

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create seven new species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae* (*Mononegavirales: Rhabdoviridae*) |
| **Code assigned:** | 2025.024P.Ac.v3.Rhabdoviridae\_Betanucleorhabdovirus\_7nsp | |

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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| W - Withdrawn |  |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** |
| *“Betanucleorhabdovirus alpiniae”* | The species epithet is derived from Alpinia, the scientific name of the plant host genera from which the sequence of the virus was obtained. |
| *“Betanucleorhabdovirus betae”* | The species epithet is derived from Beta, the scientific name of the plant host genera from which the sequence of the virus was obtained. |
| *“Betanucleorhabdovirus alphasambuci”* | The species epithet is derived from Sambucus, the scientific name of the plant host genera from which the sequence of the virus was obtained, and from the first letter of the Latin alphabet. |
| *“Betanucleorhabdovirus betasambuci”* | The species epithet is derived from Sambucus, the scientific name of the plant host genera from which the sequence of the virus was obtained, and from the second letter of the Latin alphabet. |
| *“Betanucleorhabdovirus gammasambuci”* | The species epithet is derived from Sambucus, the scientific name of the plant host genera from which the sequence of the virus was obtained, and from the third letter of the Latin alphabet. |
| *“Betanucleorhabdovirus deltasambuci”* | The species epithet is derived from Sambucus, the scientific name of the plant host genera from which the sequence of the virus was obtained, and from the fourth letter of the Latin alphabet. |
| *“Betanucleorhabdovirus epsilonsambuci”* | The species epithet is derived from Sambucus, the scientific name of the plant host genera from which the sequence of the virus was obtained, and from the fifth letter of the Latin alphabet. |
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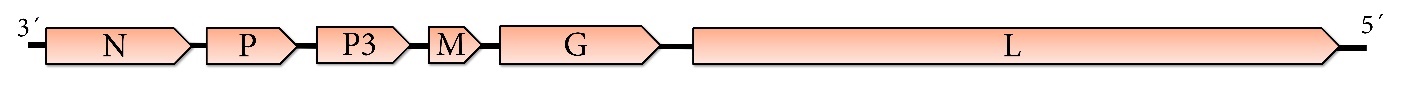
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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** | | |
| *Taxonomic rank(s) affected*:  Genus *Betanucleorhabdovirus* in the family *Rhabdoviridae*  *Description of current taxonomy*:  Genus *Betanucleorhabdovirus* belongs to the subfamily *Betarhabdovirinae*, family *Rhabdoviridae* and consists of 19 species. Viruses classified into species in the genus *Betanucleorhabdovirus* infect a wide range of plants, and 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 seven new species in the genus *Betanucleorhabdovirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. These species are proposed to be named as “*Betanucleorhabdovirus alpiniae”, “Betanucleorhabdovirus betae”, “Betanucleorhabdovirus alphasambuci”, “Betanucleorhabdovirus betasambuc”i, “Betanucleorhabdovirus gammasambuci”, “Betanucleorhabdovirus deltasambuci”* and *“Betanucleorhabdovirus epsilonsambuci”*.  *Justification*:  Seven novel rhabdoviruses were identified in *Alpinia purpurata* [1], beet [Mehrvar and Abkho, unpublished (OR227650)] and elderberry [2]. The characterization of these seven viruses showed that they should be classified into novel species within the genus *Betanucleorhabdovirus*. | | |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus *Betanucleorhabdovirus* in the family *Rhabdoviridae*    *Description of current taxonomy*:  Genus *Betanucleorhabdovirus* belongs to the subfamily *Betarhabdovirinae*, family *Rhabdoviridae* and consists of 19 species. Viruses classified into species in the genus *Betanucleorhabdovirus* infect a wide range of plants, and 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 seven new species in the genus *Betanucleorhabdovirus*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae.*  *Demarcation criteria:*  Viruses assigned to different species within the genus *Betanucleorhabdovirus* should have several of the following characteristics:  A) nucleotide identity values less than 75% for the coding-complete genome sequence  B) amino acid identity values 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*:  Seven novel rhabdoviruses were identified in *Alpinia purpurata* [1], beet [Mehrvar and Abkho, unpublished (OR227650)] and elderberry [2]. The characterization of these seven viruses showed that they should be classified into novel species within the genus *Betanucleorhabdovirus*.   1. **Alpinia vein streaking virus (ApVSV)** was identified from flowering ginger (*Alpinia purpurata*) samples collected in Hawaii, USA. The coding-complete genome (CCG) sequence of ApVSV consists of 13,153 nucleotides (OQ538192) and contains six ORFs in the order 3’-N-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 (**Figure 1**). The CCG nucleotide sequence of ApVSV has the highest identity values with that of cardamon vein clearing nucleorhabdovirus 1 (CdVCNRV1; 71.4%), while the ApVSV encoded proteins have the highest identity values with those of CdVCNRV1 (73.5%) [1]. Based on ML trees generated from complete L protein sequences, ApVSV forms a well-supported clade within betanucleorhabdoviruses with CdVCNRV1 (**Figure 2**). 2. **beet betanucleorhabdovirus 1 (BNRV1)** was identified from beet (*Beta vulgaris*) samples collected in Iran. The coding-complete genome (CCG) sequence of PyRV1 consists of 13,527 nucleotides (OR227650) and contains six ORFs in the order 3’-N-P-P3-M-G-L-5’ [Mehrvar and Abkho, unpublished] 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 CCG nucleotide sequence of BNRV1 has the highest identity values with that of tomato betanucleorhabdovirus 2 (TBRV2; 64.7%), while