

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create nine (9) new species in the family *Betaflexiviridae* |
| **Code assigned:**  | 2025.008P.Betaflexiviridae\_9nsp |

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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:** |
| *Beta-, Gamma-, Deltaflexiviridae* 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** |
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| **Submission date:** | 30/05/2025 |

**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 |  |
| 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| W - Withdrawn |  |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:** |  |

**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** |
| *Banmivirus miscanthi* | Epithet is derived from the latinized host genus name |
| *Carlavirus menthae* | Epithet is derived from the latinized host genus name |
| *Robigovirus menthae* | Epithet is derived from the latinized host genus name |
| *Capillovirus paris* | Epithet is derived from the latinized host genus name |
| *Chordovirus angelicae* | Epithet is derived from the latinized host genus name |
| *Citrivirus rudbeckiae* | Epithet is derived from the latinized host genus name |
| *Vitivirus muviti* | Epithet is derived from M in Greek and the latinized host genus name |
| *Vitivirus rhoviti* | Epithet is derived from R in Greek and the latinized host genus name |
| *Vitivirus gammactinidiae* | Epithet is derived from C - 'third' in Greek and the latinized host genus name |

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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, species*Description of current taxonomy*:The family *Betaflexiviridae* is divided into two subfamilies, *Quinvirinae* (5 genera) and *Trivirinae* (10 genera). Species in the family *Betaflexiviridae* are classified into genera as follows:*Banmivirus* (2 species), *Carlavirus* (73), *Foveavirus* (12), *Robigovirus* (5), *Sustrivirus* (1), *Capillovirus* (8), *Chordovirus* (4), *Citrivirus* (2), *Divavirus* (3), *Prunevirus* (4), *Ravavirus* (1), *Tepovirus* (5), *Trichovirus* (10), *Vitivirus* (19), *Wamavirus* (1). The currently approved species demarcation criteria based on sequence identity are <72% nucleotide identity in the replication-associated protein (Rep), or <80% amino acid identity in the capsid protein (CP).*Proposed* *taxonomic change(s):*We propose that the primary species demarcation criterion for the family *Betaflexiviridae* should be <80% aa identity of the Rep. If the aa identity is in the borderline range (78–82%), the CP aa identity (<85%) can be used as a secondary criterion [1]. Based on these new demarcation criteria, new species are proposed in 7 genera of the family *Betaflexiviridae*: *Banmivirus* (1 new species), *Carlavirus* (1), *Robigovirus* (1), *Capillovirus* (1), *Chordovirus* (1), *Citrivirus* (1) and *Vitivirus* (3). Species *Carlavirus cacti* and *Carlavirus cornutum* will be abolished. The exemplar accessions of seven carlaviruses, one foveavirus and one vitivirus will be changed to other ones which have complete or coding-complete genomes.*Justification:*Recent analyses using all complete genomes available in GenBank and published as the study case by the *Beta-, Delta-* and *Gammaflexiviridae* study group established a more adequate threshold of Rep amino acid sequence identity for species demarcation. The addition of nine new species is proposed in the family *Betaflexiviridae* since their Rep amino acid sequences identities are below 80%, according to the new species demarcation criteria described above. *Carlavirus cacti* and *Carlavirus cornutum* will be abolished due to the lack of sufficient sequence information.  |

