

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

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| **Code assigned:** | ***2023.019M*** |  |
| **Short title:** Create a new species in a new genus in the family *Phenuiviridae* and move a species into the new genus | | |
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| Francesco Di Serio |

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

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| ICTV *Phenuiviridae* Study Group |

**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** |
| ICTV *Phenuiviridae* Study Group | 9 | 0 | 0 |

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

|  |  |
| --- | --- |
| **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)** |
| N/A | N/A | N/A |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| 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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| N/A |

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

**Name of accompanying Excel module**

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| --- |
| 2023.019M.N.v1.Phenuiviridae\_1ng\_1nsp\_1spmr.xlsx |

**Abstract**

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| Botrytis cinerea bocivirus 1 (BcBV1) is a new virus identified during a metatranscriptomics study of the virome of a necrotrophic fungus (sclerotiniaceaen *Botrytis cinerea* Pers. (1794)).Here we propose to create a new genus, *Bocivirus*, including a new species in the family *Phenuiviridae* to classify this virus. Moreover, we propose to move and rename a current coguvirus species into this genus. |

**Text of proposal**

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| |  | | --- | | Botrytis cinerea bocivirus 1 (BcBV1) is a new virus during a metatranscriptomics study of the virome of a necrotrophic fungus (sclerotiniaceaen *Botrytis cinerea* Pers. (1794)) (Ruiz-Padilla et al. 2021). BvBV1 is a negative-sense RNA virus with a trisegmented genome.  The trisegmented nature of BcBV1 genome was confirmed by the identification of 5’ and 3’ termini of each segment that, as expected, have almost identical sequences. The 5’ and 3’ termini of each RNA segment are complementary, thus forming a panhandle structure (Fig. 1) likely involved in replication, as reported for other members of the order *Bunyavirales*.  BcBV1 RNA1 (6,743 nt, GenBank #MN617081) encodes a putative protein of 2,211 amino acids (aa) that, based on Blastp analysis, shares the highest sequence identity values with viruses in bunyaviral family *Phenuiviridae*, including grapevine associated cogu-like virus 1 (GaCLV1) (99% query cover, 44.05% aa sequence identity). The RNA-directed RNA polymerase (RdRp) of BcBV1 contains the typical six motifs (premotif A, motifs A–E) that are highly conserved in the RdRps of members of the order *Bunyavirales*. RNA 2 (1,653 nt, MN617080) encodes a putative protein of 470 aa with 56.43% sequence identity (92% query cover) with a protein encoded by grapevine associated cogu-like virus 2 (GaCLV2)*.* RNA3 (1,293 nt, MN617079) encodes a putative capsid protein of 356 aa sharing the highest sequence identity (41.69% aa sequence identity, 96% query cover) with the N protein encoded by grapevine associated cogu-like virus 1.  Both grapevine associated GaCLV1 and 2 have a tripartite genome (Chiapello et al. 2020). They are currently classified in phenuivirid genera *Coguvirus* and *Laulavirus*, respectively (species *Coguvirus viticulum* and *Lulavirus alphaviticulum*).  The demarcation criteria for coguvirus and laulavirus species have been established as less than 95% identity in the aa sequence of the RdRp. Since BcBV1 RdRp has an aa sequence identity below this limit with all members of these genera (Fig. 2), we propose to classify this virus as a member of a novel virus species.  A maximum likelihood phylogenetic tree was generated using amino acid (aa) sequences of the putative RdRp encoded by BcBV1, GaCLV1, and representative members of the genera of the *Phenuiviridae* family. In this tree, BcBV1 clusters in a clade together with GaCLV1 and separately from all the other known coguviruses (Fig. 3). The high bootstrap values in the phylogenetic tree strongly support the conclusion that BcBV1 and GaCLV1 are more closely related to each other than to the other members of the genus *Coguvirus*. Interestingly, while all known coguviruses have bisegmented genomes, composed of one negative-sense RNA segment and one ambisense RNA segment, both BcBV1 and GaCLV1 have trisegmented genomes*.*  Based on the data reported above we propose to create, in the family *Phenuiviridae,* a new genus, *Bocivirus*,including two species: the new species *Bocivirus botrytidis,* here proposed to be createdto classify the novel virus BcBV1 and the species *Bocivirus viticulum* here proposed to classify GaCLV1 (species moved and renamed from genus *Coguvirus*).  **Origin of the name of the species:** the genus name*Bocivirus*derives from the name of the fungus (*Botrytis cinerea* Pers. (1794)) in which BcBV1 has been identified. The species name *botrytidis* derives from the fungal genus name. | |

**Supporting evidence**

Immagine che contiene testo

Descrizione generata automaticamente

**Figure 1.** (A)Alignment of 5′ (left) and 3′ (right) termini of the genomic RNAs of Botrytis cinerea bocavirus 1 (BcBV1). Nucleotides conserved in all RNAs are denoted by an asterisk on the bottom.