the BNRV1 encoded proteins have the highest identity values with those of Sambucus betanucleorhabdovirus 4 (84.5%). Based on ML trees generated from complete L protein sequences, BNRV1 forms a well-supported clade within betanucleorhabdoviruses with TBRV2, tomato betanucleorhabdovirus 1, and Sambucus betanucleorhabdovirus 1-5 (**Figure 2**). The sequence of another beet-associated virus, that was also isolated in Iran, and named as beet leaf curl betanucleorhabdovirus (OQ784673, Zakiagal et al 2024) is the GenBank. This virus shares a 86% nt identity at genome level with BNRV1, thus beet leaf curl betanucleorhabdovirus is an isolate of BNRV1. 3. **Sambucus betanucleorhabdovirus 1 (SaBNV1)** was identified from elderberry (S*ambucus nigra*) samples collected in Czech Republic. The complete genome (CG) sequence of SaBNV1 consists of 13,488 nucleotides (PP711309) 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 SaBNV1 has the highest identity values with that of Sambucus betanucleorhabdovirus 5 (SaBNV5; 70.4%), while the SaBNV1 encoded proteins have the highest identity values with those of SaBNV5 (78.8%) [2]. Based on ML trees generated from complete L protein sequences, SaBNV1 forms a well-supported clade within betanucleorhabdoviruses with Sambucus betanucleorhabdovirus 2-5 (**Figure 2**). 4. **Sambucus betanucleorhabdovirus 2 (SaBNV2)** was identified from elderberry (S*ambucus nigra*) samples collected in Czech Republic. The complete genome (CG) sequence of SaBNV2 is 13,458 nucleotides (PP711310) in size 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 SaBNV2 has the highest identity values with that of Sambucus betanucleorhabdovirus 5 (SaBNV5; 72.3%), while the SaBNV2 encoded proteins have the highest identity values with those of SaBNV5 (82.1%) [2]. Based on ML trees generated from complete L protein sequences, SaBNV2 forms a well-supported clade within betanucleorhabdoviruses with Sambucus betanucleorhabdovirus 3-5 (**Figure 2**). 5. **Sambucus betanucleorhabdovirus 3 (SaBNV3)** was identified from elderberry (S*ambucus nigra*) samples collected in Czech Republic. The complete genome (CG) sequence of SaBNV3 consists of 13,521 nucleotides (PP711317) 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 SaBNV3 has the highest identity values with that of Sambucus betanucleorhabdovirus 5 (SaBNV5; 73.5%), while the SaBNV3 encoded proteins have the highest identity values with those of SaBNV5 (83.8%) [2]. Based on ML trees generated from complete L protein sequences, SaBNV3 forms a well-supported clade within betanucleorhabdoviruses with Sambucus betanucleorhabdovirus 4-5 (**Figure 2**). 