

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create three (3) new species, one in the genus *Alphacytorhabdovirus,* and the other two in the genus *Betacytorhabdovirus,* subfamily *Betarhabdovirinae* (*Mononegavirales*: *Rhabdoviridae*) |
| **Code assigned:** | 2025.025P.Ac.v3.Rhabdoviridae\_Alpha\_and\_Betacytorhabdovirus\_3nsp | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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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| W - Withdrawn |  |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.  It is suggested to remove the header “novel species” since it is confusing because the following paragraphs start with the virus name. |

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

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| **Response of proposer:** |
| All proposed changes were accepted, including the removal of the header “novel species” |

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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** |
| *“Alphacytorhabdovirus lonicerae”* | The species epithet is derived from *Lonicera*, the scientific name of the plant host genera from which the sequence of the virus was obtained. |
| *“Betacytorhabdovirus dioscoreae”* | The species epithet is derived from *Dioscorea*, the scientific name of the plant host genera from which the sequence of the virus was obtained. |
| *“Betacytorhabdovirus pyri”* | The species epithet is derived from *Pyrus*, the scientific name of the plant host genera from which the sequence of the virus was obtained. |

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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 *Alphacytorhabdovirus* and *Betacytorhabdovirus* in the family *Rhabdoviridae*  *Description of current taxonomy*:  Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* belong to the subfamily *Betarhabdovirinae*, family *Rhabdoviridae* and consist of 18 and 19 species, respectively. Viruses classified into species in the genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* infect a wide range of plants, and the assignment of viruses to these genera is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences  *Proposed* *taxonomic change(s)*:  Create one new species in the genus *Alphacytorhabdovirus,* and two new species in the genus *Betacytorhabdovirus,* subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. These species are proposed to be named “*Alphacytorhabdovirus lonicerae”, “Betacytorhabdovirus dioscoreae”* and *“Betacytorhabdovirus pyri”*.  *Justification*:  Three novel rhabdoviruses were identified in honeysuckle [1], *Dioscorea rotundata* [Silva et al., unpublished (ON924784)] and pear [2]. The characterization of these viruses showed that the honeysuckle-associated virus should be classified into a novel species within the genus *Alphacytorhabdovirus* [1]; while the *Dioscorea rotundata*-associated and pear-associated viruses should be assigned to novel species within the genus *Betacytorhabdovirus* [Silva et al., unpublished (ON924784) and 2, respectively]. | | |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* in the family *Rhabdoviridae*  *Description of current taxonomy*:  Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* belong to the subfamily *Betarhabdovirinae*, family *Rhabdoviridae* and consist of 18 and 19 species, respectively. Viruses classified into species in the genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* infect a wide range of plants, and the assignment of viruses to these genera is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences  *Proposed* *taxonomic change(s)*:  Create one new species in the genus *Alphacytorhabdovirus,* and two new species in the genus *Betacytorhabdovirus,* subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  *Demarcation criteria:*  Viruses assigned to different species within the genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* should have several of the following characteristics:  A) nucleotide sequence identity less than 75% for the coding-complete genome sequence  B) amino acid sequence identity less than 86% in proteins encoded by all the cognate open reading frames  C) occupy different ecological niches as evidenced by differences in hosts and/or biological vectors  *Justification*:  Three novel rhabdoviruses were identified in honeysuckle [1], *Dioscorea rotundata* [Silva et al., unpublished (ON924784)] and pear [2]. The characterization of these viruses showed that the honeysuckle-associated virus should be classified into a novel species within the genus *Alphacytorhabdovirus* [1]; while the *Dioscorea rotundata*-associated and pear-associated viruses should be classified into novel species within the genus *Betacytorhabdovirus* [Silva et al., unpublished (ON924784) and [2], respectively].  Creation of one new species in the genus *Alphacytorhabdovirus*   1. **Honeysuckle -associated cytorhabdovirus 1 (HaCV1)** was identified from honeysuckle (*Lonicera japonica*) samples collected in Henan, China. The complete genome (CG) sequence of HaCV1 consists of 13,930 nucleotides (PQ587056) and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene *P3* in the conserved location between *P* and *M* genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein gene *P6* between the *G* and *L* genes (**Figure 1**). The CG nucleotide sequence of HaCV1 has the highest identity values with that of Triticum alphacytorhabdovirus 1 (TriACRV1, 71.2%), while the HaCV1 encoded proteins have the highest identity values with those of TriACRV1 (85.3%) [1]. Based on ML trees generated from complete L protein sequences, HaCV1 forms a well-supported clade within alphacytorhabdoviruses with TriACRV1, and Pinellia alphacytorhabdovirus 1 (**Figure 2**).   HaCV1 meets the demarcation criteria A, B and C. Thus, we propose to classify HaCV1 as member of the new species “*Alphacytorhabdovirus lonicerae”* subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  Creation of two new species in the genus *Betacytorhabdovirus*   1. **Dioscorea rotundata virus 1 (DiRoV1)** was identified from white yam (*Dioscorea rotundata*) samples collected in Nigeria. The coding-complete genome (CCG) sequence of DiRoV1 is 12,751 nucleotides (ON924784) in size and contains seven ORFs in the order 3’-N-P-P3-M-G-P6-L-5’ [Silva et al., unpublished] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene *P3* in the conserved location between *P* and *M* genes, and the accessory protein *P6* gene between the *G* and *L* genes (**Figure 1**). The CCG nucleotide sequence of DiRoV1 has the highest identity values with that of mango betacytorhabdovirus 1 (ManBCRV1; 50%); while the DiRoV1 encoded proteins have the highest identity values with those of ManBCRV1 (41.74%). Based on ML trees generated from complete L protein sequences, DiRoV1 forms a well-supported clade within betacytorhabdoviruses with ManBCRV1 (**Figure 3**). 2. **pear rhabdovirus 1 (PRV1)** was identified from pear (*Pyrus communis*) samples collected in Himachal Pradesh, India. The coding-complete genome (CCG) sequence of PRV1 consists of 15,628 nucleotides (PP512586) and contains seven ORFs in the order 3’-N-P-P3-M-G-P6-L-5’ [2] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene *P3* in the conserved location between *P* and *M* genes, and the accessory protein *P6* gene between the *G* and *L* genes. Interestingly, PRV1 has a shorter G gene, like that one reported for several betacytorhabdoviruses [3] (**Figure 1**). The CCG nucleotide sequence of PRV1 has the highest identity values with that of Morus betacytorhabdovirus 1 (MorBCRV1; 49.4%); while the PRV1 encoded proteins have the highest identity values with those of MorBCRV1 (41.45%) [2]. Based on ML trees generated from complete L protein sequences, PRV1 forms a well-supported clade with those betacytorhabdoviruses that have the shorter *G* gene (**Figure 3**).   DiRoV1 and PRV1 meet the demarcation criteria A, B and C. Thus, we propose to classify DiRoV1 and PRV1 as members of the new species “*Betacytorhabdovirus dioscoreae”* and *“Betacytorhabdovirus pyri”*, respectively, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. |

