

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

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| **Code assigned:** | **2020.018P** |  |
| **Short title:** Create one new species (*Camellia japonica-associated virus 1*) 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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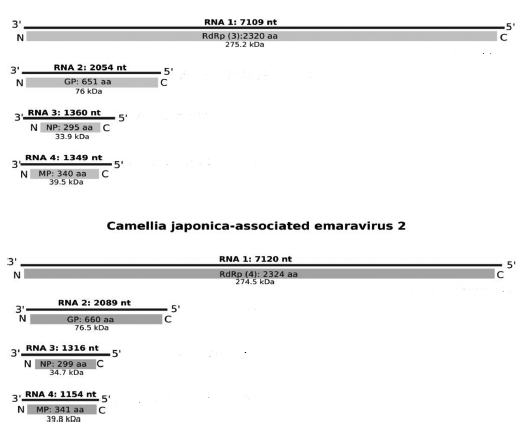
**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.018P.R.Emaravirus\_CjaV-1.xlxs |

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| **Text of proposal**   |  | | --- | | Camellia japonica-associated virus 1 (CjaV-1) 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 nine segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7109 nt, RNA2: 2054 nt, RNA3: 1360 nt, RNA4: 1349 nt, RNA5: 1246 nt, RNA6: 1474 nt, RNA7: 1297 nt, RNA8: 1335 nt; RNA9: 1155 nt (Figure 1) (in order from RNA1 to RNA9, GenBank accession numbers are MN385573 to MN385576, MN557024 to MN557028) (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 Italian isolate, ranging from 91.3% to 96.8% with a slight difference in the length (Zhang *et al*., 2020). Noteworthy mentioning that RNA5 of the Chinese isolate corresponds to RNA8 of the Italian isolate, with 93.6% of identity. 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 29 to 744 nt and from 38 to 175 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 275.2 kDa; putative glycoprotein precursor (GP, P2): 76.0 kDa; putative nucleocapsid protein (NC, P3): 33.9 kDa; putative movement protein (MP, P4): 39.5 kDa; P5 (function unknown): 21.8 kDa; P6 (function unknown): 23.9 kDa; P7 (function unknown): 25.0 kDa; P8 (function unknown): 25.7 kDa; P9 (function unknown): 33.7 kDa (Figure 1). 4. Phylogenetic relationships: the phylogenetic trees constructed using amino acid sequences of putative RdRP (Figure 2), GP, NC and MP proteins resulted in similar topologies, with CjaV-1 clustering into a clade close to CjaV-2, and forming a separate branch with HPWMoV and palo verde witches broom virus (PVBV), RLBV, ti ringspot-associated virus (TiRSaV) and jujube yellow mottle-associated virus (JYMaV). The aa identity between the CjaV-1 proteins and those of CjaV-2 was 68.0%, 45.5%, 44.1% and 73.5% for RdRP, GP, NC and MP, respectively, and less than 25% with those of all the other emaraviruses (Peracchio *et al*., 2020). 5. Experimental transmission: all attempts to transmit CjaV-1 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 1. 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 (Perracchio *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.