

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

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| **Code assigned:** | **2020.012P** |  |
| **Short title:** Create one new species (*Actinidia virus 2*) 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 28, 2020 |
| Date of this revision (if different to above) |  |

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

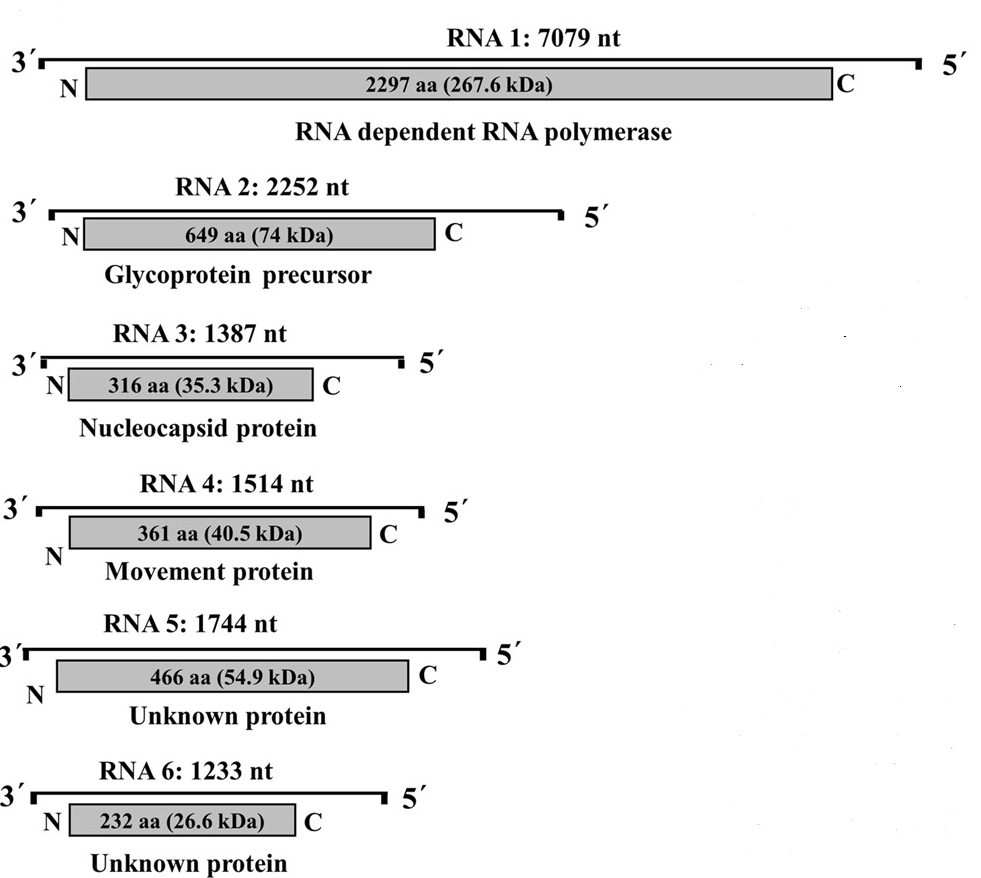
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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.012P.R.Emaravirus\_AcV-2.xlxs |

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| **Text of proposal**   |  | | --- | | Actinidia emaravirus 2 (AcV-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: supposed to be similar to those of emaraviruses, *i.e.* double-membraned bodies (DMB). 2. Genome: composed of at least of six segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus*. RNA1: 7079 nt, RNA2: 2252 nt, RNA3: 1387 nt, RNA4: 1514 nt, RNA5: 1744 nt, RNA6: 1233 nt, (Wang *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 142 to 466 nt and from 36 to 101 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 267 kDa; putative glycoprotein precursor (GP, P2): 74 kDa; putative nucleocapsid protein (NC, P3): 35.2 kDa; putative movement protein (MP, P4): 40.5 kDa; P5 (function unknown): 54.6 kDa; P6 (function unknown): 26.5 kDa (Figure 1). 4. Proteins encoded by RNAs1-4 of AcV-2 shared the highest amino acid (aa) sequence identities of 62.2%–77.3% with the corresponding proteins of FMV and PPSMV-2. P5 and P6 encoded by AcV-2 exhibited the highest identities of 44.2% and 39.2% with the corresponding proteins of PPSMV-2 (Wang *et al*., 2020). 5. Phylogenetic relationships: the phylogenetic trees constructed using amino acid sequences of putative RdRP and NC (P3) of all reported emaraviruses allocated AcV-2 close to FMV and PPSMV-2 (Figure 2). 6. Experimental transmission: no attempts to transmit the virus onto herbaceous hosts by mechanical inoculation were carried out. Transmission by eriophyid mites is suspected. 7. Natural host range: kiwifruit (*Actinidia eriantha, A. chinensis. A. delicious*) in China. | |

**Supporting evidence**

**Figure 1.** Genome organization of Actinidia emaravirus 2. The black boxes at the ends of each RNA line indicated the 13-nt stretches, conserved in all 5′ and 3′ termini of all emaraviral RNA segments. Proteins (P1–P6) encoded in all RNA segments were shown as dark gray boxes. Length, predicted molecular weight (kDa) and function of each protein are indicated.



**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**

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).

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 Virol 88:1337-1346. PMID: 17374780, DOI: 10.1099/vir.0.82715-0.

Wang Y, Zhai L, Wen S, Yang Z, Wang G, Hong N (2020) Molecular characterization of a novel emaravirus infecting *Actinidia* spp. in China. Virus Res 275:197736. PMID: 31626876, DOI: 10.1016/j.virusres.2019.197736.