

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

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| **Code assigned:** | **2020.017P** |  |
| **Short title:** Create one new species (*Ti ringspot-associated 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 28, 2020 |
| Date of this revision (if different to above) |  |

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

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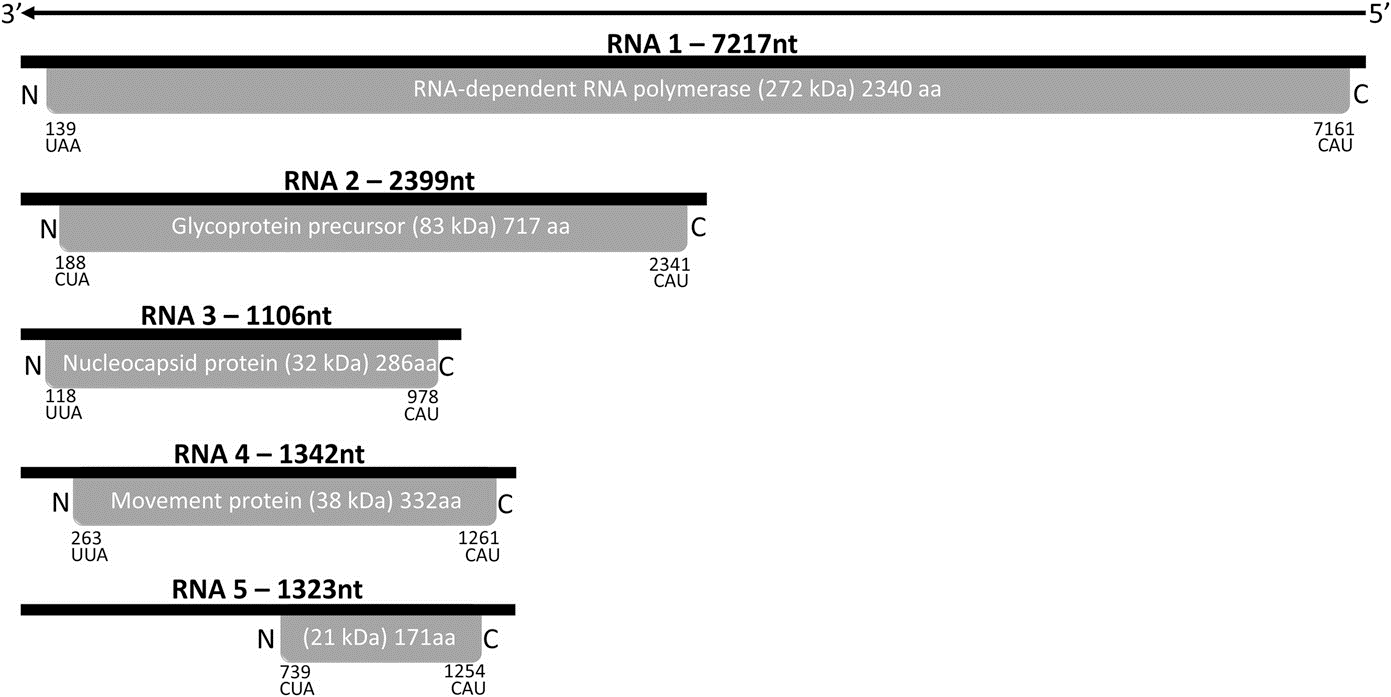
**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.017P.R.Emaravirus\_TiRSaV.xlxs |

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| **Text of proposal**   |  | | --- | | Ti ringspot-associated Emaravirus (TiRaV) 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 85 nm in diameter, in the cytoplasm or in cytoplasmic vesicles. 2. Genome: composed of nine segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7217 nt, RNA2: 2399 nt, RNA3: 1220 nt, RNA4: 1144 nt, RNA5: 1129 nt, (Figure 1) (in order from RNA1 to RNA5, GenBank accession numbers are MH223635 to MH223639) (Olmedo-Velarde *et al*., 2019). 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 117 to 738 nt and from 56 to 128 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-Polymerase (RdRP, P1): 272 kDa; putative glycoprotein precursor (GP, P2): 83 kDa; putative nucleocapsid protein (GP, P3): 32 kDa; putative movement protein (MP, P4): 37 kDa; p5 (function unknown): 21 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 TiRaV clustering into a clade composed of RLBV, HPWMoV, Palo verde witches broom virus (PVBV), and jujube yellow mottle-associated virus (JYMaV). The aa identity between the TiRaV proteins and those of RLBV was 45%, 38%, 39% and 48% for RdRP, GP, NC and MP, respectively (Olmedo-Velarde *et al*., 2019). Four of the TiRaV proteins (P1, P2, P3 and P5) showed the highest homology with their homologue of RLBV, whereas P4 showed the highest homology to that of HPWMoV (51%) (Olmedo-Velarde *et al*., 2019). 5. Transmission: TiRSaV is mechanically transmissible to *Nicotiana benthamiana, Nicotiana tabacum* and some cucurbit species. Two different and unidentified eriophyid mites were found associated with diseased plants in nature. 6. Natural host range: ti (*Cordyline fruticosa* L.)in islands of Oahu, Maui, and Hawaii. | |

**Supporting evidence**



**Figure 1**. Genome organization of ti ringspot-associated virus. Shaded boxes represent the predicted open reading frame (ORF) for each RNA. The putative protein product for each ORF, start and stop codons, function (when known), and estimated molecular weight are provided. The genomic RNAs are not drawn to scale.



**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.

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.

Olmedo-Velarde A, Park AC, Sugano J, Uchida JY, Kawate M, Borth WB, Hu JS, Melzer MJ (2019) Characterization of ti ringspot-associated virus, a novel emaravirus associated with an emerging ringspot disease of *Cordyline fruticosa* (L.). Plant Dis 103:2345-2352. PMID: 31306086, DOI: 10.1094/PDIS-09-18-1513-RE.