

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

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| **Code assigned:** | **2021.011P** |  |
| **Short title:** Create one new species (*Emaravirus chrysanthemi*) in the genus *Emaravirus* (*Bunyavirales*: *Fimoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ***Fimoviridae* 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 26, 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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| 2021.011P.A.v1.Emaravirus\_1ns.xlsx |

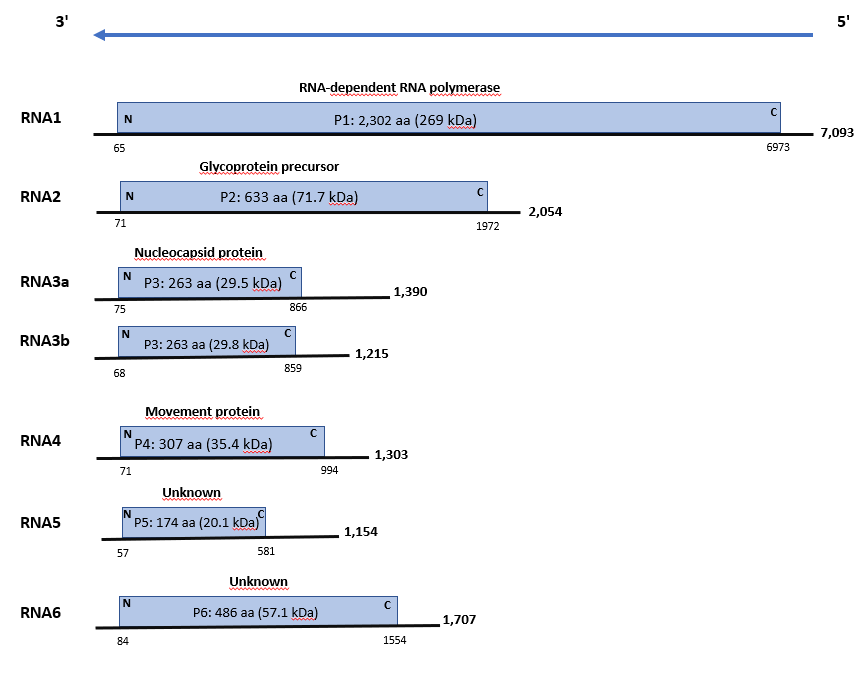
**Abstract**

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| The creation of the new species *Emaravirus chrysantemi* in the genus *Emaravirus*, family *Fimoviridae,* is proposed to accommodate chrysanthemum mosaic-associated emaravirus (ChMaV), identified in Japan on chrysanthemum plants, as its exemplar virus isolate. The new species consists of six segmented, linear, single-stranded (ss), negative sense RNA genomes, fully sequenced, which show features common to homologous RNAs of other known emaravirus species, but from which it differs significantly in nucleotide and amino acid sequences. |

**Text of proposal**

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| |  |  | | --- | --- | | Chrysanthemum mosaic-associated emaravirus (ChMaV) has been recently identified in chrysanthemum (*Chrysanthemum indicum*) of cv. Kin-nishiki in Japan and its genome has been completely sequenced (Kubota et al. 2021). ChMaV possesses all molecular and biological features to be considered as a new member of the genus *Emaravirus*, which currently comprises the following species: *Actinidia chlorotic ringspot-associated emaravirus* (AcCRaV), *Actinidia emaravirus 2* (AcV-2), *Aspen mosaic-associated emaravirus* (AsMaV), *Blackberry leaf mottle associated emaravirus* (BLMaV), *Camellia japonica-associated emaravirus 1* (CjaV-1), *Camellia japonica-associated emaravirus 2* (CjaV-2), *Fig mosaic emaravirus* (FMV)*,* *High Plains wheat mosaic emaravirus* (HPWMV), *Jujube yellow mottle-associated virus* (JYMaV), *Lilac chlorotic ringspot-associated virus* (LiCRaV), *Palo verde broom virus* (PVBV), *Pear chlorotic leaf spot-associated emaravirus* (PCLSaV), *Perilla mosaic emaravirus* (PerMV), *Pigeonpea sterility mosaic emaravirus 1* (PPSMV-1)*,* *Pigeonpea sterility mosaic emaravirus* *2* (PPSMV-2), *Pistacia emaravirus B* (PEB), *Raspberry leaf blotch emaravirus* (RLBV)*,* *Redbud yellow ringspot-associated emaravirus* (RYRSaV), *Rose rosette emaravirus* (RRV), *Ti ringspot-associated emaravirus* (TiRSaV)*,* and *European mountain ash ringspot-associated emaravirus* (EMARaV) (Elbeaino et al. 2018; Mielke and Muehlbach 2007). The RNA-dependent RNA polymerase (RdRP), glycoprotein precursor (GP), nucleocapsid (NC) and p4 (MP) proteins show different levels of sequence identity with ortholog proteins of other emaraviruses.    **Virus properties**   1. Genome: resembles that of members of the genus *Emaravirus.* It is composed of six segments of negative sense ssRNA. RNA-1: 7,093 nucleotides (nt), RNA-2: 2,054 nt, RNA3a and RNA3b 1,390 and 1,215 nt, RNA-4: 1,303 nt, RNA-5: 1,154 nt, RNA-6: 1,707 nt (Fig.1) (in order from RNA-1 to RNA-6, accession numbers in DDBJ/ENA/GenBank are: LC576445–LC576451) (Kubota et al. 2021). Each segment is monocistronic, encoding a single protein translated from the complementary strand (Figure 1). Untranslated regions (UTRs) at the 5’ and 3’ termini of all RNA segments extended from 57 to 84 nt and from 83 to 574 nt, respectively. 2. Virus-encoded proteins: RNA-dependent RNA-polymerase (p1): 269.0 kDa; putative glycoprotein precursor (p2): 71.7 kDa; putative nucleocapsid protein (p3a): 29.5 kDa and (p3b): 29.8 kDa; putative movement protein (p4): 35.4 kDa; p5 (function unknown, but hypothetical suppressor of RNA silencing): 20.1 kDa; p6 (function unknown): 57.1 kDa (Figure 1). 3. Phylogenetic relationships: RdRP, GP, NC and MP proteins of ChMaV consistently segregated with those of PCLSaV and formed a cluster with PerMV, CjaEV1, and CjaEV2 (Figure 2). The aa identity between the ChMaV proteins and those of PCLSaV was 45.0 %, 32.6%, 39.8%, 36.4% and 59.6% for the RdRP, GP, NCa, NCb and MP, respectively, and up to 31.3%, 22.4%, 21.6%, 21.0 and 19.3% with those of all the other emaraviruses. 4. Experimental transmission: No experimental transmission onto other herbaceous or woody plants were carried out. The eriophyid mite *Paraphytoptus kikus* is the putative vector of this virus in nature. 5. Natural host range: Chrysanthemum (*Chrysanthemum indicum*) of cv. Kin-nishiki.   The detected identities fulfilling the demarcation criteria for species in the genus [aa sequence of relevant gene products of RNA1 (RdRP), RNA2 (GP) and RNA3 (NP) differing by more than 25%], and the genome organization typical of emaraviruses clearly indicate that ChMaV represents a new species in the genus *Emaravirus*. Therefore, the creation of the new viral species *Emaravirus chrysantemi* within the genus *Emaravirus*, which contains ChMaV as the exemplar isolate, is proposed. |  | |

