

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

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| **Code assigned:** | **2020.016P** |  |
| **Short title:** Create one new species (*Pear chlorotic leaf spot-associated virus*) in the genus *Emaravirus* (*Bunyavirales*: *Fimoviridae*) | | |
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**Author(s) and email address(es)**

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| Liu H, Wang G, Yang Z, Wang Y, Zhang Z, Li L, Waqas M, Zhang J, Xu L, Qi L, Hong J, Hong N | whni@mail.hzau.edu.cn |

**Corresponding author**

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| --- |
| Ni Hong (whni@mail.hzau.edu.cn) |

**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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| 2020.016P.R.Emaravirus\_PCLSaV.xlxs |

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| **Text of proposal**   |  | | --- | | Pear chlorotic leaf spot-associated virus (PCLSaV) 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 80-100 nm in diameter, in the cytoplasm of mesophyll cells, near endoplasmic reticulum (ER) membranes. 2. Genome: composed of five segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7100 nt, RNA2: 2045 nt, RNA3: 1296 nt, RNA4: 1543 nt, RNA5: 1253 nt (in order from RNA1 to RNA5, GenBank accession numbers are MK602177 to MK602181) (Liu *et al*., 2020). 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 86 to 464 nt and from 69 to 116 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 268 kDa; putative glycoprotein precursor (GP, P2): 69.3 kDa [Gn (22 kDa) and Gc (47 kDa)]; putative nucleocapsid protein (NC, P3): 30 kDa; putative movement protein (MP, P4): 37 kDa; P5 (function unknown): 29 kDa (Liu et al., 2020). 4. Phylogenetic relationships: the phylogenetic trees constructed using amino acid sequences of putative RdRp, GP, NC and MP proteins resulted in similar topologies, with pear chlorotic leaf spot-associated virus (PCLSaV) clustering close to clade enclosing Perilla mosaic virus (PerMV), Camellia japonica-associated virus 1 (CjaV-1) and CjaV-2 (Figure 1). 5. Experimental transmission: no natural insect vectors were searched. 6. Natural host range: pear plants *(P. pyrifolia)* in China. | |

**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.

Liu H, Wang G, Yang Z, Wang Y, Zhang Z, Li L, Waqas M, Zhang J, Xu L, Qi L, Hong J, Hong N (2020) Identification and characterization of pear chlorotic leaf spot-associated virus, a novel emaravirus associated with a severe disease of pear trees in China. Plant Dis, DOI 10.1094/PDIS-01-20-0040-RE.

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.