

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

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| **Code assigned:** | **2021.001M** |  |
| **Short title:**  Create one new species in the genus *Alphanucleorhabdovirus*, one new species in the genus *Betanucleorhabdovirus*, and five new species in the genus *Cytorhabdovirus*, 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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| The proposal was supported by all 12 of the 15 members of *Rhabdoviridae* SG who voted. |

**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 28, 2021 |
| 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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| 2021.001M.R.Betarhabdovirinae\_7nsp |

**Abstract**

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

**Text of proposal**

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| |  | | --- | | We propose the taxonomic classification of seven novel plant-infecting rhabdoviruses in seven new species in three established genera in the *subfamily Betarhabdovirinae,* family *Rhabdoviridae*:  **One new species in the genus *Alphanucleorhabdovirus***  **1) Joa yellow blotch associated virus (JYBaV)** was identified in joa (*Solanum aculeatissimum* L.) plants from Manaus, State of Amazonas, Brazil. The complete genome sequence of 12,965 nucleotides (isolate Manaus, MW014292) has been determined [1]. The JYBaV genome is similar in organization to that of the alphanucleorhabdoviruses constricta yellow dwarf virus (CYDV), eggplant mottle dwarf virus (EMDV), physostegia chlorotic mottle virus (PhCMoV) and potato yellow dwarf virus (PYDV), containing the five canonical rhabdovirus structural protein genes (N, P, M, G, and L) plus additional accessory genes X (unknown function; between N and P genes) and Y (movement protein gene; between P and M genes) [1] (**Figure 1**). Based on ML trees generated from complete L protein sequences, JYBaV forms a well-supported clade with other alphanucleorhabdoviruses, and is most closely related to CYDV and PYDV (**Figure 2**). The genome nucleotide sequence identity between JYBaV and CYDV and PYDV is 69.5% and 69.4%, respectively; whereas the highest amino acid sequence identity of JYBaV and CYDV and PYDV encoded proteins is 74.4% and 73.11%, respectively [1].  We propose to classify JYBaV in the new species *Alphanucleorhabdovirus joa* in the genus *Alphanucleorhabdovirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae*.  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.  * JYBaV meets criteria A and B.   **One new species in the genus *Betanucleorhabdovirus***  **2) Bacopa monnieri virus 2 (BmV2)** was identified from *in silico* analysis of transcriptome data of water hyssop (*Bacopa monnieri* L.) tissues from Lucknow, India. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BmV2 has 13,165 nucleotides (isolate BM, BK014480), 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 BmV2 has the highest sequence identity with that of datura yellow vein virus (DYVV; 71%) [2]. Based on ML trees generated from complete L protein sequences, BmV2 forms a well-supported clade with other betanucleorhabdoviruses, and is most closely related to DYVV (**Figure 2**).  We propose to classify BmV2 in the new species *Betanucleorhabdovirus* *bacopae*, in the genus *Betanucleorhabdovirus*, subfamily *Betarhabdovirinae,* family *Rhabdoviridae.*  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.  * BmV2 meets criteria A and B.   **Five new species in the genus *Cytorhabdovirus***  **3) Bacopa monnieri virus 1 (BmV1)** was identified from *in silico* analysis of transcriptome data of water hyssop (*Bacopa monnieri* L.) tissues from Lucknow, India. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BmV1 has 13,332 nucleotides (isolate BM, BK014479), and contains seven ORFs in the order 3’-N-P-P3-M-G-P6-L-5’ [2] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 1**). BmV1 is most closely related to Wuhan insect virus 4 (WhIV4). The CCG nucleotide sequence of BmV1 is 54.3% identical to that of WhIV4. In a BlastP search, BmV1 N, G and L protein sequences are 48%, 46% and 52% identical to the cognate proteins of WhIV4 [2]. Based on ML trees generated from complete L protein sequences (**Figure 2**), BmV1 is placed within a subclade of cytorhabdoviruses, most closely related to WhIV4.  **4) Chrysanthemum yellow dwarf associated virus (CYDaV)** was identified in a chrysanthemum plant collected from Chongqing, China. The complete genome (CG) sequence of CYDaV has 14,086 nucleotides (isolate cq, MW039593) and contains seven ORFs in the order 3’-N-P-P3-M-G-P6-L-5’ [3] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 1**). CYDaV is most closely related to alfalfa dwarf virus (ADV), raspberry vein chlorosis virus (RVCV) and strawberry crinkle virus (SCV). The CG nucleotide sequence of CYDaV is 45.99%, 46.22% and 46.67% identical to that of ADV, RVCV and SCV, respectively. In a BlastP search, CYDaV L protein sequence is 50.6%, 49.7 and 50% identical to the L protein of ADV, RVCV and SCV, respectively [3]. Based on ML trees generated from complete L protein sequences (**Figure 2**), CYDaV is placed within a subclade of the cytorhabdoviruses, with ADV, RVCV, and SCV.  **5) Cucurbit cytorhabdovirus 1 (CuCV1)** was identified in zucchini (*Cucurbita pepo* L.) plants from Greece. The complete genome (CG) sequence of CuCV1 has 13,069 nucleotides (isolate ND4, MT381995), and contains seven ORFs in the order 3’-N-P-P3-P4-M-G-L-5’ [4] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P4 between the P3 and M genes (**Figure 1**). CuCV1 is most closely related to yerba mate chlorosis-associated virus (YmCaV). The CG nucleotide sequence of CuCV1 is 45.8% identical to that of YmCaV. In a BlastP search, CuCV1 N, G and L protein sequences are 31.18%, 33.4% and 41.51% identical to the cognate proteins of YmCaV [4]. Based on ML trees generated from complete L protein sequences (**Figure 2**), CuCV1 is placed within a subclade of cytorhabdoviruses, with YmCaV.  **6) Paper mulberry mosaic associated virus (PMuMaV)** was identified in paper mulberry (*Broussonetia papyrifera* L.) plants from Chongqing, China. The complete genome (CG) sequence of PMuMaV has 13,736 nucleotides (isolate SWU, MN872813), and contains six ORFs in the order 3’-N-P-P3-M-G-L-5’ [5] 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**). PMuMaV is most closely related to barley yellow striate mosaic virus (BYSMV) and northern cereal mosaic virus (NCMV). The CG nucleotide sequence of PMuMaV is 38.97% and 38.86% identical to that of NCMV and BYSMV, respectively. In a BlastP search, PMuMaV L protein sequence is 39.9% and 38.7% identical to the L protein of NCMV and BYSMV, respectively [5]. Based on ML trees generated from complete L protein sequences (**Figure 2**), PMuMaV is placed within a subclade of cytorhabdoviruses, with NCMV, rice stripe mosaic virus (RSMV), colocasia bobone associated virus (CBDaV), maize associated cytorhabdovirus, maize yellow striate virus, and BYSMV.  **7) Rose virus R (RVR)** was identified in a rose ‘Hugh Dickson’ plant from Maryland, USA. The complete genome (CG) sequence of RVR has 13,601 nucleotides (isolate MDR92016, MT952336), and contains seven ORFs in the order 3’-N-P-P3-M-G-P6-L-5’ [6] 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, and the accessory protein P6 between the G and L genes (**Figure 1**). RVR is most closely related to RSMV and CBDaV. The CG nucleotide sequence of RVR is 48.38% and 49.54% identical to that of RSMV and CBDaV, respectively. In a BlastP search, RVR L protein sequence is 39% and 43% identical to the L protein of RSMV and CBDaV, respectively [6]. Based on ML trees generated from complete L protein sequences (**Figure 2**), RVR is placed within a subclade of cytorhabdoviruses, with BYSMV, RSMV, NCMV, maize associated cytorhabdovirus, maize yellow striate virus, and CBDaV.  We propose to classify BmV1, CYDaV, CuCV1, PMuMaV and RVR in the new species *Cytorhabdovirus bacopae*, *Cytorhabdovirus chrysanthemi*, *Cytorhabdovirus cucurbitae*, *Cytorhabdovirus broussonetiae*,and *Cytorhabdovirus rosae* in the genus *Cytorhabdovirus*, subfamily *Betarhabdovirinae,* family *Rhabdoviridae.*  --------  Viruses assigned to different species within the genus *Cytorhabdovirus*have several of the following characteristics:   1. nucleotide sequence identity less than 75% for the complete genome sequence; 2. amino acid sequence identity in all cognate open reading frames less than 80%; 3. occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors.  * BmV1, CYDaV, CuCV1, PMuMaV and RVR meet criteria A, B and C. | |

**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 *Cytorhabdovirus*, *Alphanucleorhabdovirus* and *Betanucleorhabdovirus.* Abbreviations: N: nucleoprotein; P: phosphoprotein; P3: putative cell-to-cell movement protein; P4: protein 4; M: matrix protein; G: glycoprotein; P6: Protein 6; L: RNA-dependent RNA polymerase; Y: putative movement protein. Virus name abbreviations: Bacopa monnieri virus 1 (BmV1), chrysanthemum yellow dwarf associated virus (CYDaV), cucurbit cytorhabdovirus 1 (CuCV1), paper mulberry mosaic associated virus (PMuMaV), rose virus R (RVR), joa yellow blotch associated virus (JYBaV) and Bacopa monnieri virus 2 (BmV2).



**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. Seven viruses potentially belonging to the new species are indicated with green squares. The tree is rooted to two animal rhabdoviruses as outgroup. Numbers at the nodes indicate bootstrap support (1000 replicates).

**References**

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