

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

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| **Code assigned:** | **2021.012P** |  |
| **Short title:** Create one new species (*Emaravirus quercus*) 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** |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | May 26, 2021 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2021.012P.A.v1.Emaravirus\_1ns.xlsx |

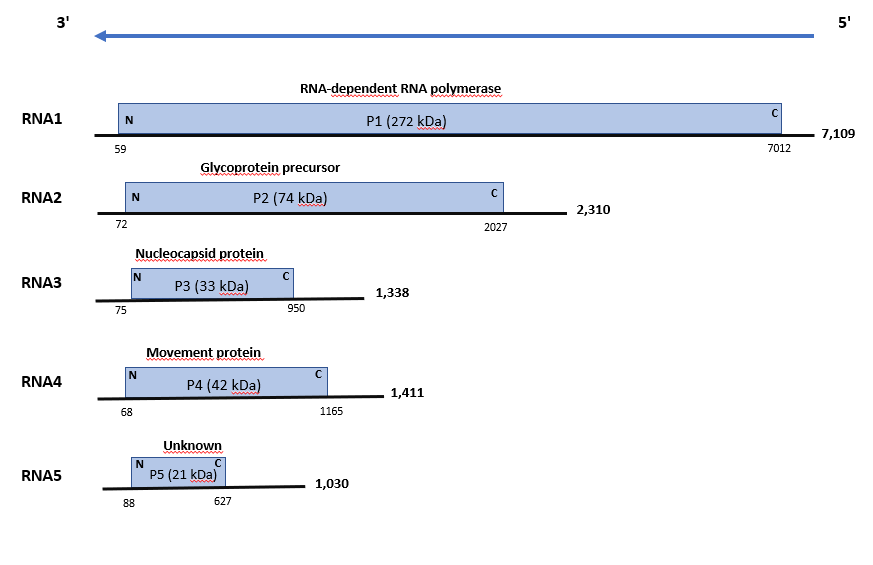
**Abstract**

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| The creation of the new species *Emaravirus quercus* in the genus *Emaravirus*, family *Fimoviridae*, is proposed to accommodate common oak ringspot-associated emaravirus (CORaV), identified in Germany and in Scandinavia on oak trees as its exemplar virus isolate. The new species consists of five segmented, linear, single-stranded, negative sense RNA genomes, fully sequenced, which show features common to homologous RNAs of other known *Emaravirus* species, but from which it differs significantly in nucleotide and amino acid sequences. |

