

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

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| **Code assigned:** | **2020.021P** |  |
| **Short title:** Create one new species (*Perilla mosaic virus*) in the genus *Emaravirus* (*Bunyavirales*: *Fimoviridae*) | | |
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**Author(s) and email address(es)**

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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 2020 |
| Date of this revision (if different to above) |  |

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

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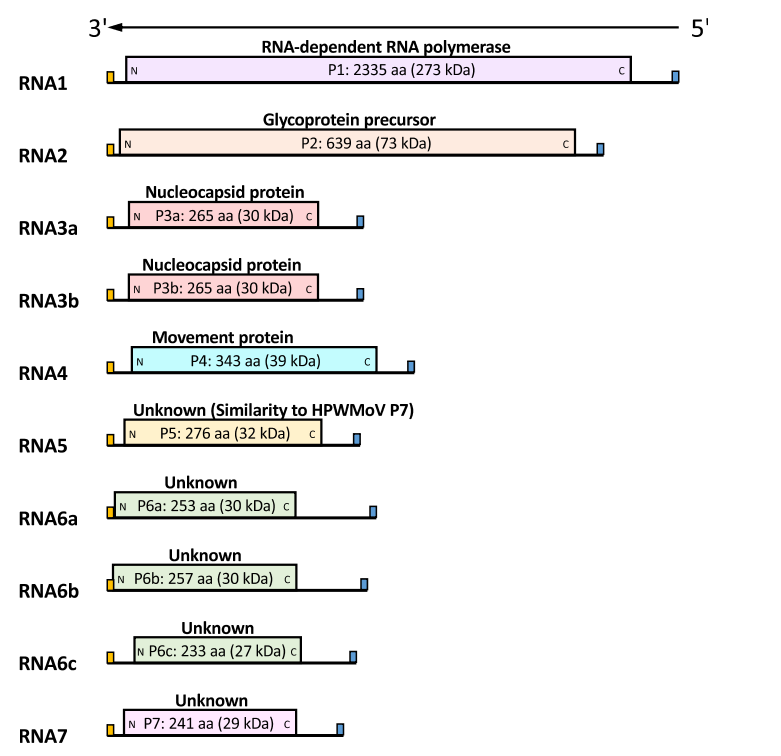
**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.021P.R.Emaravirus\_PerMV.xlxs |

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| **Text of proposal**   |  | | --- | | Perilla mosaic emaravirus (PerMV) 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*, *Blackberry leaf mottle associated emaravirus*, *Fig mosaic emaravirus,* *High Plains wheat mosaic emaravirus*, *Pigeonpea sterility mosaic emaravirus 1*, *Pigeonpea sterility mosaic emaravirus* *2*, *Pistacia emaravirus B*, *Raspberry leaf blotch emaravirus*, *Redbud yellow ringspot-associated emaravirus*, *Rose rosette emaravirus* and *European mountain ash ringspot-associated emaravirus* as the type species of the genus (Elbeaino *et al*., 2018; Mielke and Muehlbach, 2007).  **Virus properties**   1. Virus particles: supposed to be similar to those of emaraviruses, i.e. double-membraned bodies (DMB). 2. Genome: composed of nine segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7291 nt, RNA2: 2092 nt, RNA3a and 3b: 1080 and 1078 nt, RNA4: 1294 nt, RNA5: 1066 nt, RNA6a, b and c: 1128, 1097 and 1050 nt, RNA7: 998 nt, (Figure 1) (in order from RNA-1 to RNA-7, GenBank accession numbers are LC496090-LC496099 (Kubota *et al*., 2020). 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 118 to 333 nt and from 22 to 114 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 272.9 kDa; putative glycoprotein precursor (GP, P2): 73.2 kDa [2.5 kDa (Gs), 20.6 kDa (Gn), and 50.2 kDa (Gc)]; putative nucleocapsid protein (NC, P3): 30.1 and 30.0 kDa; putative movement protein (MP, P4): 39.0 kDa; P5 (function unknown): 31.8 kDa; P6a, b and c (function unknown): 29.7 kDa, 30.2 kDa, and 26.8 kDa, respectively; P7 (function unknown): 28.5 kDa (Figure 1). 4. Phylogenetic analyses, inferred from amino acid sequence alignment of RdRp (Figure 2) showed that PerMV is a distinct and highly divergent member of the genus *Emaravirus*. Phylogenetic analyses of GP, NC and MP proteins resulted in similar tree topologies. Only PerMV P4 clustered together with the subgroup III of emaraviruses containing ti ringspot-associated virus (TiRSaV) (Kubota *et al*., 2019). The amino acid sequence identities of P1 to P3 of PerMV and those of other emaraviruses ranged from 19.9% (P3a) to 33.0% (P1). 5. Experimental transmission: Lamiaceae species (*Perilla frutescens, P. citridora, P. hirtella, P. setoyensis*) inoculated by mites. *Nicotiana benthamiana* can be infected with PerMV by both mite-borne and mechanical inoculation. In nature, PerMV is transmitted by *Shevtchenkella* sp. (Acari: *Eriophyidae*) with a minimum 30 min acquisition access period. 6. Natural host range: shiso (*Perilla frutescens*)*,* Japan | |

**Supporting evidence**



**Figure 1.** Genome organization of Perilla mosaic virus. Open reading frames are shown by rectangles and those with amino acid sequence similarities to one another are colored the same. The 11- and 12-nucleotide conserved sequences at the 5’ and 3’ termini on each segment are represented by blue and yellow boxes, respectively. Function of each protein (P1-P7), if known, encoded in all RNA segments are reported above boxes, whereas their predicted molecular weight (kDa) are indicated inside boxes. Figure not drawn to scale.



**Figure 2.** Phylogenetic tree constructed with amino acid sequences encoded by RNA1 (RdRP), of recognized emaraviruses and corresponding proteins encoded by representatives of proposed new 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**

Elbeaino T, Digiaro M, Mielke-Ehret N, Muehlbach HP, Martelli GP and ICTV Report Consortium (2018) ICTV Virus Taxonomy Profile: *Fimoviridae*. J Gen Virol 99:1478-1479. PMID: 30204080 DOI: 10.1099/jgv.0.001143

Kubota K, Usugi T, Tomitaka Y, Shimomoto Y, Takeuchi S, Kadono F, Yanagisawa H, Chiaki Y, Tsuda S (2020) Perilla mosaic virus is a highly divergent emaravirus transmitted by *Shevtchenkella* sp. (Acari: Eriophyidae). Phytopathology 110:1352-1361. PMID: 32202482 DOI: 10.1094/PHYTO-01-20-0013-R.

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.