

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

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| **Code assigned:** | **2020.033P** |  |
| **Short title:** Create two new species in the genus *Pelarspovirus* (*Tolivirales*: *Tombusviridae*) | | |
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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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| *Tombusviridae* SG |

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

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| Small changes were incorporated into the proposal. |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | Aug 6, 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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| 2020.033P.R.Pelarspovirus\_2nsp.xlsx |

**Abstract**

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| Two new pelarspoviruses infecting *Jasminum* sp. have been found. Jasmine virus H was found in many areas of China, and USA states of Hawaii, California, and Maryland. Jasmine mosaic-associated virus has been found in Hawaii and Washington DC. |

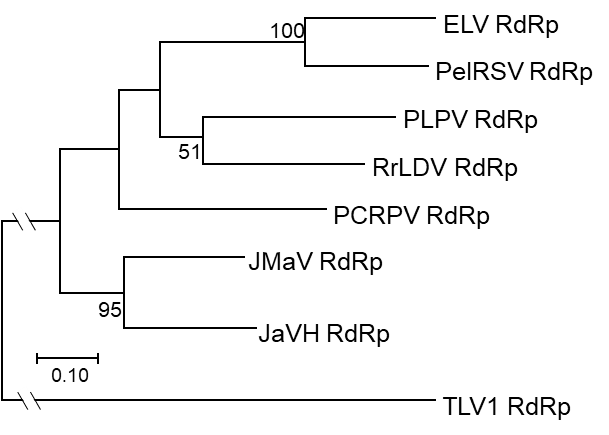
**Text of proposal**

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| |  | | --- | | Viruses from two new species that are related to ICTV-recognized pelarspoviruses have been characterized. Jasmine virus H (JaVH) was first identified in jasmine (*Jasminum sambac* (L.) Aiton) in Fujian province, China [1], and sequences of the same virus have been found in jasmine from 8 other provinces in China. JaVH was also found in Hawaii, USA, infecting 32/32 samples of star jasmine (*Jasminum multiflorum*) and in angelwing jasmine (*J. nitidum*) at the US National Arboretum, Washingtion DC. It has also been found in *J. sambac* in the US state of Maryland [1, 2].  A different virus, jasmine mosaic-associated virus (JMaV), was also detected in half of the Hawaiian samples, the Washington, DC *J. nitidum* sample, and a *Jasminum* sp. sample from California USA [2]. [Note: the virus names noted in the GenBank accessions for the DC and HI sequences will be updated from JMaV-1 and -2 to the appropriate JaVH and JMaV, respectively],  Listed below [3] are the species demarcation criteria for genus *Pelarspovirus*:  <75% amino acid sequence identity in RdRps and  <75% amino acid sequence identity in CPs  Natural host range  The host range for JMaV overlaps that of JaVH, but the RdRp and CP sequences are below the cut-off level for each other, other pelarspoviruses currently recognized by ICTV, and their closest relative, trailing lespedeza virus [4, 5; Table 1, Figs. 1 and 2]. Therefore, both of these viruses qualify as new species. Note that three currently recognized pelarspoviruses infect members of *Pelargonium* ssp., so it appears that pelarspoviruses can readily speciate within some closely related plants. | |

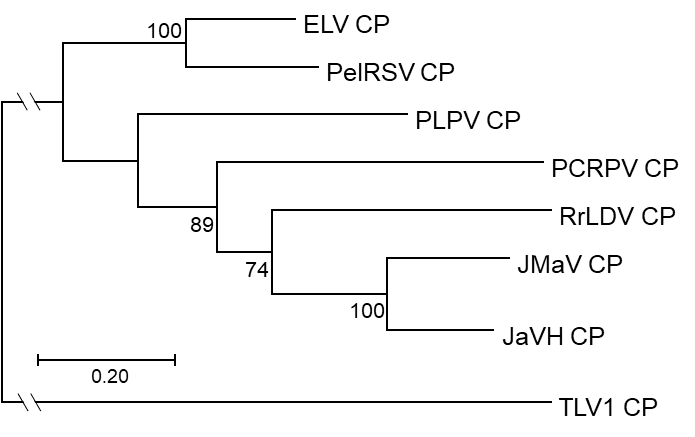
**Supporting evidence**

**Table 1.** Percent identity of CPs and RdRps for type isolates of Jasmine virus H (JaVH-Fujian) and Jasmine mosaic-associated virus (JMaV—HI) compared to current genus members.

