

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create one new species in the genus *Trirhavirus,* subfamily *Betarhabdovirinae* (*Mononegavirales: Rhabdoviridae*) |
| **Code assigned:** | 2025.023P.Ac.v3.Rhabdoviridae\_Trirhavirus\_1nsp | |

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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| W - Withdrawn |  |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** |
| *“Trirhavirus rubi”* | The species epithet is derived from *Rubus*, 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*:  Genus *Trirhavirus,* subfamily *Betarhabdovirinae*, family *Rhabdoviridae*  *Description of current taxonomy*:  Five virus species are currently classified in the recently created genus *Trirhavirus,* whose main feature is the tri-segmented genomic organization of their members. The assignment of viruses to this genus is based on their genome composition, and 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 *Trirhavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. This species is proposed to be named “*Trirhavirus rubi”*.  *Justification*:  A novel tri-segmented rhabdovirus was identified in Rubus [1]. The characterization of the genome sequence showed that it should be assigned to a novel species within the genus *Trirhavirus* [1] based on the nucleotide sequence divergence from previously reported trirhaviruses and phylogenetic placement. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus *Trirhavirus,* subfamily *Betarhabdovirinae*, family *Rhabdoviridae*  *Description of current taxonomy*:  Five virus species are currently classified in the recently created genus *Trirhavirus,* whose unique feature is the tri-segmented genomic organization of their members. The assignment of viruses to this genus is based on their genome composition, and 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 *Trirhavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  *Demarcation criteria:*  We propose that viruses assigned to different species within the genus *Trirhavirus*, should have several of the following characteristics:   1. nucleotide sequence identity lower than 80% for the *L* ORF 2. nucleotide sequence identity lower than 80% in RNA2 3. nucleotide sequence identity lower than 80% in RNA 3 4. occupy different ecological niches as evidenced by differences in hosts     *Justification*:  A novel tri-segmented rhabdovirus was identified in Rubus [1]. The characterization of this virus showed that it should be assigned to a novel species within the genus *Trirhavirus* [1] based on the nucleotide sequence divergence from previously reported trirhaviruses and phylogenetic placement (see below).   1. **Rubus trirhavirus 1(RTV1)** was identified from Rubus samples collected in South Carolina, USA. RTV1 genome is tri-segmented with a coding-complete genome (CCG) RNA1 of 6,557 nucleotides (nt), RNA2 of 4,040 nt and RNA3 of 4,191 nt (PQ317245, PQ317246 and PQ317247, respectively) [1]. RNA1 contains one large open reading frame (ORF) encoding the L polymerase protein while RNA2 and RNA 3 contain four ORFs (**Figure 1**). The nt and amino acid (aa) sequences of RTV1 *L* gene have the highest identity values with that of Picris trirhavirus 1 (PiTRV1, 64% and 65%, respectively); while the RTV1 RNA2 and RNA3 have the highest nt identities values with that of PiTRV1 with 57% and 51%, respectively [1]. Based on ML trees generated from complete L protein sequences, RTV1 is placed within a subclade of trirhaviruses with PiTRV1 and Erysimum trirhavirus 1 (**Figure 2**).   RTV1 meets the demarcation criteria A, B, C and D. Thus, we propose to classify RTV1 as the new species “*Trirhavirus rubi”* subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. |

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| **References:** |
| [1] Schnabel E, Diniz Xavier C, Whitfield A, Dubrow Z, Pham G, Cieniewicz E (2025). Exploring the virome of blackberry and wild *Rubus* spp. in South Carolina. Phytobiomes. doi: <https://doi.org/10.1094/PBIOMES-11-24-0106-R>. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.023P.A.v1.Rhabdoviridae\_Trirhavirus\_1nsp | Excel sheet |
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| **Tables, Figures:** |
| Diagrama**Figure 1**. Genome graphs depicting the architecture and gene products of the proposed virus (Rubus trirhavirus 1) to be included in the species within the genus *Trirhavirus.* Abbreviations: N: nucleoprotein; L: RNA-dependent RNA polymerase; P2: protein 2; P3: protein 3; P4: protein 4; P6: protein 6; P7: protein 7; P8: protein 8; P12: protein 12.    **Tabla**  **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 (Rubus trirhavirus 1), potentially belonging to a new species is indicated with a green square. Numbers at the nodes indicate bootstrap support (1000 replicates). |