

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

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| **Code assigned:** | **2020.035P** |  |
| **Short title:** Create one new species in the genus *Alphacarmovirus* (*Tolivirales*: *Tombusviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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**List the ICTV Study Group(s) that have seen this proposal**

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| *Tombusviridae* Study Group |

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

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| Minor editing changes; no negative responses were received |

**Submission dates**

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| Date first submitted to SC Chair | August 26,2020 |
| 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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| 2020.035P.R.Alphacarmovirus\_1nsp.xlsx |

**Abstract**

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| A new virus infecting *Adonis ramosa* (*Ranunculaceae*) was found in Saitama Prefecture, Japan, and the virus was identified by the authors as a carmovirus. AdMV causes mosaic and yellowing in *Adonis ramosa*, and it was purified via mechanical inoculation to *Chenopodium quinoa* followed by single lesion amplification in this host. Analyses (below) indicates *Adonis mosaic virus* fits the criteria as a new species in genus *Alphacarmovirus*. |

**Text of proposal**

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| |  | | --- | | The GenBank sequence LC171345 [7] appears to contain the complete genome of this virus. The genome organizations of alphacarmoviruses, betacarmoviruses, gammacarmoviruses, and pelarspoviruses are similar, and all express their replicases via stop-codon readthrough, but only pelarspoviruses express all downstream genes from a sgRNA, which is facilitated by using a noncanonical start codon for movement protein 2. AdMV has an AUG start codon for all ORFs, and its CP has a MW of 38 kDa. Below are the current genus demarcation criteria in the family *Tombusviridae*, and species demarcation criteria within genus *Alphacarmovirus* [5]. Note that recombination between tombusvirids has produced species such that the RdRp and CP genes do not produce similarly branched trees (Figs.1 & 2). The only anomalous data for AdMV is the reported size of virions of 28 nm [7], but the scale bar on the figure suggests that they are closer to the reported range of other species with large CPs that form protruding domains (32-35 nm) [4].  Genus demarcation criteria in the family *Tombusviridae* [5]  • Structural criteria: spherical virions with either a smooth or granular appearance.  • Genomic criteria: genome organization, number of genome segments, size of genome,  number of subgenomic RNAs.  • Polymerase criteria: gene interrupted by a termination codon or a -1 ribosomal  frameshifting element that is periodically read through; differential branching of  phylogenetic trees based on complete RdRp.  Species demarcation criteria within genus *Alphacarmovirus* [5]  1) Less than 75% aa sequence identity in the polymerase and  2) Less than 75% aa sequence identity in the coat protein. | |  | |

**Supporting evidence**

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| Table 1. Percent identities of alphacarmovirus RdRps and CPs | | | | | | | | | |
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|  |  | **Coat Proteins** | | | | | | | |
|  |  | **AdMV** | CarMV | PFBV | HoRV | NLVCV | CbMV | SgCV | AnFBV |
| **RdRps** | **AdMV** | **100** | 56.1 | 39.9 | 39.5 | 37.4 | 33.8 | 39.5 | 32.7 |
| CarMV | 66.5 | **100** | 37.6 | 38.9 | 36.3 | 33.1 | 41.4 | 35.3 |
| PFBV | 59.2 | 58.0 | **100** | 55.2 | 39.1 | 40.1 | 44.3 | 37.1 |
| HoRV | 58.5 | 57.9 | 66.1 | **100** | 35.9 | 37.1 | 43.2 | 34.0 |
| NLVCV | 53.5 | 51.6 | 51.0 | 52.3 | **100** | 32.5 | 33.2 | 29.6 |
| CbMV | 53.1 | 50.3 | 56.4 | 55.5 | 53.7 | **100** | 43.9 | 27.8 |
| SgCV | 54.5 | 54.1 | 56.2 | 55.6 | 49.3 | 53.7 | **100** | 30.9 |
| AnFBV | 53.5 | 52.4 | 54.5 | 54.5 | 49.5 | 50.1 | 51.5 | **100** |





**References**

1. Edgar RC (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity. BMC Bioinf 5:113. PMC 517706 DOI:10.1186/1471-2105-5-113

2. Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32:1792-1797. PMC 390337 DOI: 10.1093/nar/gkh340

3. Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for bigger datasets. Mol Biol Evol 33:1870-1874 PMID: 27004904DOI:10.1093/molbev/msw054.

4. Rochon D, Rubino L, Russo M, Martelli GP, Lommel S (2011) *Tombusviridae*. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Virus taxonomy: classification and nomenclature of viruses. Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, San Diego. pp. 1111-1138.

5. Scheets K, White KA, Rubino L, Martelli G, Rochon DA (2015) ICTV taxonomic proposal 2015.007a-rP.A.v1.split\_Carmovirus. Divide the genus *Carmovirus* into three new genera: *Alphacarmovirus*, *Betacarmovirus*, and *Gammacarmovirus*.

https://talk.ictvonline.org/files/ictv\_official\_taxonomy\_updates\_since\_the\_8th\_report/m/plant-official/5841

6. Tam AW, Smith MM, Guerra ME, Huang CC, Bradley DW, Fry KE, Reyes GR (1991) Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome. Virology 185:120-131. PMID: 1926770 DOI: 10.1016/0042-6822(91)90760-9

7. Yasaki M, Hirano Y, Uga H, Hanada K, Uehara-Ichiki T, Toda T, Furuya H, Fuji S-i (2017) Characterization of a new carmovirus isolated from an *Adonis* plant. Arch Virol 162:501-504. PMID: 27738845 DOI: 10.1007/s00705-016-3108-0