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| **Text of Taxonomy proposal:**  |
| ***Taxonomic rank(s) affected*:** Genus, species***Description of current taxonomy*:** *Banmivirus* genus comprises two species, *Carlavirus* comprises 73 species, *Robigovirus* comprises five species*, Capillovirus* comprises eight species, *Chordovirus* comprises four species, *Citrivirus* comprises two species and *Vitivirus* comprises 19 species. ***Proposed* *taxonomic change(s)*:** New demarcation criteria are proposed, based on amino acid sequence identity of Rep as the primary demarcation criterion and nucleotide sequence identity of the CP as a secondary criterion. Based on these new demarcation criteria, new species are proposed in 7 genera of the family *Betaflexiviridae*: *Banmivirus* (1 new species), *Carlavirus* (1), *Robigovirus* (1), *Capillovirus* (1), *Chordovirus* (1), *Citrivirus* (1) and *Vitivirus* (3). Species *Carlavirus cacti* and *Carlavirus cornutum* will be abolished. The exemplar accessions of seven carlaviruses, one foveavirus and one vitivirus will be changed to other ones which have complete or coding-complete genomes.***Demarcation criteria:***The demarcation criteria of <72% nucleotide identity, or <80% amino acid identity in the replication-associated protein (Rep) or capsid protein (CP) became incoherent among accepted species of *Betaflexiviridae.* The primary demarcation criterion for the family *Betaflexiviridae* should be less than 80% aa identity of the Rep protein between members of distinct species. If the Rep protein aa identity is in the borderline range (78–82%), CP aa identity can be used as a secondary parameter for species demarcation. The threshold of CP amino acid identity is 85% [1].Alternatively, a flexible threshold can be applied to determine species-specific thresholds when accuracy statistics can be calculated, preferentially with the aid of biological properties. Members of the same species must be monophyletic based on the Rep phylogeny. Biological characteristics, if available, should be considered when appropriate to differentiate species, especially for borderline situations.***Justification for new species*:****Miscanthus virus M** [2]Virus name: Miscanthus virus MProposed species name: “*Banmivirus miscanthi”*Genus: *Banmivirus*Origin of name: epithet is derived from the latinized host genus name NCBI accession: ON986335 – Miscanthus virus M isolate NG77022Submitted: 13-JUL-2022Original host: *Miscanthus* sp*.*Geographic location: USASequencing approaches: Illumina, 5' and 3' RACE**Amino acid sequence identity of Rep and CP**:The recalculated highest amino acid (aa) identities are 42.8% for Rep with banana mild mosaic virus (AF314662, *Banmivirus*), matching the reference [2]. However, the highest CP aa identity was 38.1% with apricot latent virus (HQ339956, *Foveavirus*). In the reference, the closest CP aa identity was 38.9% with another foveavirid species, apple stem pitting virus (D21829) [2]. By our recalculations, the CP aa identity with the ASPV (D21829) was 37.9%. According to the genus demarcation criteria, the virus can be classified into the genus *Banmivirus* based on the Rep aa identity. Nevertheless, the lower CP aa identity with *Banmivirus*, closer to that of *Foveavirus*, suggests potential recombination. Therefore, its taxonomic position may change in the future.**Mint virus C** [3]Virus name: mint virus CProposed species name: “*Carlavirus menthae”* Genus: *Carlavirus*Origin of name: epithet is derived from the latinized host genus name NCBI accession: PQ562895 - mint virus C isolate Me1, complete genomeSubmitted: 04-NOV-2024Original host: *Mentha spicata*Geographic location: ItalySequencing approaches: Illumina, 5' RACE**Amino acid sequence identity of Rep and CP:**BLASTp analysis revealed the highest amino acid (aa) identity values of 52.31% (Rep) and 52.38% (CP) with poplar mosaic virus (PopMV, species *Carlavirus populi*) isolate DSMZ PV-0341 (ON924213). Based on our recalculations, the highest Rep aa identity (54.1%) was observed with the ICTV-recognized reference sequence for poplar mosaic virus, isolate PV-0341 (AY505475). The highest CP aa identity (47.1%) was with the reference for elderberry carlavirus D (SVD, species *Carlavirus deltasambuci*) isolate EBCVD (KJ572563). Our phylogenetic analyses based on the Rep aa sequences placed mint virus C (PQ562895) in the genus *Carlavirus* of the family *Betaflexiviridae*. Based on these data and according to current species demarcation criteria, mint virus C can be classified as a member of the newly established species “*Carlavirus menthae”*, within the genus *Carlavirus*.