

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

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| **Code assigned:** | **2022.007P** |  |
| **Short title:** Create four new species in the family *Caulimoviridae*  |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| *Caulimoviridae* SG |

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

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| *Caulimoviridae* SG |  |  | X |

**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 | 23 May 2022 |
| Date of this revision (if different to above) | 27 May 2022 |

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

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

**Name of accompanying Excel module**

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| 2022.007P.N.v1.Caulimoviridae\_4ns.xlxs |

**Abstract**

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| We propose the creation of one new species in the genus *Badnavirus*: *Badnavirus meliae*; one new species in the genus *Caulimovirus*: *Caulimovirus metaplexis*; one new species in the genus *Soymovirus*: *Soymovirus* *eleocharis*; and one new species in the genus *Tungrovirus*: *Tungrovirus agapanthi*. Complete genomes of the type members of all these proposed new species were published recently. |

**Text of proposal**

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| 1. **Creating species *Badnavirus meliae* in the genus *Badnavirus***

*Badnavirus meliae* can be considered a new species in the genus *Badnavirus* for the following reasons:1. Its exemplar isolate, chinaberry tree badnavirus 1 (ChTBV1), has a 7,018 bp circular double-stranded (ds) DNA genome with an organization typical of members of the genus *Badnavirus* with 3 putative open reading frames (ORF1 to ORF3). Its ORF3 encodes a putative polyprotein containing the conserved viral aspartic protease (AP), a zinc knuckle finger, a reverse transcriptase (RT), and RNase H domains.
2. The genome of ChTBV1 harbors a tRNAMet primer binding site.
3. In phylogenetic analyses using the RT/RH1 domain nucleotide sequence, ChTBV1 groups within the genus *Badnavirus* (Fig. 1). Its closest relative is fig badnavirus 1 (FBV1; Fig. 1; Table 1).
4. ChTBV1 displays only 68.1% nucleotide (nt) sequence identity with FBV1 in the RT/RH1 domain, which is below the species demarcation criterion of 80% nt sequence identity, justifying the classification of *Badnavirus meliae* as a separate species.
5. **Creating species *Caulimovirus metaplexis* in the genus *Caulimovirus***

*Caulimovirus metaplexis* can be considered a new species in the genus *Caulimovirus* for the following reasons:1. Its exemplar isolate, Metaplexis yellow mottle-associated virus (MeYMaV), has a 7,733bp circular double-stranded (ds) DNA genome with an organization typical of members of the genus *Caulimovirus* with 6 putative open reading frames (ORF1 to ORF6) encoding a putative movement protein, a putative aphid transmission factor, a putative DNA-binding protein, a putative coat protein with a zinc finger domain, a putative polymerase polyprotein with conserved domains for a peptidase, a reverse transcriptase (RT) and an RNase H and a protein with homology to the P6 protein of CaMV with a viroplasmin domain, respectively.
2. The genome of MeYMaV has TATA-like boxes and polyadenylation signals in the large and small intergenic regions, that are hallmarks of members of the genus *Caulimovirus*.
3. In phylogenetic analyses using the RT/RH1 domain nucleotide sequence, MeYMaV groups within the genus *Caulimovirus* (Fig. 1). Its closest relative is strawberry vein banding virus (SVBV; Fig. 1; Table 1).
4. MeYMaV displays only 64.7% nucleotide (nt) sequence identity with SVBV in the RT/RH1 domain, which is below the species demarcation criterion of 80% nt sequence identity, justifying the classification of *Caulimovirus metaplexis* as a separate species.
5. **Creating species *Soymovirus eleocharis*****in the genus *Soymovirus***

*Soymovirus eleocharis* can be considered a new species in the genus *Soymovirus* for the following reasons:1. Its exemplar isolate, water chestnut soymovirus 1 (WCSV1) has a 7,355bp circular double-stranded (ds) DNA genome with an organization typical of members of the genus *Soymovirus* with 9 putative open reading frames encoding a putative movement protein with an RNA-binding domain, 4 small proteins of unknown function, a putative coat protein with a zinc binding domain, a putative polymerase with RT, RNAse H, aspartic protease domains, a putative transactivator protein and a protein of unknown function, respectively.
2. The genome of WCSV1 harbors a tRNAMet primer binding site
3. In phylogenetic analyses using the RT/RH1 domain nucleotide sequence, WCSV1 groups within the genus *Soymovirus* (Fig. 1). Its closest relative is peanut chlorotic streak virus (PCSV; Fig. 1; Table 1).
4. WCSV1 displays only 57.5% nucleotide (nt) sequence identity with PCSV in the RT/RH1 domain, which is below the species demarcation criterion of 80% nt sequence identity, justifying the classification of *Soymovirus eleocharis* as a separate species.
5. **Creating species *Tungrovirus agapanthi*****in the genus *Tungrovirus***

*Tungrovirus agapanthi* can be considered a new species in the genus *Tungrovirus* for the following reasons:1. Its exemplar isolate, Agapanthus tungro virus (AgTV) has a 7,942 bp circular double-stranded (ds) DNA genome with an organization typical of members of the genus *Tungrovirus* with 4 putative open reading frames encoding two putative proteins of unknown function, a polyprotein with putative RT, RNAse H and aspartic protease domains and a virion-associated protein.
2. The genome of AgTV harbors a tRNAMet primer binding site
3. In phylogenetic analyses using the RT/RH1 domain nucleotide sequence, AgTV groups within the genus *Tungrovirus* (Fig. 1). Its closest relative is rice tungro bacilliform virus (RTBV; Fig. 1; Table 1).
4. AgTV displays only 63.9% nucleotide (nt) sequence identity with RTBV in the RT/RH1 domain, which is below the species demarcation criterion of 80% nt sequence identity, justifying the classification of *Tungrovirus agapanthi* as a separate species.
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**Supporting evidence**

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**Figure 1: Phylogenetic tree showing placement of chinaberry tree badnavirus 1 (ChTBV1; species *Badnavirus meliae*), Metaplexis yellow mottle-associated virus (MeYMaV: species *Caulimovirus metaplexis*), water chestnut soymovirus 1 (WCSV1; species *Soymovirus eleocharis*) and Agapanthus tungro virus (AgTV; *Tungrovirus agapanthi*).**Maximum likelihood analysis with 1000 bootstrap sets were performed on nucleotide sequences corresponding to the RT/RH1 domain. Alignments were performed using CLUSTALW and the phylogenic tree was built using the Maximum Likelihood method and Hasegawa-Kishino-Yano model (Hasegawa et al., 1985) of the MEGA X package (Kumar et al., 2018). The tree with the highest log likelihood is shown. Bootstrap values are given above nodes when above 70 % and GenBank accession numbers are provided. The scale bar shows the number of substitutions per site. *Saccharomyces cerevisiae Ty3 virus* (SceTy3V; family *Metaviridae*, genus *Metavirus*) was included in the analysis as an outgroup. Colored dots indicate genera. Type members of the proposed new species are shown with open circles and in red boxes.

**Table 1: Percent nucleotide identities for the *Caulimoviridae* in *pol* gene nucleotide sequences.**

Figures corresponding to type members of the proposed new species are highlighted in orange.



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