(B) Panhandle structure formed by complementary termini of each BcBV1 genomic segment (Figure modified with permission from Ana Ruiz-Padilla et al., 2023).

Torzella virus 1 100.00

Brassica campestris chinensis-coguvirus 1 (UFE16634.1) 88.50 100.00

Watermelon crinkle leaf-associated virus 2 (ASY01343) 52.68 52.36 100.00

Yunnan Paris negative-stranded virus (QVU28732.1) 54.29 54.11 69.74 100.00

Edgeworthia chrysantha mosaic associated virus (ON602044) 54.57 53.93 70.41 74.88 100.00

Watermelon crinkle leaf-associated virus 1 (ASY01340.1) 55.43 55.02 59.51 60.71 60.06 100.00

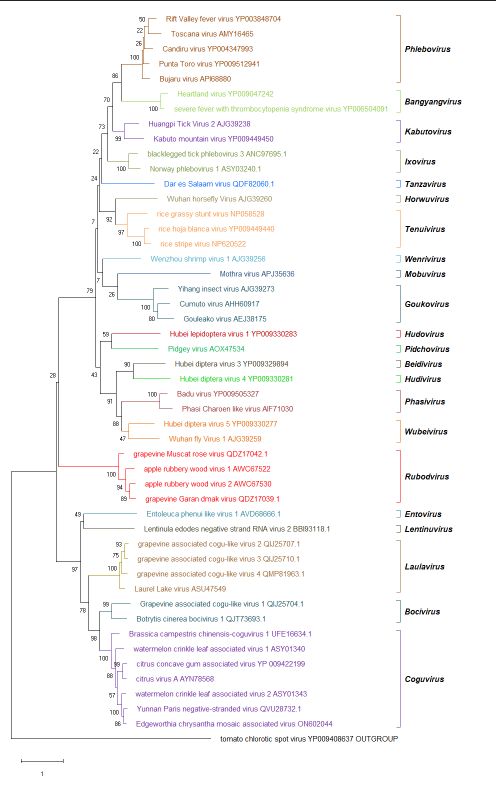
Citrus concave gum-associated virus (YP 009422199.1) 55.52 55.20 58.30 59.82 59.41 62.64 100.00

Citrus virus A (AYN78568.1) 55.94 56.21 57.79 59.82 58.67 63.06 76.65 100.00

Grapevine associated cogu-like virus 1 (QIJ25704.1) 37.47 38.06 38.85 37.94 37.27 38.57 37.61 38.99 100.00

Botrytis cinerea bocivirus 1 (QJT73693.1) 38.99 39.17 38.71 38.97 38.22 38.86 38.73 38.50 44.18 100.00

**Figure 2.** Amino acid identity matrix (values in % of identity) of RdRp (panel A) and NP (panel B) proteins of ECMaV and all the current and proposed members of the genus *Coguvirus*

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**Figure 3** Phylogenetic tree of the RNA-directed RNA polymerase (RdRp) of Botrytis cinerea bocivirus 1, grapevine associated cogu-like virus 1, representative members of all phenuivirid genera, and tomato chlorotic spot virus (bunyaviral *Tospoviridae*) as the outgroup. Maximum likelihood method adopting the LG + G amino acid substitution model was used to infer the phylogenetic tree. Bootstrap probability values (1,000 replicates) are shown at branch nodes. Tree branches are proportional to the genetic distances, with the scale bar indicating substitutions per amino acid site.

**References**

Ruiz-Padilla A, Rodríguez-Romero J, Gómez-Cid I, Pacifico D, Ayllón MA. 2021. Novel mycoviruses discovered in the mycovirome of a necrotrophic fungus. mBio 12:e03705-20. <https://doi.org/10.1128/mBio.03705-20>

Chiapello M, Rodríguez-Romero J, Nerva L, Forgia M, Chitarra W, Ayllón MA, Turina M. 2020. Putative new plant viruses associated with *Plasmopara* *viticola*-infected grapevine samples. Ann Appl Biol 176:180–191.