**Mentha arvensis robigovirus 1** [4]Virus name: Mentha arvensis robigovirus 1Proposed species name: *"Robigovirus menthae"*Genus: *Robigovirus*Origin of name: epithet derived from the latinized host genus nameNCBI accession: OR397129 – Mentha arvensis robigovirus 1 isolate dehongSubmitted: 03-AUG-2023Original host: wild mint (*Mentha arvensis*)Geographic location: West Yunnan, ChinaSequencing approaches: Illumina (mRNA and small RNA sequencing), RT-PCR, RACE **Amino acid sequence identity of Rep and CP:**The complete genome of Mentha arvensis robigovirus 1 is 7,617 nucleotides in length and encodes five open reading frames (ORFs): replication-associated protein (Rep), TGB1, TGB2, TGB3, and coat protein (CP), consistent with the genomic organization typical of the genus *Robigovirus*. The highest amino acid (aa) identity for the Rep (WNN29044) was 49.39% with cherry robigovirus 5 (QEJ80616), while the CP (WNN29048) shared 46.36% aa identity with the same reference species (QEJ80621). Both the replicase and CP aa identities fall well below the 80% species demarcation threshold established for members of *Robigovirus*. Based on these results, Mentha arvensis robigovirus 1 should be considered as a member of a novel species within the genus *Robigovirus*.**Paris polyphylla chlorotic mottle virus** [5]Virus name: Paris polyphylla chlorotic mottle virus Proposed species name: “*Capillovirus paris”*Genus: *Capillovirus*Origin of name: epithet derived from the latinized host genus nameNCBI accession: MW822017 – Paris polyphylla severe chlorotic mottle virus isolate YunnanSubmitted: 28-Aug-2020Original hosts: *Paris polyphylla* var. yunnanensis Geographic location: Yunnan, ChinaSequencing approaches: Illumina, RT-PCR, 5' and 3' RACE **Amino acid sequence identity of Rep and CP:**The genome of Paris polyphylla severe chlorotic mottle virus contains two open reading frames (ORFs): ORF1 encodes a polyprotein comprising both the replication-associated protein (Rep) and coat protein (CP), while ORF2 encodes the movement protein (MP). The highest amino acid (aa) identity for the Rep was 68% with Hobart betaflexivirus 1 (AWK77906), and for the CP, 54.84% with Rhodiola betaflexivirus 1 (QQG34587). Both Rep and CP aa identities are well below the 80% species demarcation threshold established for the genus *Capillovirus*. Based on these findings, Paris polyphylla severe chlorotic mottle virus should be recognized as a novel species within the genus *Capillovirus.***Angelica chordovirus** [6]Virus name: Angelica chordovirusProposed species name: “*Chordovirus angelicae”*Genus: *Chordovirus*Origin of name: derived from the latinized host genus name NCBI accession: OR656535 – Angelica chordovirus isolate AlT0 Submitted: 05-FEB-2025Original host: *Angelica lignescens*Geographic location: PortugalSequencing approaches: HTS, Sanger, 5' and 3' RACEThis virus was identified by HTS (siRNA), the genome sequence was confirmed by Sanger sequencing, and the extremities were obtained by a RACE on a single plant. The general structure of the genome conforms with the members of the subfamily *Trivirinae* (four ORFs: ORF1= REP, ORF2 = MP, ORF3= CP and a short hypothetical ORF4).**Amino acid sequence identity of Rep and CP:**The closest relative is Carrot chordovirus 4 (OP886458) with 71% nts identity over the full genome. The amino acid (aa) identities are 79.85 % for Rep and 81.95% for the CP.According to the new species demarcation criteria, the virus is very close to the 80% aa threshold of the Rep, but below the 85% aa threshold for the CP, so it can be accepted as a new species of the genus *Chordovirus*.**Rudbeckia citrivirus A** [7]Virus name: Rudbeckia citrivirus A Proposed species name: “*Citrivirus rudbeckiae”*Genus: *Citrivirus*Origin of name: derived from the latinized host genus nameNCBI accession: ON216317 - Rudbeckia citrivirus A Submitted: 18-Oct-2022Original host: *Rudbeckia* sp. Geographic location: GermanySequencing approaches: HTS, Sanger, 5' and 3' RACE on seed lot.This virus was identified from a seed lot (RNA extraction followed by HTS), the genome sequence was confirmed by Sanger sequencing, and the extremities were obtained by a RACE. The general structure of the genome conforms with the members of the subfamily *Trivirinae* (three ORFs: ORF1= REP, ORF2 = MP, ORF3= CP).**Amino acid sequence identity of Rep and CP:**The closest relative is Citrus leaf blotch virus (MT863785) with 57% aa identity for Rep (56% with Polyscias citrivirus 1; ON240064) and 54% for the CP of CLBV (52% with Polyscias citrivirus 1).