

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:**  | Create three (3) new species in the genus *Varicosavirus,* subfamily *Betarhabdovirinae* (*Mononegavirales: Rhabdoviridae*) |
| **Code assigned:**  | 2025.026P.Rhabdoviridae\_Varicosavirus\_3nsp |

|  |
| --- |
| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
| Nicolas | Bejerman | UFyMA INTA-CONICET, Argentina | bejerman.nicolas@inta.gob.ar | X |
| Humberto | Debat | UFyMA INTA-CONICET, Argentina | debat.humberto@inta.gob.ar |  |
| Ralf G | Dietzgen  | QAAFI, UQ, Australia | r.dietzgen@hotmail.com |  |
| Juliana | Freitas-Astua | EMBRAPA Mandioca e Fruticultura, Brazil | juliana.astua@embrapa.br |  |
| Hideki | Kondo | Okayama University, Japan | hkondo@rib.okayama-u.ac.jp |  |
| Pedro Luis | Ramos-Gonzalez  | Instituto Biológico de São Paulo, Brazil | plrg1970@gmail.com |  |
| Anna E | Whitfield  | NC State University, USA | awhitfi@ncsu.edu |  |
| Peter J | Walker | UQ, Australia | peter.walker@uq.edu.au |  |

**Part 1b: Taxonomy Proposal Submission**

|  |
| --- |
| **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  |  |

|  |
| --- |
| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| *Rhabdoviridae* study group |

|  |
| --- |
| **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 |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** |  21/05/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

|  |  |
| --- | --- |
| **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 |  |

|  |
| --- |
| **Comments from the Executive Committee:** |
|  |

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

|  |
| --- |
| **Response of proposer:**  |
|  |

|  |  |
| --- | --- |
| **Revision date:** |  |

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

|  |
| --- |
| **Taxonomic changes proposed:**  |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

|  |
| --- |
| **Etymology (origin) of proposed taxonomic names:**  |
| **Taxon name**  | **Etymology of the term** |
| *Varicosavirus agastachi* | The species epithet is derived from *Agastache*, the scientific name of the plant host genera from which the sequence of the virus was obtained. |
| *Varicosavirus orychophragmi* | The species epithet is derived from *Orychophragmi,* the scientific name of the plant host genera from which the sequence of the virus was obtained. |
| *Varicosavirus 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. |

|  |
| --- |
| **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*: Species*Description of current taxonomy*: Viruses classified in the genus *Varicosavirus* are bi-segmented and infect a wide range of plants. The assignment of viruses to this genus is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences.*Proposed* *taxonomic change(s):* Create three new species in the genus *Varicosavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. These species are proposed to be named “*Varicosavirus agastachi”, “Varicosavirus orychophragmi”* and *“Varicosavirus rubi”*. *Justification*: Three novel rhabdoviruses were identified in *Agastache rugosa* [1], *Orychophragmus violaceus* [2] and *Rubus* spp. [3]. The characterization of these three viruses showed that they should be assigned to novel species within the genus *Varicosavirus* based on the nucleotide sequence divergence from previously reported varicosaviruses and phylogenetic placement.  |

|  |
| --- |
| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Species *Description of current taxonomy*: Viruses classified in the genus *Varicosavirus* are bi-segmented and infect a wide range of plants. The assignment of viruses to this genus is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences.*Proposed* *taxonomic change(s)*: Create three new species in the genus *Varicosavirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. *Demarcation criteria:*Viruses assigned to different species within the genus *Varicosavirus* 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. occupy different ecological niches as evidenced by differences in hosts

*Justification*: Three novel rhabdoviruses were identified in *Agastache rugosa* [1], *Orychophragmus violaceus* [2] and *Rubus* spp. [3]. The characterization of these three viruses showed that they should be assigned to novel species within the genus *Varicosavirus*, based on the nucleotide sequence divergence from previously reported varicosaviruses and phylogenetic placement (see below).**Novel species**1. **Agastache rugosa associated varicosavirus (ARaVV)** was identified from Korean mint (*Agastache rugosa*) samples collected in Lianoning, China. ARaVV genome is bi-segmented with a coding-complete genome (CCG) RNA1 of 6,428 nucleotides and RNA2 of 3,862 nucleotides (PP987314 and PP987315) [1]. RNA1 contains one large ORF for the L polymerase protein, while RNA2 contains three ORFs (**Figure 1**). The nucleotide sequence of ARaVV L protein has the highest identity values with that of Centaurea virus 1(CenV1; 56.8%), while the ARaVV RNA2 has the highest nt identities values with that of Raphanus virus 1 with 40.6% [1]. The nucleotide sequence identity between the ARaVV genomic segments and those of the closest relative is below 75%. Based on ML trees generated from complete L protein sequences, ARaVV is placed within a subclade of varicosaviruses with CenV1 (**Figure 2**).
2. **Orychophragmus violaceus varicosavirus (OVVV)** was identified from Chinese violet cress (*Orychophragmus violaceus*) samples collected in Beijing, China. OVVV genome is bi-segmented with a complete genome (CG) RNA1 of 6,795 nucleotides and RNA2 of 5,895 nucleotides [2]. RNA1 contains one large ORF for the L polymerase protein, while RNA2 contains four ORFs (**Figure 1**). The nucleotide sequence of OVVV L protein has the highest identity values with that of Brassica virus 2 (BrV2; 66.5%), while the OVVV RNA2 has the highest nt identities values with that of BrV2 with 42.9%. Based on ML trees generated from complete L protein sequences, OVVV is placed within a subclade of varicosaviruses with BrV2 (**Figure 2**).
3. **Rubus varicosavirus 1(RVV1)** was identified from Rubus samples collected in South Carolina, USA. RVV1 genome is bi-segmented with a coding-complete genome (CCG) RNA1 of 6,480 nucleotides and RNA2 of 5,630 nucleotides (PQ317243 and PQ317244) [3]. RNA1 contains one large ORF for the L polymerase protein, while RNA2 contains five ORFs (**Figure 1**). The nucleotide sequence of RVV1 L protein has the highest identity values with that of Vincetoxicum virus 1(VinV1; 62 %), while the RVV1 RNA2 has the highest nt identities values with that of VinV1 with 53% [2]. Based on ML trees generated from complete L protein sequences, RVV1 is placed within a subclade of varicosaviruses with VinV1 (**Figure 2**).

ARaVV, OVVV and RVV1 meet the demarcation criteria A and B. Thus, we propose to classify ARaVV, OVVV and RVV1 into the new species “*Varicosavirus agastachi”, “Varicosavirus orychophragmi”* and *“Varicosavirus rubi”*. subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. |

|  |
| --- |
| **References:**  |
| [1] Yang C, Yang L, Li Y, Cui X, Bai X, Zhang S, Cao M (2024). Molecular identification of a putative novel varicosavirus identified from Agastache rugosa in China. Arch Virol 169:212. PMID: 39365443 DOI: 10.1007/s00705-024-06141-0.[2] Chen Y, Li Q, Yu J, Zhou Y, Fei S, Wu J, Fu S (2025). A novel varicosavirus associated with Orychophragmus violaceus in China. Arch Virol 170:121. PMID: 40329141 DOI: 10.1007/s00705-025-06283-9[3] 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>.  |

|  |
| --- |
| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| 2025.026P.N.v2.Rhabdoviridae\_Varicosavirus\_3nsp | Excel sheet |
|  |  |

**Tables, Figures:**

****

**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.



**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).