

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

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| **Code assigned:** | **2020.014P** |  |
| **Short title:** Create one new species (*Lilac chlorotic 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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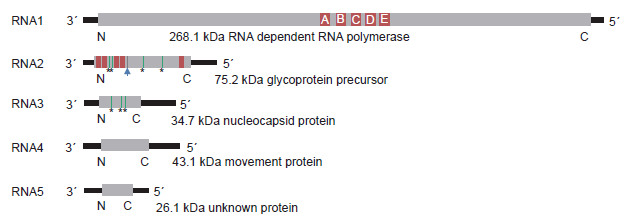
**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.014P.R.Emaravirus\_LiCRaV.xlxs |

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| **Text of proposal**   |  | | --- | | Lilac chlorotic ringspot-associated virus (LiCRaV) 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 five segments of negative sense ssRNA, resembling those of members of the genus *Emaravirus*. RNA1: 7047 nt, RNA2: 2268 nt, RNA3: 1557 nt, RNA4: 1651 nt, RNA5: 1269 nt, (Figure 1) (in order from RNA1 to RNA5, GenBank accession numbers are MT112174-MT112178) (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 41 to 95 nt and from 96 to 539 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 268.1 kDa; putative glycoprotein precursor (GP, P2): 75.2 kDa (Gn: 22.7 kDa and Gc: 52.4 kDa); putative nucleocapsid protein (NC, P3): 34.7 kDa; putative movement protein (MP, P4): 43.1 kDa; P5 (function unknown): 26.1 kDa (Figure 1). 4. Phylogenetic relationships: the phylogenetic trees constructed using amino acid sequences of putative RdRP, GP, NC and MP proteins resulted in similar topologies, with LiCRaV clustering into a clade close to RYRSaV, AcCRaV and EMARaV (Figure 2). The aa identity between the lilac chlorotic ringspot-associated virus (LiCRaV) proteins and those of RYRSaV was 64.9%, 47.8%, 63.6% and 54.6% for RdRP, GP, NC and MP, respectively (Wang *et al*., 2020). 5. Experimental transmission: LiCRaV is mechanically transmitted onto *Nicotiana benthamiana* plants. 6. Natural host range: lilac (*Syringa vulgaris* L) at Yan’an, Shaanxi, China. | |

**Supporting evidence**



**Figure 1.** Genome organization of Lilac chlorotic ringspot-associated virus (LiCRaV). Predicted expression products of each RNA are represented as gray boxes. RNA1, *Bunyaviridae* replicases motifs A-E are indicated in red boxes: RNA2, asterisks and arrows indicate four putative glycosylation sites and predicted protease cleavage sites, respectively. Red boxes represent five putative transmembrane helices; RNA3, asterisks indicate three conserved nucleocapsid motifs (Wang *et al*., 2020).



**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 Virol88:1337-1346. PMID: 17374780, DOI: 10.1099/vir.0.82715-0.

Wang YQ, Yu S, Cao MJ, Cheng Q, Wu JX, Hu, T (2020) Identification of a novel emaravirus infecting lilac through next-generation sequencing. J Integ Agric 19:2064-2071. DOI: 10.1016/S2095-3119(19)62806-6