

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create two (2) new species in the genus *Dichorhavirus* (*Mononegavirales: Rhabdoviridae*) |
| **Code assigned:**  | 2025.027P.Ac.v3.Rhabdoviridae\_Dichorhavirus\_2nsp |

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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:**  |
| *Rhabdoviridae* 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** |
| *Rhabdoviridae* | 11 | 0 | 3 |
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| **Submission date:** |  21/05/2025 |

**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 | **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| W - Withdrawn |  |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 proposed changes were accepted  |

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| **Revision date:** | 19/08/2025 |

**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** |
| *“Dichorhavirus chilense”* | The species epithet is adopted from the geographical origin of the samples where the virus was identified. Vinca chlorotic spot virus was detected in a region south of Santiago, Chile. It is the first dichorhavirus detected in that country.  |
| *“Dichorhavirus piracicabense”* | The species epithet is adopted from the geographical origin of the samples where the virus was identified. So far, Clerodendrum leaf spot virus has been detected infecting three plant species, all collected in or near the city of Piracicaba. Piracicaba is a word of Tupi-Guarani origin (an indigenous language of Brazil) and means "the place where the fish stops" or "the river where the fish pauses". |

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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**  |
|  |  |  |
| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: Genus *Dichorhavirus* in the family *Rhabdoviridae**Description of current taxonomy*: Genus *Dichorhavirus*, family *Rhabdoviridae,* encompasses viruses assigned to six species. They are plant-infecting viruses transmitted by mites of the genus *Brevipalpus* [1]. The genome of dichorhaviruses includes bi-segmented, negative-sense, single-stranded RNA molecules, in which genes *N*, *P*, *P3*(*ORF3*), *M*, and *G* are located in RNA1, whereas the gene *L* is in RNA2. In nature, dichorhaviruses cause non-systemic diseases, mostly producing chlorotic and necrotic spots; however, sometimes orchid fleck virus (OFV) can induce systemic infection in orchids. Dichorhaviruses also replicate in their vectors [1, 2].*Proposed* *taxonomic change(s):* Create two new species in the genus *Dichorhavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. The two new taxa are proposed to be named “*Dichorhavirus chilense”* and *“Dichorhavirus piracicabense”*, respectively.*Justification*: Two novel viruses were identified in bleeding-heart vine (*Clerodendrum thomsoniae*) and large periwinkle (*Vinca major*) plants, respectively (Ramos-González et al., unpublished results). Biological and molecular characterization of these viruses demonstrated that they should be classified as novel species within the genus *Dichorhavirus*. The complete sequences of RNA1 and *L* ORF in the RNA2 of both viruses share less than 80% of nucleotide sequence identity with known dichorhaviruses. Phylogenetic analyses using the L proteins place both viruses in a subclade with viruses of the known species of the genus. |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Genus *Dichorhavirus* in the family *Rhabdoviridae**Description of current taxonomy*: Genus *Dichorhavirus*, family *Rhabdoviridae,* encompasses viruses assigned to six species. Viruses classified in the genus *Dichorhavirus* produce short, bacilliform virions, 40 × 100–110 nm in size, which appear not to be enveloped. Their genomes are bi-segmented, single-stranded, negative-sense (-) RNA molecules of approximately 6.0 kb with six canonical open reading frames (ORFs). Dichorhaviruses infect plants and are persistently transmitted by *Brevipalpus* mites in a propagative manner. The assignment of viruses to this genus is also based on the placement of the viruses on Maximum Likelihood trees inferred from complete *L* protein sequences. *Proposed* *taxonomic change(s)*: Create two new species in the genus *Dichorhavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. The two new taxa are proposed to be named “*Dichorhavirus chilense”* and *“Dichorhavirus piracicabense”*, respectively.