

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

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| **Code assigned:** | **2021.003P** |  |
| **Short title:** Create two new species and abolish one species (*Schefflera ringspot virus)* in the genus *Badnavirus* (*Ortervirales*: *Caulimoviridae*) | | |
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**Author(s) and email address(es)**

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| --- | --- |
| Umber M, Teycheney P-Y | marie.umber@inrae.fr;  teycheney@cirad.fr |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| INRAE, UR ASTRO, F-97170, Petit-Bourg, Guadeloupe, France [MU]  CIRAD, UMR AGAP Institut, 97130 Capesterre Belle Eau, France [PYT]  UMR AGAP Institut, Univ Montpellier, CIRAD, INRAE, Institut Agro, 97130 Capesterre Belle Eau, France [PYT] |

**Corresponding author**

|  |
| --- |
| Pierre-Yves Teycheney – teycheney@cirad.fr |

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

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| *Caulimoviridae* Study Group |

**ICTV study group comments and response of proposer**

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**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 21, 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**

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

**Name of accompanying Excel module**

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| 2021.003P.R.Badnavirus\_2ns\_1as |

**Abstract**

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| We propose the creation of two new species, *Badnavirus aucubae* and *Badnavirus castaneae*, in the genus *Badnavirus*, for which complete genomes were published recently. We also propose to abolish one species,*Schefflera ringspot virus*, in the genus *Badnavirus* because its exemplar virus isolate, for which a partial genome sequence is available, displays 99.4% nucleotide sequence identity with the fully sequenced exemplar isolate of an existing species, *Ivy ringspot-associated virus*, in this genus. |

**Text of proposal**

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| |  | | --- | | 1. **Two new species in the genus *Badnavirus***     1. **Creating the species *Badnavirus aucubae***   *Badnavirus aucubae* can be considered a new species in the genus *Badnavirus* for the following reasons:   1. Bacilliform-shaped virions measuring 30 × 180 nm were observed in *Aucuba japonica* diseased plants 2. Its exemplar isolate, aucuba ringspot virus (AuRV) has a 9,092 bp circular double-stranded (ds) DNA genome with an organization typical of members of the genus *Badnavirus* with 3 open reading frames (ORF1 to ORF3). Its ORF3 encodes a putative polyprotein containing the conserved movement protein, coat protein, aspartic protease, reverse transcriptase (RT) and RNase H domains. 3. The genome of AuRV harbors a tRNAMet primer binding site. 4. In phylogenetic analyses using the RT/RH1 domain nucleotide sequence, AuRV groups within the genus *Badnavirus* (Fig. 1). Its closest relative is green Sichuan pepper vein clearing-associated virus(GSPVCaV)(Fig. 1; Table 1). 5. AuRV displays only 70.1% nucleotide (nt) sequence identity with GSPVCaV in the RT/RH1 domain, which is below the species demarcation criterion of 80% nt sequence identity, justifying the classification of *Badnavirus aucubae* as a separate species.    1. **Creating the species *Badnavirus castaneae***   *Badnavirus castaneae* can be considered a new species in the genus *Badnavirus* for the following reasons:   1. Its exemplar isolate, chestnut mosaic virus (ChMV) has a 7,160 bp circular dsDNA genome with an organization typical of a member of the genus *Badnavirus* with 3 ORFs. Its ORF3 encode a putative polyprotein containing the conserved movement protein, coat protein, aspartic protease, reverse transcriptase (RT) and RNase H domains. 2. The genome of ChMV harbors a tRNAMet primer binding site. 3. In phylogenetic analyses using the RT/RH1 domain nucleotide sequence, ChMV groups within the genus *Badnavirus* (Fig. 1). Its closest relative is birch leaf roll-associated virus(BLRaV)(Fig. 1; Table 1). 4. ChMV displays only 67.5% nt identity with BLRaV in the RT/RH1 domain, which is below the species demarcation criterion of 80% nt sequence identity, justifying the classification of *Badnavirus castaneae* as a separate species. 5. **Abolish species *Schefflera ringspot virus* in genus *Badnavirus***   Schefflera ringspot virus (SRV), the exemplar isolate of the species *Schefflera ringspot virus*, was characterized from infected scheffleras and aralias (Lockhart & Olszewski, 1996). SRV has bacilliform particles and is transmitted by the citrus mealybug (*Planococcus citri*). Only a 555 bp partial genome sequence (MH475920) is available for SRV and this sequence overlaps only partially the RT/RH1 sequence that is used for establishing phylogenetic relationships among members of family *Caulimoviridae* (Teycheney et al. 2020), therefore preventing the accurate phylogenetic placement of this virus.  Ivy ringspot-associated virus (IRSaV) was characterized in 2020 from ivy (*Hedera helix*), a member of family Araliaceae like scheffleras and aralias (Bester et al., 2020). Its complete genome was sequenced (MN850490). IRSaV shows 99.4% nt sequence identity to the 555 bp partial SRV sequence deposited in GenBank. It can therefore safely be assumed that SRV and IRSaV belong to the same virus.  We propose to abolish the species *Schefflera ringspot virus* and retain the species *Ivy ringspot-associated virus* based on the fact that only viruses for which complete genome sequences are available are included in the taxonomy of the *Caulimoviridae*. | |

**Supporting evidence**

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**Figure 1: Phylogenetic tree showing placement of aucuba ringspot virus (AuRV, species *Badnavirus aucubae*) and chestnut mosaic virus (ChMV, species *Badnavirus castaneae*)in genus *Badnavirus*.** Maximum likelihood analysis with 1000 bootstrap sets were performed on nucleotide sequences corresponding to the RT/RH1 domain. Alignments were performed using CLUSTAW and the phylogenic tree was built by 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 (-42110,31) 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. The exemplar isolates 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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