**Supporting evidence**



**Figure 1.** Genome organization of chrysanthemum mosaic-associated virus (ChMaV). Colored boxes represent the protein encoding region (ORF) for each RNA, and those with the amino acid sequence similarity to one another have the same color. The length of RNAs, the putative protein product for each ORF, function (if known), and estimated molecular weight are provided. The genomic RNAs are not drawn to scale. The 13- and 11- nucleotide conserved sequences at the 5’ and 3’ terminus on each segment are represented by blue and yellow boxes, respectively.

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**Figure 2.** Phylogenetic tree constructed with amino acid sequences encoded by RNA1 (RdRP), of recognized emaraviruses and corresponding tentative species (indicated by a red square). Alignment was obtained using ClustalW, and analyzed by the Neighbor-Joining method, with 1000 bootstrap replicates. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap is shown next to the branches (when >70%). TSWV (tomato spotted wilt virus), a tospovirus of the family *Tospoviridae*, was used as an outgroup species.

Actinidia chlorotic ringspot-associated virus (AcCRaV), Actinidia virus 2 (AcV-2), aspen mosaic-associated virus (AsMaV), blackberry leaf mottle associated virus (BLMaV), Camellia japonica-associated virus 1 (CjaV-1), Camellia japonica-associated virus 2 (CjaV-2), **chrysanthemum mosaic-associated virus (ChMaV)**, common oak ringspot-associated virus (CORaV), fig mosaic virus (FMV), High Plains wheat mosaic virus (HPWMoV), jujube yellow mottle-associated virus (JYMaV), lilac chlorotic ringspot-associated virus (LiCRaV), maple mottle-associated virus (MaMaV), palo verde broom virus (PVBV), pear chlorotic leaf spot-associated virus (PCLSaV), perilla mosaic virus (PerMV), pigeonpea sterility mosaic virus 1 (PPSMV-1), pigeonpea sterility mosaic virus 2 (PPSMV-2), pistacia virus B (PiVB), raspberry leaf blotch virus (RLBV), redbud yellow ringspot-associated virus (RYRSaV), rose rosette virus (RRV), ti ringspot-associated virus (TiRSaV), and European mountain ash ringspot-associated virus (EMARaV).

**References**

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Mielke N, Muehlbach HP (2007) A novel, multipartite, negative-strand RNA virus is associated with the ringspot disease of European mountain ash (*Sorbus aucuparia* L.). J GenVirol 88:1337–1346. PMID: 17374780. DOI 10.1099/vir.0.82715-0

Kubota K, Yanagisawa H, Chiaki Y, Yamasaki J, Horikawa H, Tsunekawa K, Morita Y, Kadono F (2021) Complete nucleotide sequence of chrysanthemum mosaic-associated virus, a novel emaravirus infecting chrysanthemum. Arch Virol 166:1241–1245. PMID: 33566195. DOI: [10.1007/s00705-021-04979-2](https://doi.org/10.1007/s00705-021-04979-2)