

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2022.001M** |  |
| **Short title:** Create two new species in the genus *Alphanucleorhabdovirus*, and four new species in the genus *Betanucleorhabdovirus*, subfamily *Betarhabdovirinae* (*Mononegavirales*: *Rhabdoviridae*) |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Rhabdoviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| Minor corrections |

**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Rhabdoviridae* Study Group | 12 | 0 | 2 |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 23, 2022 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2022.001M.N.v1.Alpha and betanucleorhabdoviruses\_6nsp.xlsx |

**Abstract**

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| Viruses classified in the family *Rhabdoviridae* infect vertebrates, invertebrates, and plants. Six new plant-infecting rhabdoviruses were discovered recently and their complete or coding-complete genome sequences were determined. This proposal aims to classify taxonomically these six viruses in six new species in the genera *Alphanucleorhabdovirus* and *Betanucleorhabdovirus.*  |

**Text of proposal**

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| We propose the taxonomic classification of six novel plant-infecting rhabdoviruses in six new species in two established genera in the subfamily *Betarhabdovirinae,* family *Rhabdoviridae*: **Two new species in genus *Alphanucleorhabdovirus*****1)** **Agave tequilana virus 1 (ATV1)** was identified during an *in silico* analysis of transcriptome data of blue agave (*Agave tequilana* Weber var. azul) tissues from Guanajuato, Mexico. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ATV1 has 13,166 nucleotides (GenBank #BK014297) 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 ATV1 has the highest sequence identity with that of maize mosaic virus (MMV; 49.3%) [1]. Based on ML trees generated from complete large protein (L) sequences, ATV1 forms a well-supported clade with the monocot-infecting alphanucleorhabdoviruses MMV, maize Iranian mosaic virus, Morogoro maize-associated virus, and taro vein chlorosis virus (**Figure 2**).**2)** **Artemisia capillaris nucleorhabdovirus 1 (ArtCaNV1)** was identified during an *in silico* analysis of transcriptome data of capillary wormwood (*Artemisia capillaris* Thunb) tissues from Kyoto, Japan. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArtCaNV1 has 13,939 nucleotides (isolate YK,GenBank #OM372677), and contains six ORFs in the order 3’-N-P-P3-M-G-L-5’ [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 ArtCaNV1 has the highest sequence identity with that of wheat yellow striate virus (WYSV; 51.8%) [unpublished]. Based on ML trees generated from complete L sequences, ArtCaNV1 forms a well-supported clade with the alphanucleorhabdoviruses rice yellow stunt virus and WYSV (**Figure 2**).Viruses assigned to different species within the genus *Alphanucleorhabdovirus* have several of the following characteristics: 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.

ATV1 and ArtCaNV1 meet criteria A and B. Consequently, we propose to classify ATV1 and ArtCaNV1 in two new alphanucleorhabdovirus species.**Four new species in the genus *Betanucleorhabdovirus*****1) Asclepias syriaca virus 2 (AscSyV2)** was identified during an *in silico* analysis of transcriptome data of common milkweed (*Asclepias syriaca* L.) tissues from Illinois, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of AscSyV2 has 12,940 nucleotides (GenBank #BK014299) 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 AscSyV2 has the highest sequence identity with that of apple rootstock virus A (ApRVA; 51.3%) [1]. Based on ML trees generated from complete L sequences, AscSyV2 is placed within a subclade of betanucleorhabdoviruses with ApRVA (**Figure 2**).**2) Cnidium virus 1 (CnV1)** was identified in *Cnidium officinale* plants from Seoul, South Korea. The complete genome (CG) sequence of CnV1 has 14,002 nucleotides (isolate SK, GenBank #MZ983390), 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**). CnV1 is most closely related to black currant-associated rhabdovirus (BCaRV) and cardamom vein clearing virus (CdVCV). The CG nucleotide sequence of CnV1 is 54% and 56% identical to that of BCaRV and CdVCV, respectively [2]. Based on ML trees generated from complete L sequences (**Figure 2**), CnV1 is placed within a subclade of betanucleorhabdoviruses with BCaRV and CdVCV.**3) Plectranthus aromaticus virus 1 (PleArV1)** was identified during an *in silico* analysis of transcriptome data of Cuban oregano (*Plectranthus aromaticus* Lour.) tissues from Malaysia. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PleArV1 has 12,994 nucleotides (GenBank #BK014300) 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 PleArV1 has the highest sequence identity with that of datura yellow vein virus (DYVV; 62.1%) [1]. Based on ML trees generated from complete L sequences, PleArV1 is placed within a subclade of betanucleorhabdoviruses with DYVV and Bacopa monnieri virus 2 (**Figure 2**).**4) Rhododendron delavayi virus 1 (RhoDeV1)** was identified during an *in silico* analysis of transcriptome data of red rhododendron (*Rhododendron delavayi* Franch) tissues from Yunnan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of RhoDeV1 has 13,719 nucleotides (GenBank #BK014301) 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 RhoDeV1 has the highest sequence identity with that of black currant-associated rhabdovirus (BCaRV; 53.1%) [1]. Based on ML trees generated from complete L sequences, RhoDeV1 forms a well-supported clade with other betanucleorhabdoviruses (**Figure 2**).Viruses assigned to different species within the genus *Betanucleorhabdovirus* have several of the following characteristics: 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.

AscSyV2, CnV1, PleArV1, and RhoDeV1 meet criteria A and B. Consequently, we propose to classify AscSyV2, CnV1, PleArV1, and RhoDeV1 into four new betanucleorhabdovirus species. |

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**Supporting evidence**

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**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; P: phosphoprotein; P3: putative cell-to-cell movement protein; M: matrix protein; G: glycoprotein; L: large protein. Virus name abbreviations: Agave tequilana virus 1 (ATV1), Artemisia capillaris nucleorhabdovirus 1 (ArtCaNV1), Asclepias syriaca virus 2 (AscSyV2), Cnidium virus 1 (CnV1), Plectranthus aromaticus virus 1 (PleARV1), and Rhododendron delavayi virus 1 (RhoDeV1).

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**Figure 2.** AMaximum Likelihood (ML) phylogenetic tree of plant-infecting rhabdovirus L 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. Six viruses potentially belonging to the new species are indicated with green squares. Numbers at the nodes indicate bootstrap support (1000 replicates).

**References**

[1] Bejerman N, Dietzgen RG, Debat H (2021). Illuminating the Plant Rhabdovirus Landscape through Metatranscriptomics Data. Viruses 13:1303. PMID: 34372509, doi: 10.3390/v13071304.

[2] Belete M, Igori D, Kim S, Lee S, Moon J (2022) Complete genome sequence of cnidium virus 1, a novel betanucleorhabdovirus infecting Cnidium officinale. Arch Virol 167:973-977. PMID: 35112199, doi:10.1007/s00705-021-05348-9.