*Demarcation criteria*: Viruses assigned to different species within the genus *Dichorhavirus* have several of the following characteristics [8]: A) minimum nucleotide sequence divergence of 20% in *L* genes B) minimum nucleotide sequence divergence of 20% in RNA1 C) can be distinguished in serological tests D) occupy different ecological niches as evidenced by differences in plant hosts and/or arthropod vectors. *Justification*: This taxonomic proposal aims to classify Vinca chlorotic spot virus (ViCSV) and Clerodendrum leaf spot virus (ClLSV) into two new species in the genus *Dichorhavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*, order *Mononegavirales*. ViCSV and ClLSV genomes are divided into two single-stranded (-) RNA molecules (Figure **1**). RNA1 segments contain five canonical ORFs detected in plant-infecting rhabdoviruses, *i*.*e*., *N*, *P*, *P3* (*ORF 3, MP*), *M*, and *G*. The RNA2 segments consist of a large ORF encoding the L protein. The genomes of the novel viruses show genomic arrangements that resemble those of known dichorhaviruses and phylogenetic analyses place ViCSV and ClLSV in the genus *Dichorhavirus*. Nucleotide sequences from the full-length RNA1 segment and the *L* ORF in the RNA2 of each virus share less than 80% nucleotide sequence identities with the existing members of the genus. 1. **Vinca chlorotic spot virus** (ViCSV): Particles of ViCSV isolate LPa01 were first detected by transmission electron microscopy in samples of large periwinkle (*Vinca major*) plants collected in a region south of Santiago, Chile, in 2019. Infected periwinkle leaves showed chlorotic spots on green leaves, green islands on senescent leaves, and sometimes, necrotic spots. ViCSV was successfully experimentally transmitted to *Arabidopsis thaliana* and *Nicotiana* *tabacum* plants using viruliferous *Brevipalpus chilensis* mites previously collected from naturally infected plants. The virus has been detected in large periwinkle samples collected in 2020-2021 and 2023. The complete viral genome of ViCSV was detected by high-throughput sequencing and RACE analysis from plants and *B. chilensis* mites. Sequences were deposited in GenBank (RNA1: OR372158 and RNA2: OR372159). Pairwise comparisons of ViCSV\_LPa01 RNA1 and *L* ORF sequences with other dichorhaviruses showed identity values below 56% (Table **1**), and the highest values corresponded to the alignments with citrus bright spot virus (CiBSV, *Dichorhavirus australis*) [3] and citrus leprosis virus N (CiLV-N, *Dichorhavirus leprosis*) [4]. Based on a maximum likelihood (ML) tree generated from L protein sequences, ViCSV shares a branch with CiBSV and CiLV-N (Figure **2**).
2. **Clerodendrum leaf spot virus** (ClLSV): ClLSV isolate Prb1 was first detected in bleeding-heart vine (*Clerodendrum thomsoniae*) plants in 2017. Once a specific molecular diagnostic method based on RT-PCR was available, the virus was detected in ornamentals of three other species in 2017-2020. Infected leaves show chlorotic spots and necrotic lesions have not been observed. The complete coding sequence of ClLSV\_Prb01 was detected by high-throughput sequencing. Besides the six canonical genes found in other dichorhaviruses, RNA1 of ClLSV\_Prb01 has an additional small ORF with 180 nts placed between the ORFs *P3* and *M*. The putative deduced protein is 8.5 kDa and shows a transmembrane helix. Complete coding sequences of other ClLSV isolates have been recovered by assembling overlapping amplicons generated by RT-PCR using a set of specific primers. Sequences of ClLSV\_Prb01 were deposited in the GenBank (RNA1: PV555428 and RNA2: PV555429). Pairwise comparisons of ClLSV\_Prb01 RNA1 and *L* ORF sequences with other dichorhaviruses showed identity values below 50% (Table **1**), and the highest values corresponded to the alignments with citrus bright spot virus (*Dichorhavirus australis*) [3] and coffee ringspot virus (CoRSV, *Dichorhavirus coffeae*) [5]. Based on a maximum likelihood (ML) tree generated from L protein sequences, ClLSV is placed in a basal position of the branch shared by the dichorhaviruses CoRSV, citrus chlorotic spot virus (*Dichorhavirus citri*) [6], and Clerodendrum chlorotic spot virus (ClCSV, *Dichorhavirus clerodendri*) [7] (Figure **2**). The presence of *Brevipalpus yothersi* mites has been detected in plants affected by ClLSV, which likely vector this virus. Transmission experiments under controlled conditions have not been carried out.

