

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

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| **Code assigned:** | **2020.019P** |  |
| **Short title:** Create one new species (*Camellia japonica-associated virus 2*) 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 |

**Submission dates**

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| Date first submitted to SC Chair | July 28, 2020 |
| Date of this revision (if different to above) |  |

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

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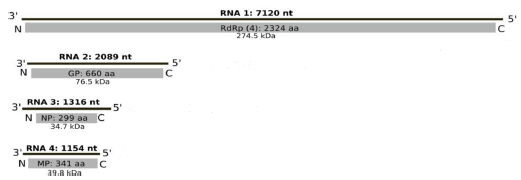
**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.019P.R.Emaravirus\_CjaV-2.xlxs |

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| **Text of proposal**   |  | | --- | | Camellia japonica-associated virus 1 (CjaV-2) 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), *Blackberry leaf mottle associated emaravirus* (BLMaV), *Fig mosaic emaravirus* (FMV)*,* *High Plains wheat mosaic emaravirus* (HPWMV), *Pigeonpea sterility mosaic emaravirus 1* (PPSMV-1)*,* *Pigeonpea sterility mosaic emaravirus* *2* (PPSMV-2), *Pistacia emaravirus B* (PiVB), *Raspberry leaf blotch emaravirus* (RLBV)*,* *Redbud yellow ringspot-associated emaravirus* (RYRSaV), *Rose rosette emaravirus* (RRV)and *European mountain ash ringspot-associated emaravirus* (EMARaV) as the type species of the genus (Elbeaino *et al*., 2018; Mielke and Muehlbach, 2007).  **Virus properties**   1. Virus particles: double membrane-bound bodies (DMBs), approximately 60-70 nm in diameter, located in proximity of the membranes of the endoplasmic reticulum of mesophyll cells. 2. Genome: composed of four segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7120 nt, RNA2: 2089 nt, RNA3: 1316 nt, RNA4: 1154 nt, (Figure 1) (RNA1 to RNA4 GenBank accession numbers are MN385577 to MN385580) (Peracchio *et al*., 2020). Five RNA segments of the same virus were detected form camellia also in China, showing a nucleotide sequence identity with the corresponding RNAs of the Italian isolate ranging from 86% to 91.5% and a slight difference in the length (Zhang et al., 2020). The fifth Chinese RNA (RNA5) is 1333 nt in length, encodes a protein of 25.5 kDa and shows a high nucleotide identity (92.2%) with the Italian RNA7 of CjaV-1. 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 28 to 300 nt and from 69 to 116 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-Polymerase (RdRP, P1): 274.5 kDa; putative glycoprotein precursor (GP, P2): 76.5 kDa; putative nucleocapsid protein (NC, P3): 34.7 kDa; putative movement protein (MP, P4): 39.8 kDa (Figure 1). 4. Phylogenetic relationships: the phylogenetic trees constructed with amino acids (aa) of putative RdRP (Figure 2), GP, NC and MP proteins resulted in similar topologies, with CjaV-2 clustering with CjEV-1 and Perilla mosaic virus (PerMV) in one clade (in the case of RdRP tree; Figure 2), while in other phylogenetic trees, it was clustered in a separate branch with HPWMoV, Palo verde witches broom virus (PVBV), RLBV, ti ringspot-associated emaravirus (TiRSaV) and jujube yellow mottle-associated virus (JYMaV) (Peracchio *et al*., 2020). The aa identity between the CjaV-2 proteins and those of CjaV-1 was 68.0%, 45.5%, 44.1% and 73.5% for RdRP, GP, NC and MP, respectively, and less than 30% with those of all the other emaraviruses (Peracchio *et al*., 2020). 5. Experimental transmission: all attempts to transmit CjaV-2 onto herbaceous hosts by mechanical inoculation were unsuccessful; no natural insect vectors were searched. 6. Natural host range: *Camellia japonica* | |

**Supporting evidence**



**Figure 1.** Genome organization of Camellia japonica-associated virus 2. Proteins (RdRP, P1; GP, P2; NC, P3; MP, P4) encoded in all RNA segments were shown as gray boxes. Length, predicted molecular weight (kDa) and function of each protein are indicated (Peracchio *et al*., 2020).



**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), and the orthologous L segment of members of the genera *Orthotospovirus* and *Orthobunyavirus*. 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%). GenBank accession numbers, names and acronyms of corresponding viruses used in the analysis are reported in the tree. GFLV (grapevine fanleaf virus), a nepovirus of the family *Secoviridae,* was used as an outgroup species.

**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 Gen Virol88:1337-1346. PMID: 17374780, DOI: 10.1099/vir.0.82715-0.

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Zhang S, Yang L, Ma L, Tian X, Li R, Zhou C, Cao M (2020) Virome of *Camellia japonica*: discovery of and molecular characterization of new viruses of different taxa in camellias. Front Microbiol 11:945. PMID: 32499772, DOI: 10.3389/fmicb.2020.00945.