6. **Sambucus betanucleorhabdovirus 4 (SaBNV4)** was identified from elderberry (S*ambucus nigra*) samples collected in Czech Republic. The coding-complete genome (CCG) sequence of SaBNV4 has 13,486 nucleotides (PP711315) 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 CCG nucleotide sequence of SaBNV4 has the highest identity values with that of Sambucus betanucleorhabdovirus 5 (SaBNV5; 74%), while the SaBNV4 encoded proteins have the highest identity values with those of SaBNV5 (84.1%) [2]. Based on ML trees generated from complete L protein sequences, SaBNV4 forms a well-supported clade within betanucleorhabdoviruses with Sambucus betanucleorhabdovirus 3 and 5 (**Figure 2**). 7. **Sambucus betanucleorhabdovirus 5 (SaBNV5)** was identified from elderberry (S*ambucus nigra*) samples collected in Czech Republic. The coding-complete genome (CCG) sequence of SaBNV5 is 13,527 nucleotides (PP711313) in size 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 CCG nucleotide sequence of SaBNV5 has the highest identity values with that of Sambucus betanucleorhabdovirus 4 (SaBNV4; 74%), while the SaBNV5 encoded proteins have the highest identity values with those of SaBNV4 (84.1%) [2]. Based on ML trees generated from complete L protein sequences, SaBNV5 forms a well-supported clade within betanucleorhabdoviruses with Sambucus betanucleorhabdovirus 3-4 (**Figure 2**).   ApVSV and BNRV1 meet the demarcation criteria A, B and C; while SaBNV1, SaBNV2, SaBNV3, SaBNV4 and SaBNV5 meet the demarcation criteria A and B. Thus, we propose to classify ApVSV, BNRV1, SaBNV1, SaBNV2, SaBNV3, SaBNV4 and SaBNV5 as the new species “*Betanucleorhabdovirus alpiniae”, “Betanucleorhabdovirus betae”, “Betanucleorhabdovirus alphasambuci”,” Betanucleorhabdovirus betasambuci”, “Betanucleorhabdovirus gammasambuci”, “Betanucleorhabdovirus deltasambuc”i* and *“Betanucleorhabdovirus epsilonsambuci”* in the subfamily *Betarhabdovirinae*, family *Rhabdoviridae*. |

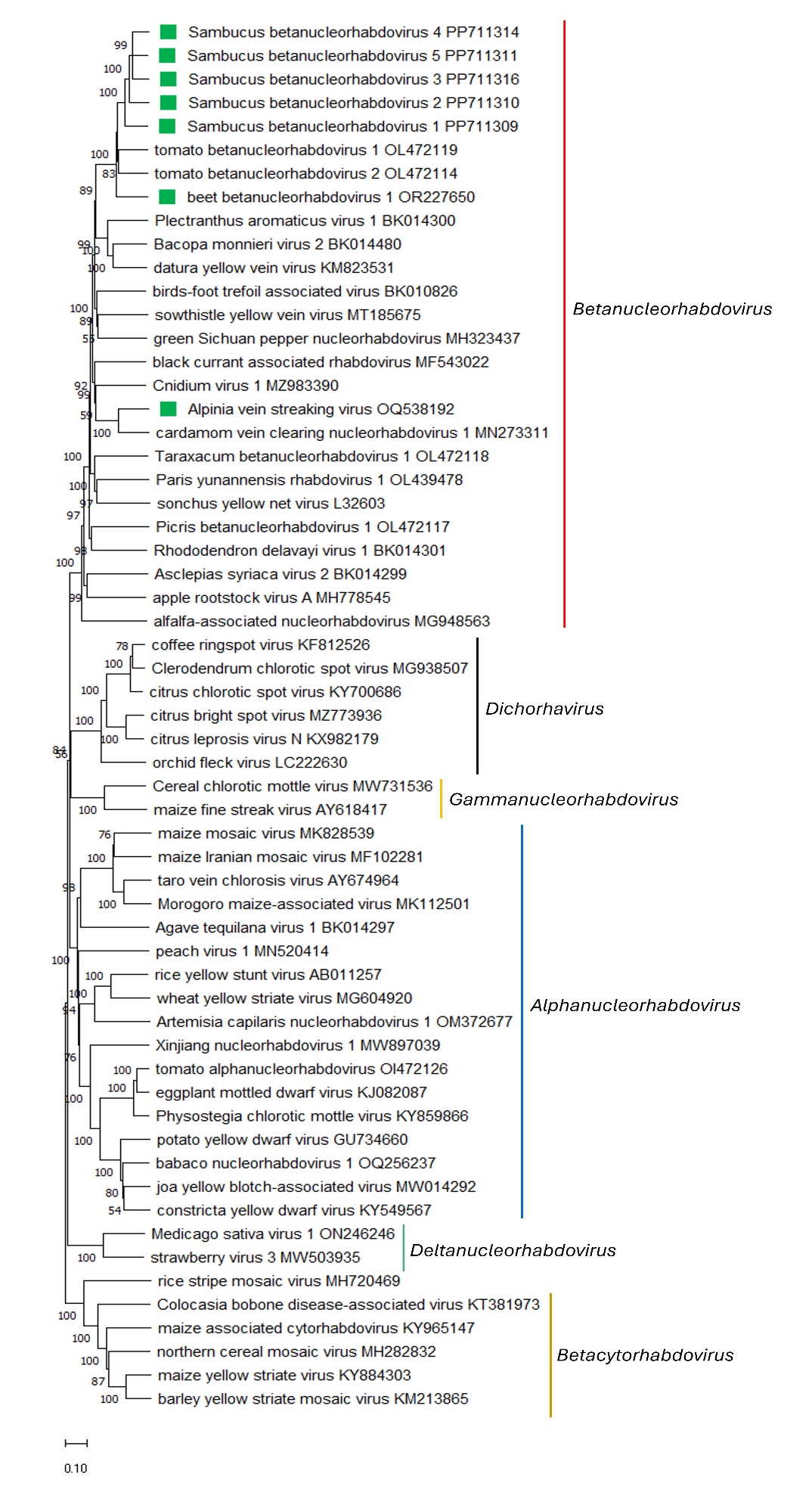
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| **References:** |
| [1] Larrea-Sarmiento A, Galanti R, Olmedo-Velarde A, Wang X, Al Rwahnih, et al. (2024). Characterization of Two Novel Viruses Within a Complex Virome from Flowering Ginger in Hawaii. Plant Dis 108:3011-3009. PMID: 39327791 DOI: 10.1094/PDIS-10-23-2181-RE.  [2] Safarova D, Candresse T, Veselska J, Navratil M (2024). Novel Betanucleorhabdoviruses Infecting Elderberry (*Sambucus nigra* L.): Genome Characterization and Genetic Variability. Pathogens 13:445. PMID: 38921743 DOI: 10.3390/pathogens13060445. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.024P.A.v1.Rhabdoviridae\_Betanucleorhabdovirus\_7nsp | Excel sheet |
|  |  |

**Tables, Figures:**

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

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**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. Seven viruses potentially belonging to the new species are indicated with green squares. Numbers at the nodes indicate bootstrap support (1000 replicates).