The serological test information required in criterion C is unavailable, but both viruses meet criteria A and B. ViCSV also meets criterion D. ClLSV partially meets criterion D since its host range partially overlaps that described for Clerodendrum chlorotic spot virus (*Dichorhavirus clerodendri*). Similarly, ClLSV is likely transmitted by *Brevipalpus yothersi* mites, the vector of ClCSV. We propose classifying ViCSV and ClLSV into the new species “*Dichorhavirus chilense”* and “*Dichorhavirus piracicabense”*, respectively, in the genus *Dichorhavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. The epithets in the binomial species names of the two viruses refer to the geographical origin of the samples from which they were first detected.  |

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| **References:**  |
|  1. Dietzgen RG, Freitas-Astúa J, Chabi-Jesus C, et al (2018) Dichorhaviruses in their Host Plants and Mite Vectors. In: Advances in Virus Research. Academic Press Inc., pp 119–148
2. de Lillo E, Freitas-Astúa J, Kitajima EW, et al (2021) Phytophagous mites transmitting plant viruses: update and perspectives. Entomologia Generalis 41:439–462. https://doi.org/10.1127/ENTOMOLOGIA/2021/1283
3. Chabi-Jesus C, Ramos-González PL, Tassi AD, et al (2023) Citrus Bright Spot Virus: A New Dichorhavirus, Transmitted by Brevipalpus azores, Causing Citrus Leprosis Disease in Brazil. Plants 12:1371. https://doi.org/10.3390/PLANTS12061371
4. Ramos-González PL, Chabi-Jesus C, Guerra-Peraza O, et al (2017) Citrus leprosis virus N: a new dichorhavirus causing Citrus Leprosis disease. Phytopathology 107:963–976. https://doi.org/10.1094/PHYTO-02-17-0042-R
5. Ramalho TO, Figueira AR, Sotero AJ, et al (2014) Characterization of Coffee ringspot virus-Lavras: a model for an emerging threat to coffee production and quality. Virology 464–465:385–96. https://doi.org/10.1016/j.virol.2014.07.031
6. Chabi-Jesus C, Ramos-González PL, Tassi AD, et al (2018) Identification and characterization of citrus chlorotic spot virus, a new dichorhavirus associated with citrus leprosis-like symptoms. Plant Dis 102:1588–1598. https://doi.org/10.1094/PDIS-09-17-1425-RE
7. Ramos-González PL, Chabi-Jesus C, Banguela-Castillo A, et al (2018) Unveiling the complete genome sequence of clerodendrum chlorotic spot virus, a putative dichorhavirus infecting ornamental plants. Arch Virol 163:2519–2524. https://doi.org/10.1007/s00705-018-3857-z
8. Rhabdoviridae study group Genus: Dichorhavirus | ICTV. https://ictv.global/report/chapter/rhabdoviridae/rhabdoviridae/dichorhavirus. Accessed 1 May 2025

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| 2025.027P.A.v1.Rhabdoviridae\_Dichorhavirus\_2nsp | Excel sheet |
|  |  |

**Tables, Figures:**

**Table 1**: Percentage of nucleotide sequence identities among RNA1 (A) and *L* ORF (B) of ViCSV, ClLSV, and other members of the genus *Dichorhavirus.* Nucleotide sequences were aligned using MAFFT or ClustalW, and the identity values from both alignments were calculated using MEGA11. Values shown were those obtained from ClustalW alignment.

