* | From the second letter of Greek alphabet and genus of the host *Ficus* |
| *“Closterovirus cnidi”* | From the name of the host plant genus *Cnidium* |
| *“Closterovirus duocarotae”* | From Latin for “two” and host species name *Daucus carota* |
| *“Closterovirus thesii”* | From the name of the host plant genus *Thesium* |
| *“Closterovirus stellariae”* | From the name of the host plant genus *Stellaria* |
| *“Closterovirus tritici”* | From the name of the host plant genus *Triticum* |
| *“Closterovirus dregeae”* | From the name of the host plant genus *Dregea* |
| *“Crinivirus kurdistanfragariae”* | From geographic region (Kurdistan) and host genus *Fragaria* |
| *“Crinivirus dioscoreae”* | From the name of the host plant genus *Dioscorea* |
| *“Crinivirus mori”* | From the name of the host plant genus *Morus* |
| *“Crinivirus papyriferae”* | From the host species *Broussonetia papyrifera* |
| *“Crinivirus arracaciae”* | From the name of host plant genus *Arracacia* |
| *“Olivavirus oleae”* | From the name of host plant genus *Olea* |
| *“Velarivirus agapanthi”* | From the name of host plant genus *Agapanthus* |
| *“Velarivirus oleae”* | From the name of host plant genus *Olea* |

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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*:  Genera *Ampelovirus, Closterovirus, Crinivirus*, *Olivavirus* and *Velarivirus* in the family *Closteroviridae*  *Description of current taxonomy*:  Family *Closteroviridae* is currently composed of seven genera that accommodate 58 species, most of which are classified in one of the four “traditional” genera: *Closterovirus* (17), *Crinivirus* (14), *Ampelovirus* (13) and *Velarivirus* (9). Two of three recently established genera (*Bluvavirus* and *Menthavirus*) are monospecific, while the genus *Olivavirus* includes 3 species.  *Proposed* *taxonomic change(s):*  We propose creation of 31 new species in the family based on recently published data on characterization of viruses with affinities with currently recognized members of the family *Closteroviridae*.  *Justification*:  During the search of GenBank, 31 viral genomes with required quality and completeness along with availability of a valid publication were selected as exemplar isolates for typifying proposed new species. All these viruses meet the molecular criteria for species demarcation in the genera as they differ in amino acid content of all 3 relevant virus-encoded proteins (HSP70h, RdRP and CP) with counterparts of 58 already recognized members of the family. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genera *Ampelovirus, Closterovirus, Crinivirus*, *Olivavirus* and *Velarivirus* in the family *Closteroviridae*  *Description of current taxonomy*:  The family *Closteroviridae* is a large and diverse group of filamentous plant viruses (particles of 650−2200 nm in length) with positive-sense (+) RNA genomes. Well-characterized members of the family can be naturally transmitted in a semi-persistent manner by aphids (closteroviruses), whiteflies (criniviruses), mealybugs or soft scales insects (ampeloviruses). The members of this family are known to affect several crops of major economic importance, such as sugar beet, citrus, tomato, lettuce, potato, sweet potato, grapevine, pineapple, cherry, and some ornamentals.  Currently, 58 virus species have been classified in the family *Closteroviridae*. They are grouped into the following seven genera: *Ampelovirus* (13 species), *Bluvavirus* (1 species), *Closterovirus* (17 species), *Crinivirus* (14 species), *Menthavirus* (1 species), *Olivavirus* (3 species) and *Velarivirus* (9 species).  *Proposed* *taxonomic change(s)*:  In the recent years, numerous new viruses related to the recognized closterovirids have been discovered and characterized from various plant hosts. Characterization of these viruses was based mostly on their genomes by using high throughput sequencing approaches. Among the many of closterovirid-related nucleotide sequences available in the GenBank on May 1, 2025, we rigorously selected those with associated published literature in peer-reviewed journals, complete or coding-complete genome sequences, and identity levels of amino acid sequences of the three taxonomically-relevant gene product (HSP70h, CP and RdRP) below current demarcation criteria when compared with orthologs of recognized members in the family.  Therefore, we propose creation of 31 new species (15 in the genus *Ampelovirus,* 8 in the genus *Closterovirus*, 5 in the genus *Crinivirus*, 1 in the genus *Olivavirus* and 2 in the genus *Velarivirus*). Virus isolates used to represent newly proposed species along with proposed species nomenclature are listed Table 1. The placement of new members within the family is depicted by the phylogenetic tree presented in Figure 1, while pairwise identity levels are illustrated in Figure 2.  Additionally, because of insufficient characterization of burdock yellows virus [22], the lack of reference material making impossible genome sequencing and its comparison with other members, we propose to abolish the species *Closterovirus flavarctii* which is typified by this virus*.*  *Demarcation criteria:*  The currently valid species demarcation criteria in the family *Closteroviridae* are: (i) particle size, (ii) coat protein size, (iii) serological specificity, (iv) genome structure and organization, (v) more than 25%difference in amino acid sequence of the relevant gene products (CP, RdRp, HSP70h) among members of distinct species, (vi) vector species and specificity, (vii) natural host range, and (vii) cytopathological features [5].  *Justification*:  All these viruses meet the molecular criteria for species demarcation in the genera as they differ more than 25% in amino acid content of all 3 relevant virus-encoded proteins (HSP70h, RdRP and CP) with counterparts of 58 already recognized members of the family. Additionally, members of some new species were identified in plants previously not reported susceptible to closterovirids, thus furthering the knowledge on natural hosts for this group of filamentous viruses with large (+)RNA genomes. |

