

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

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| **Code assigned:** | ***2023.007M*** |  |
| **Short title:** Crate a new species in the genus *Coguvirus* (*Bunyavirales : Phenuiviridae*) | | |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Navarro B, Nicoloso VM, Di Serio F | [beatriz.navarro@ipsp.cnr.it](mailto:beatriz.navarro@ipsp.cnr.it); [vittorio.nicoloso@ipsp.cnr.it](mailto:vittorio.nicoloso@ipsp.cnr.it); [francesco.diserio@ipsp.cnr.it](mailto:francesco.diserio@ipsp.cnr.it) |

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

|  |
| --- |
| Istituto per la Protezione Sostenibile delle Piante, CNR, Italy [BN, VMN, FDS] |

**Corresponding author**

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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**

|  |  |  |  |
| --- | --- | --- | --- |
| **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 |

|  |  |  |
| --- | --- | --- |
| **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, 023 |
| 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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| 2023.007M.N.v1.Coguvirus\_1nsp.xlsx |

**Abstract**

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| Edgeworthia chrysantha mosaic-associated virus(ECMaV) fulfils the criteria established by the International Committee on Taxonomy of Viruses *Phenuiviridae* Study Group to be classified as representative member of a new species in the phenuivirid genus *Coguvirus*. The name *Coguvirus* *chrysanthae* is proposed for such a species. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | Edgeworthia chrysantha mosaic-associated virus(ECMaV) has been recently identified in China as a novel virus infecting thymelaeaceaen *Edgeworthia chrysantha* Lindl (Wang et al., 2022). It is a negative-sense RNA virus with a bisegmented genome: the negative-sense RNA1 encodes the putative RNA-directed RNA polymerase (RdRp), whereas the ambisense RNA2 encodes for putative movement (MP) and nucleocapsid (NP) proteins. This genomic organization is similar to that reported previously for members of phenuivirid genus *Coguvirus*. The 5’ and 3’ terminal sequences (approximately 20 nucleotides) of each genomic RNA of ECMaV are complementary (Fig. 1), thus allowing the formation of panhandle structures (Fig. 2) typical of all members of order *Bunyavirales* and likely required for viral replication (Navarro et al., 2018a; Wang et al., 2022). In addition, the 5’ and 3’ termini of the ECMaV genomic RNA1 and RNA2 consist of the nucleotide sequences ACACA and UGUGU at the 5’ and 3’ termini, respectively (Fig. 1), which are conserved in all members of bunyaviral family *Phenuiviridae* (Tang et al., 2021). The RdRP of ECMaV contains the typical six motifs (premotif A, motifs A–E) that are highly conserved in the RdRps of members of the order *Bunyavirales* (Xin et al., 2017; Chen et al. 2021) (Fig. 3). This protein has amino acid (aa) identity ranging from 37.58 % to 74.88 % with the RdRps of classified coguviruses, with the highest identity value obtained with the RdRp encoded by Yúnnán Paris negative-stranded virus (Fig. 4A).  The amino acid (aa) sequence identities of the putative N protein with those of classified coguviruses ranges from 25.37% to 65.80 %, with the highest identity value obtained with the N protein encoded by Yúnnán Paris negative-stranded virus (Fig. 4B).  A maximum likelihood phylogenetic tree was generated using amino acid sequences of the putative RdRp encoded by ECMaV and representative members of all the genera of the *Phenuiviridae* family. In such a tree, ECMaV clusters with coguviruses (Fig. 5). The high bootstrap values in the phylogenetic tree strongly support the classification of ECMaV in the genus *Coguvirus*.  The demarcation criterion for the species of the genus *Coguvirus* has been established as less than 95% identity in the aa sequence of the RdRp (ratified taxonomic proposal 2019.026M.A.v1). Since ECMaV RdRp has an aa sequence identity ranging from 37.58% to 74.88 %, with the other members of the genus *Coguvirus*, we propose to classify ECMaV as a member of a novel species, named *Coguvirus chrysantae*.  **Origin of the name of the species:** *chrysantae* derives from the name of the plant species (*Edgeworthia chrysanta*) in which the virus has been identified for the first time. | |

**Supporting evidence**

5’ 3’

ECMaV-RNA1 **ACACA**AAGACUCUCAAACAUU....UGUGUUUGAGAUCUU**UGUGU**

ECMaV-RNA2 **ACACA**AAGAUCUCUCAACACU....ACGUUGAGAGAUCUG**UGUGU**

BCCoV1-RNA1 **ACACA**AAGACUCCCCAACUUU....AAGUUUGGGGAUCUU**UGUGU**

BCCoV1-RNA2 **ACACA**AAGA-UCCCCCUGUUU....AAGCAAGGGGGUCUU**UGUGU**

CCGaV-RNA1 **ACACA**AAGACUCCCAAACUUU....AUAGUUUGGGAUCUG**UGUGU**

CCGaV-RNA2 **ACACA**AAGA-UCCCAUAACUU....AAGUUAUGGGUUCUA**UGUGU**

CiVA-RNA1 **ACACA**AAGACUCCCAAACUUU....AAAGUUUGGGAUCUG**UGUGU**

CiVA-RNA2 **ACACA**UAGA-UCCCAUAAUUU....AAGUUAUGGGUUCUA**UGUGU**

WCLaV-1-RNA1 **ACACA**AAGACUCCCGUACUUC....UUAAUACGGGAUCUA**UGUGU**

WCLaV-1-RNA2 **ACACA**UAGA-ACCCAUAAACU....AGUUAAUGGGAUCUU**UGUGU**

WCLaV-2-RNA1 **ACACA**AAGACUCUCAAACACU....UGUGUUUGAGAUCUU**UGUGU**

WCLaV-2-RNA2 **ACACA**AAGAUCUCUCAACACA....AGUUGAAGAGAUCUG**UGUGU**

YPNSV-RNA1 CUCAAACACU--....UUUU-UUCAGUAAAC-**GUG**GU

YPNSV-RNA2 CUCAA-CACUUU....AAUAGUUGAGAGAUC**UGUG**-

**Figure 1.** Multiple alignment of 5′ (left) and 3′ (right) termini of the genomic RNAs of ECMaV and those of members of the genus *Coguvirus*. The conserved nucleotides in all members of the family *Phenuiviridae* are shown in bold. The terminal sequences of YPNSV reported in NCBI are likely incomplete.

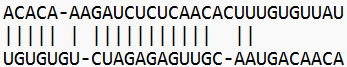
ECMaV-RNA1 **5’**

**Immagine che contiene testo

Descrizione generata automaticamente** ****

**3’**

ECMaV-RNA2 **5’**

**** ****

**3’**

**Figure 2.** Panhandle structures formed by the 5′ and 3′ termini of ECMaV RNA1 and RNA2.

Immagine che contiene tavolo

Descrizione generata automaticamente

**Figure 3.** Conserved motifs in the RdRps typical of members of the order *Bunyavirales*

**A**

**Immagine che contiene testo, tavolo

Descrizione generata automaticamente**

**B**

**Immagine che contiene tavolo

Descrizione generata automaticamente**

**Figure 4.** Amino acid identity (%) matrix of RdRp (panel A) and NP (panel B) proteins of ECMaV and all the current and proposed members of the genus *Coguviru*s.

Immagine che contiene diagramma

Descrizione generata automaticamente

**Figure 5.** Phylogenetic tree of the RNA-directed RNA polymerase (RdRp) of ECMaV, representative members of all the genera of the family *Phenuiviridae*, and tomato chlorotic spot virus (bunyaviral *Tospoviridae*) as the outgroup. Maximum likelihood method adopting the LG + G + F 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.

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