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| **References:** |
| [1] Yang J, Liu L, Li J, Chen Z, Peng B, Li Y (2025). Identification and complete genome sequence of Honeysuckle-associated cytorhabdovirus in China. Arch Virol 170:62. PMID: 39976771 DOI: 10.1007/s00705-025-06238-0.  [2] Prajapati M, Gupta N, Thapa P, Diksha D, Sharma S, Baranwal V (2025). Identification and Characterization of a Novel Cytorhabdovirus Associated with Pear (P. communis ‘Bartlett’) Through RNA‑seq. Curr Microbiol 82:39. PMID: 39680169 DOI: 10.1007/s00284-024-04010-2.  [3] Bejerman N, Dietzgen R, Debat H (2023). Novel Tri-Segmented Rhabdoviruses: A Data Mining Expedition Unveils the Cryptic Diversity of Cytorhabdoviruses. Viruses 15:2402, PMID:38140643, doi:10.3390/v15122402. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.025P.A.v1.Rhabdoviridae\_Alpha\_and\_Betanucleorhabdovirus\_3nsp | Excel sheet |
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**Tables, Figures:**

**Gráfico

El contenido generado por IA puede ser incorrecto.**

**Figure 1**. Genome graphs depicting the architecture and gene products of viruses proposed to be included in species within the genera *Alphacytorhabdovirus* and *Betacytorhabdovirus.* Abbreviations: N: nucleoprotein; P: P overlapping protein; P: phosphoprotein; P3: putative cell-to-cell movement protein; M: matrix protein; G: glycoprotein; P6: protein 6; L: RNA-dependent RNA polymerase.

Imagen que contiene Texto

El contenido generado por IA puede ser incorrecto.

**Figure 2.** Maximum Likelihood (ML) phylogenetic tree of plant-infecting rhabdovirus L polymerase protein sequences. Amino acid sequences were aligned using MUSCLE. The resulting alignment was used to generate a phylogenetic tree using Mega11 with the best-fit model LG + G + I +F. The virus potentially belonging to the new species are indicated with green square. Numbers at the nodes indicate bootstrap support (1000 replicates).

Imagen que contiene Texto

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**Figure 3** Maximum Likelihood (ML) phylogenetic tree of plant-infecting rhabdovirus L polymerase protein sequences. Amino acid sequences were aligned using MUSCLE. The resulting alignment was used to generate a phylogenetic tree using Mega11 with the best-fit model LG + G + I +F. Two viruses potentially belonging to the new species are indicated with green squares. Numbers at the nodes indicate bootstrap support (1000 replicates).