

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

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| **Code assigned:** | **2020.020P** |  |
| **Short title:** Create one new species (*Jujube yellow mottle-associated virus*) in the genus *Emaravirus* (Bunyavirales: *Fimoviridae*) | | |
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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 14, 2020 |
| Date of this revision (if different to above) |  |

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

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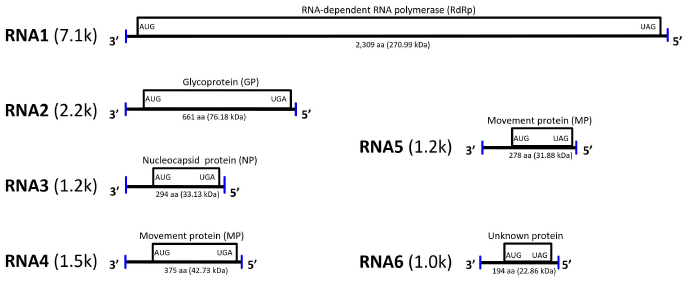
**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.020P.R.Emaravirus\_JYMaV.xlxs |

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| **Text of proposal**   |  | | --- | | Jujube yellow mottle-associated virus (JYMaV) has been recently identified in jujube trees (*Ziziphus jujube* Mill.) and its genome has been completely sequenced (Yang *et al*., 2019). JYMaV 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*, P*istacia 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). The RNA-dependent RNA polymerase (RdRP), glycoprotein precursor (GP), nucleocapsid (NC) and P4 (MP) proteins of JYMaV show different levels of sequence identity with ortholog proteins of other emaraviruses (Table 1).  **Virus properties**   1. Virus particles: double membrane-bound bodies (DMBs), approximately 100 nm in diameter, located in proximity of the membranes of the endoplasmic reticulum of mesophyll cells. 2. Genome: composed of six segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus.* RNA1: 7143 nt, RNA2: 2233 nt, RNA3: 1259 nt, RNA4: 1547 nt, RNA5: 1267 nt, RNA6: 980 nt (Figure 1) (in order from RNA1 to RNA6, GenBank accession numbers are MK305894 to MK305899) (Yang *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 112 to 321 nt and from 57 to 101 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 271.0 kDa; putative glycoprotein precursor (GP, P2): 76.2 kDa (Gn 22.3 kDa, Gs 3.0 kDa and Gc 50.9 kDa); putative nucleocapsid protein (NC, P3): 33.1 kDa; putative movement protein (MP, P4): 42.7 kDa; P5 (function unknown, but hypothetical additional movement protein): 31.9 kDa; P6 (function unknown): 22.9 kDa (Figure 1). 4. Phylogenetic relationships: in the phylogenetic trees constructed with amino acids (aa) of putative RdRP (Figure 2) jujube yellow mottle-associated virus (JYMaV) clustered into the same clade with RLBV, ti ringspot-associated virus (TiRSaV), Palo verde witches broom virus (PVBV) and HPWMoV. Phylogenetic analyses of GP, NC and MP proteins resulted in similar tree topologies. The aa identity between the JYMaV proteins and those of RLBV was 70.4%, 52.1%, 65.1% and 63.3% for the RdRP, GP, NC and MP, respectively, and 31.9-42.6%, 21.5-33.3%, 16.6-65%, and 9.2-44% with those of all the other emaraviruses (Table 1). 5. Experimental transmission: No experimental transmission onto other herbaceous or woody plants were carried out. No natural insect vectors were searched. 6. Natural host range: Jujube (*Ziziphus jujube* Mill.). | |

**Supporting evidence**

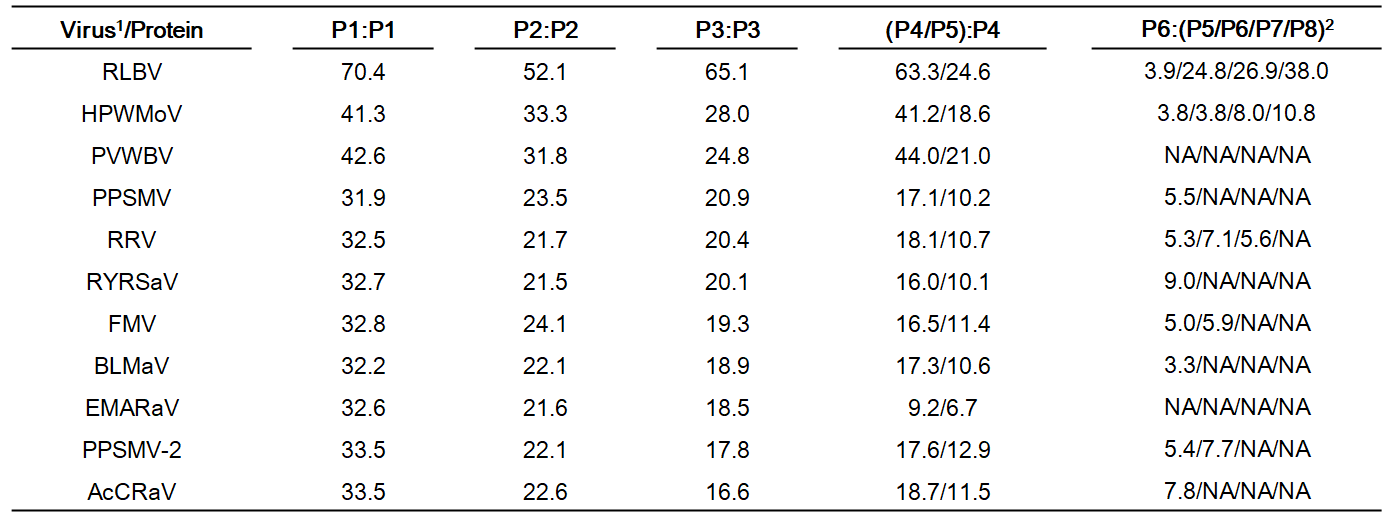


**Figure 1.** Genome organization of jujube yellow mottle-associated virus. Vertical blue lines at the ends of each RNA indicated the 13-nt stretches, conserved in all 5′ and 3′ RNA termini of emaraviruses segments. Proteins (P1-P6) encoded in all RNA segments are shown as boxes. Length, predicted molecular 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 representatives of possible 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.

**Table 1.** Pairwise percentage identity between amino acid sequences of putative proteins encoded by jujube yellow mottle-associated virus (JYMaV) genome (P1: RNA-dependent RNA Polymerase; P2: glycoprotein precursor; P3: nucleocapsid protein; P4: movement protein; P5: movement protein; P6: unknown function) and the homologous proteins encoded by recognized emaraviruses (Yang *et al*., 2020).



1AcCRaV, Actinidia chlorotic ringspot-associated virus; BLMaV, blackberry leaf mottle-associated virus, EMARaV, European mountain ash ringspot-associated virus; FMV: fig mosaic virus; HPWMoV, High Plains wheat mosaic virus; PiVB: Pistacia emaravirus B; PPSMV-1, pigeonpea sterility mosaic virus 1; PPSMV-2, pigeonpea sterility mosaic virus 2; RLBV, raspberry leaf blotch virus; RRV, rose rosette virus; RYRSaV, redbud yellow ringspot-associated virus. 2NA, not available.

**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

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.

Yang C, Zhang S, Han T, Fu J, Di Serio F, Cao M (2019) Identification and characterization of a novel emaravirus associated with jujube (*Ziziphus jujuba* Mill.) Yellow Mottle Disease. Front Microbiolo 10:1417. PMID: 31293549 DOI: 10.3389/fmicb.2019.01417.