**Grapevine virus M** [8]Virus name: grapevine virus MProposed species name: “*Vitivirus muviti”*Genus: *Vitivirus*Origin of name: epithet is derived from M in Greek and the latinized host genus nameNCBI accession: MK492703 – Grapevine virus M isolate TX-WATSubmitted: 29-APR-2019Original host: *Vitis* sp*.* cv. Blanc du BoisGeographic location: USASequencing approaches: HTS, Sanger sequencing, 5’ and 3’ RACEThe virus was first identified by HTS (RNASeq) from a pooled sample of 51 grapevines collected from a 32-year-old Blanc du Bois vineyard. Using PCR primers designed from HTS, vitivirus sequences were obtained, and it was further confirmed that the virus is only present in 11.8% (6/51) of the samples. The near complete genome of the virus was obtained by two overlapping PCR fragments from three positive samples. The terminal ends of the virus were obtained by RACE. The genomic structure is typical of the members of the genus *Vitivirus*, subfamily *Quinvirinae* consisting of five ORFs (ORF1=Rep, hypothetical ORF2, ORF3=MP, ORF4=CP and ORF5=RBP). **Amino acid sequence identity of Rep and CP:**The closest vitivirus relative is grapevine virus H (MF521889), with Rep and CP amino acid (aa) identity values corresponding to 74.7% and 88.8%, respectively. Based on the new species demarcation criteria, grapevine virus M can be accepted as a member of a new species of the genus *Vitivirus*.**Grapevine virus P** [9]Virus name: grapevine virus PProposed species name: “*Vitivirus rhoviti”*Genus: *Vitivirus*Origin of nams: Epithet is derived from R in Greek and the latinized host genus name NCBI accession: LC746753 – grapevine virus P isolate g12-C1434Submitted: 28-DEC-2024Original host: *Vitis vinifera* cv. NachubearmarieGeographic location: JapanSequencing approaches: HTS, Sanger sequencing, 5’ and 3’ RACEHTS (RNASeq) was initiated from a pool of 174 samples (grouped into 20 batches comprising of 6-10 vines per group) collected from the grapevine genetic resources collection of the Japanese National Agriculture and Food Organization. The virus was identified from bulk sample g12 (group 12). Using PCR primers designed from HTS-obtained vitivirus-like contig, it was further confirmed that the virus is only present in one sample (single vine) out of the 10 vines that comprised g12. The near complete genome of the virus was obtained from three overlapping PCR fragments from the g12 positive vine. 3’ RACE resulted in the completion of the 3’ terminal end sequence of the virus, whereas results from 5’ RACE were not successful; however, resequencing/remapping of short reads showed multiple reads matching to the first 20 nucleotide sequence of the 7,461 nt vitivirus-like HTS-obtained contig. The genomic structure is typical of the members of the genus *Vitivirus*, subfamily *Quinvirinae* consisting of five ORFs (ORF1=Rep, hypothetical ORF2, ORF3=MP, ORF4=CP and ORF5=RBP). **Amino acid sequence identity of Rep and CP:**The closest vitivirus relative is grapevine virus D (MF774336) for Rep and grapevine virus A (X75433) for CP, with amino acid (aa) identity values corresponding to 57.5% and 72.7%, respectively. Based on the new species demarcation criteria, grapevine virus P can be accepted as a member of a new species of the genus *Vitivirus*.**Actinidia virus C** [10]Virus name: Actinidia virus CProposed species name: “*Vitivirus gammactinidiae”*Genus: *Vitivirus*Origin of name: Epithet is derived from C ('third' in Greek) and the latinized host genus nameNCBI accession: MN022352– Actinidia virus C isolate ZhouzhiSubmitted: 01-MAR-2021Original host: *Actinidia deliciosa*Geographic location: ChinaSequencing approaches: HTS, Sanger sequencing, 5’ and 3’ RACETwo genomic virus sequences were obtained by HTS (RNASeq) from a symptomatic plant and confirmed Sanger sequencing; the Sanger derived sequence was used in further analysis. The terminal end sequences were determined by RACE from tissues of the symptomatic plant used in HTS. The genomic structure is typical of the members of the genus *Vitivirus*, subfamily *Quinvirinae* consisting of five ORFs (ORF1=Rep, hypothetical ORF2, ORF3=MP, ORF4=CP and ORF5=RBP). **Amino acid sequence identity of Rep and CP:**The closest vitivirus relative is Actinidia virus A (JN427014) sharing 69.2% genomic sequence identity, while Rep and CP amino acid (aa) identity values correspond to 75.3% and 87.4%, respectively. Based on the new species demarcation criteria, Actinidia virus C can be accepted as a new member of a species of the genus *Vitivirus*.  |

