

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

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| **Code assigned:** | **2020.015P** |  |
| **Short title:** Create one new species (*Palo verde broom 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 27, 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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| 2020.015P.R.Emaravirus\_PVBV.xlxs |

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| **Text of proposal**   |  | | --- | | Palo verde broom virus (PVBV) 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: supposed to be similar to those of emaraviruses, i.e. double-membraned bodies (DMB). 2. Genome: composed of four segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7022 nt, RNA2: 2104 nt, RNA3: 1369 nt, RNA4: 1478 nt (in order from RNA1 to RNA4, GenBank accession numbers are MF766025, MF766030, MF766035, MF766040) (Ilyas *et al*., 2018). Each segment is monocistronic, encoding a single protein translated from the complementary strand. Untranslated regions (UTRs) at the 5′ and 3′ termini of all RNA segments extended from 111 to 400 nt and from 55 to 90 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 268.3 kDa; putative glycoprotein precursor (GP, P2): 74.3 kDa; putative nucleocapsid protein (NC, P3): 33.4 kDa; putative movement protein (MP, P4): 41.9 kDa. 4. Phylogenetic relationships: the phylogenetic trees constructed using amino acid sequences of putative RdRP, GP, NC and MP proteins resulted in similar topologies, with PVBV clustering into a clade close to HPWMV, ti ringspot-associated virus (TiRSaV), RLBV and jujube yellow mottle-associated virus (JYMaV) (Figure 1); and shared similarity scores ranging from 60 to 65% with the analogous RNAs 1 to 4 of HPWMV (Ilyas *et al*., 2018). 5. Transmission in nature: the natural transmission through the eriophyid mite *Aculus cercidi* is suspected. 6. Natural host range: blue palo verde tree (*Parkinsonia florida*) in Arizona (USA). | |

**Supporting evidence**



**Figure 1.** 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**

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

[Ilyas](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-01-18-0124-PDN) M,  [Avelar](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-01-18-0124-PDN) S,  [Schuch](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-01-18-0124-PDN) U K,  [Brown](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-01-18-0124-PDN) J K (2018) First report of an emaravirus associated with witches' broom disease and eriophyid mite infestations of the blue palo verde tree in Arizona. Plant Dis 102:1863. PMID: 30125163, DOI: 10.1094/PDIS-01-18-0124-PDN.

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.