**Text of proposal**

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| |  | | --- | | Common oak ringspot-associated emaravirus (CORaV) has been recently identified in oak (*Quercus robur* L*.*) in Germany and in Scandinavia and its genome has been completely sequenced (Rehanek et al. 2021). CORaV 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), *Actinidia emaravirus 2* (AcV-2), *Aspen mosaic-associated emaravirus* (AsMaV), *Blackberry leaf mottle associated emaravirus* (BLMaV), *Camellia japonica-associated emaravirus 1* (CjaV-1), *Camellia japonica-associated emaravirus 2* (CjaV-2), *Fig mosaic emaravirus* (FMV)*,* *High Plains wheat mosaic emaravirus* (HPWMoV), *Jujube yellow mottle-associated virus* (JYMaV), *Lilac chlorotic ringspot-associated virus* (LiCRaV), *Palo verde broom virus* (PVBV), *Pear chlorotic leaf spot-associated emaravirus* (PCLSaV), *Perilla mosaic emaravirus* (PerMV), *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), *Ti ringspot-associated emaravirus* (TiRSaV)*,* and *European mountain ash ringspot-associated emaravirus* (EMARaV) (Elbeaino et al. 2018; Mielke and Muehlbach 2007). The RNA-dependent RNA polymerase (RdRP), glycoprotein precursor (GP), nucleocapsid (NC) and p4 (MP) proteins show different levels of sequence identity with ortholog proteins of other emaraviruses.    **Virus properties**   1. Genome: resembles that of members of the genus *Emaravirus.* It is composed of six segments of negative sense ssRNA. RNA1: 7,109 nucleotides (nt); RNA2: 2,310 nt; RNA3: 1,338 nt; RNA4: 1,411 nt, RNA5: 1,030 nt) (Fig.1) (in order from RNA-1 to RNA-5, accession numbers in GenBank are: LR828198–LR828202) (Rehanek et al. 2021). 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 58 to 87 nt and from 97 to 403 nt, respectively. 2. Virus-encoded proteins: RNA-dependent RNA-polymerase (p1): 2317 amino acids (aa), 271.7 kDa; putative glycoprotein precursor (p2): 651 aa, 74.2 kDa; putative nucleocapsid protein (p3a): 291 aa, 32.9 kDa; putative movement protein (p4): 365 aa, 41.7kDa; putative silencing suppressor p5 (function unknown): 179 aa, 21.1 kDa (Figure 1). 3. Phylogenetic relationships: RdRP, GP, NC and MP proteins of CORaV consistently segregated with those of TiRSaV, HPWMoV, RLBV, JYMaV, and PVBV, regardless of the protein considered (Figure 2). Deduced aa sequences of CORaV identified in oak showed 21-38% (RNA 3), 18-58% (RNA 4), and 18-41% (RNA 5) sequence identity to the corresponding protein sequences encoded by High Plains wheat mosaic virus (HPWMoV), raspberry leaf blotch virus (RLBV), ti ringspot-associated virus (TiRSaV), jujube yellow mottle-associated virus (JYMaV), and palo verde broom virus (PVBV). 4. Experimental transmission: Symptoms of chlorotic lesions, ringspots and chlorotic mottle were transmitted on young oak seedlings after grafting. The causing agent was not transmissible by mechanical inoculation of plant sap to indicator plants. 5. Natural host range: oak *(Quercus robur* L*.*).   The detected identities fulfilling the demarcation criteria for species in the genus [aa sequence of relevant gene products of RNA1 (RdRP), RNA2 (GP) and RNA3 (NP) differing by more than 25%], and the genome organization typical of emaraviruses clearly indicate that CORaV represents a new species in the genus *Emaravirus*. Therefore, the creation of the new viral species *Emaravirus quercus* within the genus *Emaravirus*, which contains CORaV as the exemplar isolate, is proposed. | |

**Supporting evidence**



**Figure 1.** Genome organization of common oak ringspot-associated emaravirus. Boxes represent the protein encoding region (ORF) for each RNA. The length of RNAs, the putative protein product for each ORF, function (if known), and estimated molecular weight are provided. The genomic RNAs are not drawn to scale.

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**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). 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%). TSWV (tomato spotted wilt virus), a tospovirus of the family *Tospoviridae*, was used as an outgroup species.

Actinidia chlorotic ringspot-associated virus (AcCRaV), Actinidia virus 2 (AcV-2), aspen mosaic-associated virus (AsMaV), blackberry leaf mottle associated virus (BLMaV), Camellia japonica-associated virus 1 (CjaV-1), Camellia japonica-associated virus 2 (CjaV-2), chrysanthemum mosaic-associated virus (ChMaV), **common oak ringspot-associated virus (CORaV)**, fig mosaic virus (FMV), High Plains wheat mosaic virus (HPWMoV), jujube yellow mottle-associated virus (JYMaV), lilac chlorotic ringspot-associated virus (LiCRaV), maple mottle-associated virus (MaMaV), palo verde broom virus (PVBV), pear chlorotic leaf spot-associated virus (PCLSaV), perilla mosaic virus (PerMV), pigeonpea sterility mosaic virus 1 (PPSMV-1), pigeonpea sterility mosaic virus 2 (PPSMV-2), pistacia virus B (PiVB), raspberry leaf blotch virus (RLBV), redbud yellow ringspot-associated virus (RYRSaV), rose rosette virus (RRV), ti ringspot-associated virus (TiRSaV), and European mountain ash ringspot-associated virus (EMARaV).

**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(11):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

Rehanek M, von Bargen S, Bandte M, Karlin DG, Büttner C (2021) A novel emaravirus comprising five RNA segments is associated with ringspot disease in oak. Arch Virol 166:987–990, PMID: 33462672. DOI: 10.1007/s00705-021-04955-w