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| **References:**  |
| [1] Silva J M F, Melo FL, Elena SF, Candresse T, Sabanadzovic S, Tzanetakis IE, Blouin AG, Villamor DE, Mollov D, Constable F, Cao M, Saldarelli P, Cho WK, Nagata T (2022) Virus classification based on in-depth sequence analyses and development of demarcation criteria using the Betaflexiviridae as a case study. *Journal of General Virology* 103:001806. doi.org/10.1099/jgv.0.001806.[2] Abrahamian P, Grinstead S., Kinard GR. et al. Complete sequence and genome characterization of miscanthus virus M, a new betaflexivirus from *Miscanthus* sp. Arch Virol 169, 27 (2024). <https://doi.org/10.1007/s00705-024-05966-z>.[3] Forgia M, Vallino M, Marra M, Mussano P, Lanteri AP, Accotto GP, Ciuffo M. (2025) Characterization of mint virus C, a new member of the genus Carlavirus. Arch Virol 170:35. doi: 10.1007/s00705-025-06222-8.[4] Weng HT, Li YY, Chen JP, Zhang CX, Li JM, Xu ZT. Complete genome sequence of a novel robigovirus infecting *Mentha arvensis*. Arch Virol. 169(1):19 (2024) https://doi: 10.1007/s00705-023-05944-x. [5] He Q, Chen B, Zheng H, Cao Y, Hua M, Yin Y, Peng J, Li J, Chen J, Yan F, Song X, Lin L. Complete genome sequence of Paris polyphylla chlorotic mottle virus infecting *Paris polyphylla* var. yunnanensis in southwest China. Arch Virol. 168(12):292. (2023) https://doi: 10.1007/s00705-023-05896-2. PMID: 37966521. [6] Luna S, Lopes MS, Dias E. et al. Identification of a chordovirus hosted by *Angelica lignescens*. J Plant Pathol 107, 1201–1206 (2025). https://doi.org/10.1007/s42161-025-01842-0[7] Kim, J., Jun, M., Lee, DS. et al. Complete genome and molecular characterization of a putative novel citrivirus from *Rudbeckia* sp. Virus Genes 59, 158–162 (2023). <https://doi.org/10.1007/s11262-022-01936-2>[8] Alabi, O.J., McBride, S., Appel, D.N., Al Rwahnih, M., Pontasch, F.M. Grapevine virus M, a novel vitivirus discovered in the American hybrid bunch grape cultivar Blanc du Boi in Texas. Arch Virol. 164:1739-1741 (2019). https://doi.org/10.1007/s00705-019-04252-7[9] Ito, T. First reports of several viruses and a viroid including a novel vitivirus in Japan, found through virome analysis of bulk grape genetic resources. Virus Genes 60:684-694. <https://doi.org/10.1007/s11262-024-02101-7>[10] Zhao, L., Cao, M., Huang, Q., Jing, M., Bao, W., Zhang, Y., Hou, C. Wu, Y., Wang, Q.C. Occurrence and molecular characterization of Actinidia virus C (AcVC), a novel vitivirus infecting kiwifruit (*Actinidia* spp.) in China. Plant Pathol. 69:775-782 (2020). https://doi.org/10.1111/ppa.13171 |

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| **Accompanying files:** |
| **Filename** | **Description of contents** |
| 2025.008P.N.v2.Betaflexiviridae\_9nsp | spreadsheet |
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| **Tables, Figures:**  |

Figure 1. Approximately-maximum-likelihood phylogenetic tree based on amino acid sequences of the replication-associated protein (Rep) of members of the family *Betaflexivifidae*. The tree was inferred using FastTree and a Rep multiple sequence alignment prepared using Mafft linsi method. Bootstrap values >70% are shown. Tree branches are proportional to genetic distances between sequences, and the scale bar at the bottom indicates substitutions per amino acid site. Accession numbers are shown next to the respective virus taxon. Novel species proposed in extant genera are indicated by a black circle and the changed exemplar accession numbers are indicated by a black diamond.