

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

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| **Code assigned:** | **2020.013P** |  |
| **Short title:** Create one new species (*Aspen mosaic-associated virus*) in the genus *Emaravirus* (*Bunyavirales*: *Fimoviridae*) | | |
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**Author(s) and email address(es)**

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| von Bargen S, Al Kubrusli R, Gaskin T, Fürl S, Hüttner F, Blystad D, Karlin DG, Jalkanen R, Büttner C | susanne.von.bargen@agrar.hu-berlin.de |

**Corresponding author**

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| Susanne von Bargen (susanne.von.bargen@agrar.hu-berlin.de) |

**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**

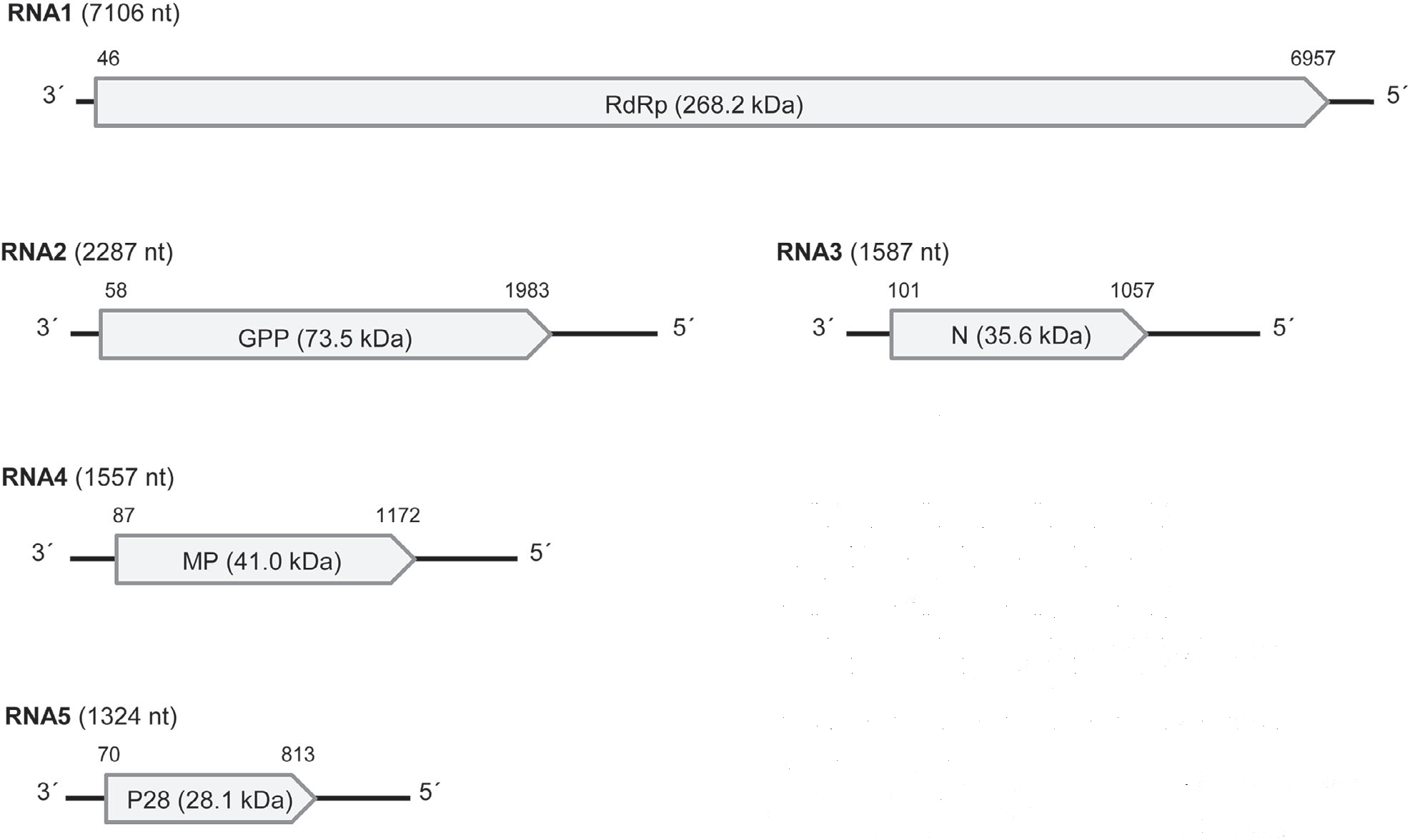
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**Part 3:** **TAXONOMIC PROPOSAL**

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| 2020.013P.R.Emaravirus\_AsMaV.xlxs |

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| **Text of proposal**   |  | | --- | | Aspen mosaic-associated virus (AsMaV) ) 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: 7106 nt, RNA2: 2287 nt, RNA3: 1587 nt, RNA4: 1557 nt, RNA5: 1324 nt (Fig.1) (in order from RNA1 to RNA5, GenBank accession numbers are  LR742461 to LR742465) (Von Bargen *et al*., 2020). Each segment is monocistronic, encoding a single protein translated from the complementary strand (Fig. 1). Untranslated regions (UTRs) at the 5′ and 3′ termini of all RNA segments extended from 45 to 100 nt and from 149 to 530 nt, respectively. 3. Virus-encoded proteins: RNA-dependent RNA-polymerase (RdRP, P1): 268.2 kDa; putative glycoprotein precursor (GP, P2): 73.5 kDa; putative nucleocapsid protein (NC, P3): 35.6 kDa; putative movement protein (MP, P4): 41.0 kDa; P5 (function unknown): 28.1 kDa (Figure 1). 4. Phylogenetic relationships: the phylogenetic trees constructed with amino acids (aa) of RdRp, GP, NC and MP proteins resulted in similar topologies, with AsMaV clustering into a clade close to PiVB, PPSMV-2, FMV, RRV and BLMaV (Figure 2). The aa identity between the AsMaV proteins and those of PiVB is 76.3%, 58.3%, 56.1% and 67.3% for RdRP, GP, NC and MP, respectively (Von Bargen *et al*., 2020). 5. Experimental transmission: AsMaV was experimentally transmitted by grafting onto Eurasian aspen seedlings and rootstocks. Galls induced by different mite species (*Phyllocoptes populi* and *Eriophyes diversipunctatus*) were regularly found in AsMaV-affected Eurasian aspen trees in Fennoscandia. Specific transmission experiments need to be established. 6. Natural host range: Eurasian aspen (*Populus tremula*) in Norway, Finland and Sweden (Fennoscandia). | |

**Supporting evidence**



**Figure 1.** Schematic genome organization of aspen mosaic-associated virus (AsMaV) identified in *Populus tremula*. Genome segments of the ss(-)RNA virus are displayed as mRNA with the encoded open reading frames (ORFs) as arrows indicating the first and last nucleotide above the arrow. The locations of the replicase (RdRP) on RNA1, the glycoprotein precursor (GP) on RNA2, the nucleocapsid protein (NC) on RNA3, the movement protein (MP) on RNA4 and the protein of unknown function (P28) encoded by RNA5, are shown and are given with the deduced molecular weight.



**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.

Von Bargen S, Al Kubrusli R, Gaskin T, Fürl S, Hüttner F, Blystad D-R, Karlin DG, Jalkanen R, Büttner C (2020) Characterisation of a novel emaravirus identified in mosaic-diseased Eurasian aspen (*Populus tremula*). Ann Appl Biol 176:210-222. DOI:10.1111/aab.12576.