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| **References:** |
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Arch Virol. 2022 Jun;167(6):1491-1494. doi: 10.1007/s00705-022-05448-0. Epub 2022 Apr 26. PMID: 35474497. 8. Hajizadeh M, Zandan NG, Koloniuk I, Sierra-Mejia A, Tzanetakis IE. Characterization, Detection, and Prevalence of a Novel Strawberry Crinivirus. Plant Dis. 2025 May;109(5):988-991. doi: 10.1094/PDIS-08-24-1682-SC. Epub 2025 May 18. PMID: 39636284. 9. Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS. UFBoot2: Improving the Ultrafast Bootstrap Approximation. *Mol Biol Evol*. 2018;35(2):518-522. doi:10.1093/molbev/msx281 PMID: **29077904.** 10. Ito T, Sato A. Three novel viruses detected from Japanese persimmon ‘Reigyoku’ associated with graft-transmissible stunt. *Eur J Plant Pathol*, 2020;158: 163–175. <https://doi.org/10.1007/s10658-020-02063-0> 11. Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS. ModelFinder: fast model selection for accurate phylogenetic estimates. Nat Methods. 2017 Jun;14(6):587-589. doi: 10.1038/nmeth.4285. Epub 2017 May 8. 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Discovery and Characterization of a Novel Ampelovirus on Firespike. *Viruses*. 2020;12(12):1452. Published 2020 Dec 16. doi:10.3390/v12121452 PMID: **33339381** 31. Zamorano A, Gamboa C, Camilla C, Beltrán F, Magni C, Vaswani S, Martínez-Herrera E, Fiore N. A New Species of *Ampelovirus* Detected in *Persea lingue* (Ruiz & Pav.) Nees ex Kopp, a Common Tree of the Threatened Chilean Sclerophyll Forest. Forests. 2023; 14(6):1257. <https://doi.org/10.3390/f14061257> 32. Zhang P, Han TT, Tang JX, Zhong K, Ma Y, Smith WK, Zhao WG, Lu QY. Whole genome sequence of mulberry crinivirus, a new member of the genus Crinivirus. Arch Virol. 2023 Jan 7;168(2):50. doi: 10.1007/s00705-022-05657-7. PMID: 36609709. 33. Zhang S, Yang C, Qiu Y, Liao R, Xuan Z, Ren F, Dong Y, Xie X, Han Y, Wu D, Ramos-González PL, Freitas-Astúa J, Yang H, Zhou C, Cao M. Conserved untranslated regions of multipartite viruses: Natural markers of novel viral genomic components and tags of viral evolution. Virus Evol. 2024 Jan 12;10(1):veae004. doi: 10.1093/ve/veae004. PMID: 38361819 |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.019P.A.v1.Closteroviridae\_31nsp\_abolish\_1sp |  |
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| **Tables, Figures:** |

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A screen shot of a computer

AI-generated content may be incorrect.**Figure 1.** Phylogenetic tree showing reorganized family *Closteroviridae* with viruses representing proposed new species reported in red bold font*.* Maximum-likelihood phylogenetic tree was constructed on the MAFFT-aligned amino acid sequences of HSP70 protein using IQ-TREE v 1.6.11 [23] with the 1,000 replicates ultrafast bootstrap [9] under best-fit model “LG+F+I+G4” according to BIC as estimated by ModelFinder [11] and visualized with iTOL v7 [16]. The GenBank accession numbers of HSP70h proteins used for analyses along with virus names are indicated at the tips of branches. Presence of red dot on branching point indicates statistical support of >90% with size corresponding to level of bootstrap values. Different genera in the family are color-coded. A blue and red pixelated triangle

AI-generated content may be incorrect.

