

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

|  |  |
| --- | --- |
| **Title:**  | Create one new species in the genus *Alphanucleorhabdovirus*, and one species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae* (*Mononegavirales: Rhabdoviridae*)  |
| **Code assigned:**  | 2024.014P.A.v1.Rhabdoviridae\_2nsp |

|  |
| --- |
| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)**  |
| Bejerman M | UFyMA INTA-CONICET, Argentina | bejerman.nicolas@inta.gob.ar | X |
| Debat H | UFyMA INTA-CONICET, Argentina | debat.hmberto@inta.gob.ar |  |
| Dietzgen R | QAAFI, UQ, Australia | r.dietzgen@uq.edu.au |  |
| Freitas-Astua J | EMBRAPA Mandioca e Fruticultura, Brazil | juliana.astua@embrapa.br |  |
| Kondo H | Okayama University, Japan | hkondo@rib.okayama-u.ac.jp |  |
| Ramos-Gonzalez P | Instituto Biológico de São Paulo, Brazil | plrg1970@gmail.com |  |
| Whitfield A | NC State University, USA | awhitfi@ncsu.edu |  |
| Walker P | 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 | **X** | 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** |
| *Rhabdovridae* SG | 10 | 0 | 4 |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** |  10/06/2024 |

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

|  |  |
| --- | --- |
| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| 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:** |  DD/MM/YYYY |

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

|  |
| --- |
| **Name of accompanying Excel module:**  |
| 2024.014P.A.v1.Rhabdoviridae\_2nsp.xslx |

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

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person:**  | N |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
|  |  |  |
|  |  |  |
|  |  |  |

|  |
| --- |
| **Abstract of Taxonomy Proposal:**  |
| ***Taxonomic rank(s) affected***: Species***Description of current taxonomy***: Viruses classified in the genera *Alphanucleorhabdovirus* and *Betanucleorhabdovirus* 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 *Alphanucleorhabdovirus* and one new species in the genus *Betanucleorhabdovirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. These species are proposed to be named *Alphanucleorhabdovirus babaci* and *Betanucleorhabdovirus paridis*, respectively. ***Justification***: Two novel rhabdoviruses were identified in babaco [1] and *Paris polyphylla* [2]. The characterization of both viruses showed that the babaco-associated virus should be classified as a novel species within the genus *Alphanucleorhabdovirus* [1] while the *Paris polyphylla*-associated virus should be classified as a novel species within the genus *Betanucleorhabdovirus* [2].  |

|  |
| --- |
| **Text of Taxonomy proposal:**  |
| ***Taxonomic rank(s) affected***: Species ***Description of current taxonomy***: Viruses classified in the genera *Alphanucleorhabdovirus* and *Betanucleorhabdovirus* 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 *Alphanucleorhabdovirus* and one new species in the genus *Betanucleorhabdovirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.***Demarcation criteria****:* Members of the genera *Alphanucleorhabdovirus* and *Betanucleorhabdovirus* have several of the following characteristics (<https://ictv.global/report/chapter/rhabdoviridae/rhabdoviridae>; accessed on March 8th): 1. nucleotide sequence identity lower than 75% in the complete genome sequence;
2. occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors; and
3. can be clearly distinguished in serological tests or by nucleic acid hybridization.

***Justification***: Two novel rhabdoviruses were identified in babaco [1] and *Paris polyphylla* [2]. The characterization of both viruses showed that the babaco-associated virus should be classified as a novel species within the genus *Alphanucleorhabdovirus* [1] while the *Paris polyphylla*-associated virus should be classified as a novel species within the genus *Betanucleorhabdovirus* [2].One new species in the genus *Alphanucleorhabdovirus*1. **Babaco nucleorhabdovirus 1 (BabRV1)** was identified from babaco (*Vasconcellea × heilbornii*) samples collected in the Azuay Province, Ecuador. The complete genome (CG) sequence of BabRV1 has 12,802 nucleotides (OQ256237) and contains seven ORFs in the order 3’-N-X-P-P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes and the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, as well as the accessory ORF encoding the X protein between the N and P genes (**Figure 1**). The CG nucleotide sequence of BabRV1 has the highest sequence identity with that of Joa yellow blotch-associated virus (JYBaV, 68%) [1]. Based on ML trees generated from complete L protein sequences, BabRV1 forms a well-supported clade within alphanucleorhabdoviruses with JYBaV, constricta yellow dwarf virus, and potato yellow dwarf virus (**Figure 2**).

BabRV1 meets the demarcation criteria A and B. Thus, we propose to classify BabRV1 in the new species *Alphanucleorhabdovirus babaci*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.One new species in the genus *Betanucleorhabdovirus*1. **Paris yunnanensis rhabdovirus 1 (PyRV1)** was identified from *Paris polyphylla* var. *yunnanensis* samples collected in Yunnan Province, China. The complete genome (CG) sequence of PyRV1 has 13,709 nucleotides (OL439478) and contains six ORFs in the order 3’-N-P-P3-M-G-L-5’ [2] representing the five canonical rhabdovirus structural protein genes and the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 1**). The CG nucleotide sequence of PyRV1 has the highest sequence identity with that of sonchus yellow net virus (SYNV; 55.1%) [2]. Based on ML trees generated from complete L protein sequences, PyRV1 forms a well-supported clade within betanucleorhabdoviruses with SYNV and Taraxacum betanucleorhabdovirus 1 (**Figure 2**).

PyRV1 meets the demarcation criteria A and B. Thus, we propose to classify PyRV1 in the new species *Betanucleorhabdovirus paridis*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  |

|  |
| --- |
| **References:**  |
| [1] Reyes-Proaño E, Cañada-Bautista M, Cornejo-Franco J, Alvarez-Quinto R, Mollov D, Sanchez-Timm E, Quito-Avila D (2023). The virome of Babaco (Vasconcellea × heilbornii) expands to include new members of the *Rhabdoviridae* and *Bromoviridae*. Viruses 15:1380, PMID:37376679, doi: 10.3390/v15061380.[2] Hu J, Miao T, Que K, Siddiqur Rahman M, Zhang L, Dong J, Ji P, Dong J (2023). Identification, molecular characterization and phylogenetic analysis of a novel nucleorhabdovirus infecting *Paris polyphylla* var. *yunnanensis*. Sci Rep 13:10040, PMID:37340012, doi:10.1038/s41598-023-37022-2.   |

|  |
| --- |
| **Tables, Figures:** **Diagrama  Descripción generada automáticamente****Figure 1**. Genome graphs depicting architecture and gene products of proposed viruses to be included in species within genera *Alphanucleorhabdovirus* and *Betanucleorhabdovirus.* Abbreviations: N: nucleoprotein; X; X protein; P: phosphoprotein; P3: putative cell-to-cell movement protein; M: matrix protein; G: glycoprotein; L: RNA-dependent RNA polymerase. Virus name abbreviations: babaco nucleorhabdovirus 1 (BabRV1) and Paris yunnanensis rhabdovirus 1 (PyRV1).Diagrama, Esquemático  Descripción generada automáticamente**Figure 2.** AMaximum 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 MegaX 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). |