1. **Complete RNA1 segment (nts)**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Dichorhavirus RNA1 | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| 1 | Citrus chlorotic spot virus (CiCSV) strain Trs1 NC 055208.1 |  |  |  |  |  |  |  |
| 2 | Citrus leprosis virus N (CiLV-N) strain ibi1 NC 052230.1 | 24.58 |  |  |  |  |  |  |
| 3 | Clerodendrum chlorotic spot virus (ClCSV) isolate Prb1 NC 043648.1 | 65.84 | 25.64 |  |  |  |  |  |
| 4 | Coffee ringspot virus (CoRSV) strain Lavras NC 038756.1 | 66.70 | 26.99 | 67.53 |  |  |  |  |
| 5 | Orchid fleck virus (OFV) strain So NC 009608.1 | 17.14 | 18.44 | 16.29 | 18.16 |  |  |  |
| 6 | Citrus bright spot virus (CiBSV) strain PFd01 MZ773933.1 | 27.51 | 63.43 | 28.08 | 28.93 | 18.71 |  |  |
| 7 | **Vinca chlorotic spot virus (ViCSV) strain LPa01 OR372158.1** | 24.76 | **41.18** | 22.92 | 23.48 | 16.57 | **41.96** |  |
| 8 | **Clerodendrum leaf spot virus (ClLSV) strain Prb1 PV555428.1** | **32.40** | 22.56 | 31.46 | **32.32** | 15.88 | 22.56 | 19.80 |

1. ***L* ORF (nts)**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Dichorhavirus *L* gene | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| 1 | CiLV-N\_Ibi/gene |  |  |  |  |  |  |  |
| 2 | OFV\_So/L gene | 39.69 |  |  |  |  |  |  |
| 3 | CoRSV\_Lavras/L gene | 46.13 | 40.56 |  |  |  |  |  |
| 4 | CiBSV\_PFd01/L gene | 68.99 | 39.02 | 47.51 |  |  |  |  |
| 5 | CiCSV\_Trs01/L gene | 46.29 | 41.24 | 73.36 | 47.88 |  |  |  |
| 6 | ClCSV\_Prb01/L gene | 47.50 | 39.91 | 73.94 | 47.76 | 70.88 |  |  |
| 7 | **ViCSV\_LPa01/L gene** | **55.07** | 39.18 | 44.24 | 54.53 | 46.17 | 45.49 |  |
| 8 | **ClLSV\_Prb1/L gene** | 46.46 | 37.71 | **49.09** | 45.60 | 48.53 | 47.91 | 41.11 |

1. **Vinca chlorotic spot virus (ViCSV)**

3’

*L*

*N*

*P*

*P3*

*M*

*G*

3’

5’

5’

RNA2

RNA1

1. **Clerodendrum leaf spot virus (ClLSV)**

*G*

*M*

*L*

*N*

*P*

*P3*

5’

5’

3’

3’

RNA2

RNA1

**Figure 1.** Schematic representations of the genomic organization of Vinca chlorotic spot virus (ViCSV) and Clerodendrum leaf spot virus (ClLSV), members of the proposed new species of the genus *Dichorhavirus*. Open reading frames are represented with solid boxes containing a letter that indicates the name of each viral gene. Small, non-canonical ORF in ClLSV is fill with a purple grid pattern. Abbreviations: *N*: nucleoprotein, *P*: phosphoprotein, *P3*: putative cell-to-cell movement protein, *M*: matrix protein, *G*: glycoprotein, and *L*: RNA-dependent RNA polymerase.

**Figure 2.** Phylogenetic reconstruction for viruses of the subfamily *Betarhabdovirinae* (family *Rhabdoviridae*). Vinca chlorotic spot virus and Clerodendrum leaf spot virus are highlighted in red. The maximum-likelihood phylogenetic tree was inferred using IQ-tree software based on the deduced amino acid sequences of L proteins. The alignment was constructed in MAFFT using the E-INS-I iterative refinement method. Phylogenetically informative regions of the multiple sequence alignment included 578 residues selected using BMGE software and its evolutionary history was inferred based on the model LG+F+I+G4. The bootstrap support values (1,000 replications) of branches greater than 50% are indicated next to the corresponding nodes. The tree was rooted using viruses of the genera *Varicosavirus*, *Alphagymnorhavirus,* and *Betagymnorhavirus* as an external group. The scale bar specifies the average number of amino acid substitutions per site, and the tree is drawn to scale.