**Figure 2.** Pairwise identity matrix among the members of the family *Closteroviridae* based on the HSP70h amino acid sequences. The viruses representing 30 new species are included. The matrix was created in SDT v1.3 [21] on the sequences aligned with ClustalW. Color code key indicating % identities is presented.

**Table 1.** List of the proposed new species in the family with representative isolates and corresponding GenBank accessions and associated publication.

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| --- | --- | --- | --- | --- |
| **Genus** | **Species name** | **Virus name** | **GenBank** | **Ref** |
| *Ampelovirus* | *Ampelovirus allamandae* | Allamanda chlorotic virus A | PP212980 | 3 | |
|  | *Ampelovirus alpiniae* | Alpinia vein clearing virus | OQ550018 | 15 | |
|  | *Ampelovirus unesculentae* | Manihot esculenta associated ampelovirus 1 | MT773586 | 13 | |
|  | *Ampelovirus duesculentae* | Manihot esculenta associated ampelovirus 2 | MT773592 | 13 | |
|  | *Ampelovirus unocitri* | citrus associated ampelovirus 1 | MW365401 | 18 | |
|  | *Ampelovirus duocitri* | citrus associated ampelovirus 2 | MW365402 | 18 | |
|  | *Ampelovirus odontonemae* | firespike leafroll-associated virus | MW147758 | 30 | |
|  | *Ampelovirus pentananas* | pineapple mealybug wilt-associated virus 5 | OQ850040 | 19 | |
|  | *Ampelovirus hexananas* | pineapple mealybug wilt-associated virus 6 | OP860296 | 14 | |
|  | *Ampelovirus septananas* | pineapple mealybug wilt-associated virus 7 | OQ850042 | 19 | |
|  | *Ampelovirus sacchari* | sugarcane mild mosaic virus | MN116751 | 20 | |
|  | *Ampelovirus croton* | croton golden spot associated virus A | OR041673 | 2 | |
|  | *Ampelovirus alphaolivae* | olive virus A | OQ863254 | 25 | |
|  | *Ampelovirus kaki* | persimmon ampelovirus | LC488185 | 10 | |
|  | *Ampelovirus perseae* | lingue ampelovirus 1 | OQ805851 | 31 | |
| *Closterovirus* | *Closterovirus alphafici* | fig virus A | MN817232 | 24 | |
|  | *Closterovirus betafici* | fig virus B | MN817233 | 24 | |
|  | *Closterovirus cnidi* | Cnidium closterovirus 1 | OL804208 | 7 | |
|  | *Closterovirus duocarotae* | carrot closterovirus 2 | OP886455 | 28 | |
|  | *Closterovirus thesii* | Thesium chinense closterovirus 1 | OM801605 | 29 | |
|  | *Closterovirus stellariae* | Stellaria aquatica virus C | PP280820 | 1 | |
|  | *Closterovirus tritici* | wheat closterovirus 1 | LC735716 | 12 | |
|  | *Closterovirus dregeae* | Dregea volubilis virus 1 | MZ779122 | 17 | |
| *Crinivirus* | *Crinivirus kurdistanfragariae* | strawberry Kurdistan virus | OR387513-4 | 8 | |
|  | *Crinivirus dioscoreae* | yam virus 1 | PP378481-3 | 6 | |
|  | *Crinivirus mori* | mulberry crinivirus | ON931610-11 | 32 | |
|  | *Crinivirus papyriferae* | paper mulberry crinivirus 1 | OL344036-7 | 33 | |
|  | *Crinivirus arracaciae* | arracacha latent virus C | KY451034-5 | 4 | |
| *Olivavirus* | *Olivavirus oleae* | olive leaf mottling virus | PP869314 | 27 | |
| *Velarivirus* | *Velarivirus agapanthi* | Agapanthus velarivirus | MT533601 | 26 | |
|  | *Velarivirus oleae* | olive virus V | OQ863266 | 25 | |