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| **RdRp** |  | **Coat Protein** | | | | | | | |
| **TLV1** | **ELV** | **PelRSV** | **RrLDV** | **PLPV\_OK** | **PCRPV** | **JaVH** | **JMaV** |
| **TLV1** | **100** | 38 | 39 | 40 | 40 | 40 | 41 | 40 |
| **ELV** | 33 | **100** | 69 | 57 | 57 | 55 | 56 | 54 |
| **PelRSV** | 32 | 71 | **100** | 58 | 57 | 56 | 55 | 54 |
| **RrLDV** | 31 | 44 | 43 | **100** | 61 | 61 | 60 | 59 |
| **PLPV** | 32 | 50 | 48 | 46 | **100** | 58 | 58 | 55 |
| **PCRPV** | 28 | 44 | 45 | 49 | 44 | **100** | 58 | 59 |
| **JaVH** | 32 | 50 | 51 | 53 | 51 | 49 | **100** | **72** |
| **JMaV** | 34 | 48 | 47 | 55 | 48 | 49 | **70** | **100** |



**Figure 1.** Phylogenetic (distance) analysis of the complete RdRps for current members and 2 proposed pelarspoviruses. Alignments of the 8 sequences were made using MUSCLE [6] while trees were generated in Mega 7 [7] with the Maximum Likelihood (ML) algorithm using 1000 bootstrap replicates (showing values >50%). Positions with <50% site coverage were eliminated, leaving 761 positions in the final dataset for RdRps. Brackets connecting to TLV1 were proportionally shortened.

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**Figure 2.** Phylogenetic (distance) analysis of the complete CPs for current members and 2 proposed pelarspoviruses. Alignments of the 8 sequences were made using MUSCLE [6] while trees were generated in Mega 7 [7] with the ML algorithm using 1000 bootstrap replicates (showing values >50%). Positions with <50% site coverage were eliminated, leaving 339 positions in the final dataset. Brackets connecting to TLV1 were proportionally shortened.

**References**

1 Zhuo T, Zhu L-J, Lu C-C, Jiang C-Y, Chen Z-Y, Zhang G, Wang Z-H, Jovel J, Han Y-H (2018) Complete nucleotide sequence of jasmine virus H, a new member of the family *Tombusviridae*. Arch Virol 163:731-735. PMID: 29214362 DOI: 10.1007/s00705-017-3663-z

2 Dey KK, Leite M, Hu JS, Jordan R, Melzer MJ (2018) Detection of Jasmine virus H and characterization of a second pelarspovirus infecting star jasmine (*Jasminum multiflorum*) and angelwing jasmine (J. nitidum) plants displaying virus-like symptoms. Arch Virol 163:3051-3058. PMID: 30069855 DOI: 10.1007/s00705-018-3947-y

3 Scheets K, Jordan R, White KA, Hernández C (2015) *Pelarspovirus*, a proposed new genus in the family *Tombusviridae*. Arch Virol 160:2385-2893. PMID: 26149249 DOI: 10.1007/s00705-015-2500-5

4 Scheets K, Blinkova O, Melcher U, Palmer MW, Wiley GB, Ding T, Roe BA (2011) Detection of members of the *Tombusviridae* in the Tallgrass Prairie Preserve, Osage County, Oklahoma, USA. Virus Res 160:256-263. PMID: 21762736 DOI: 10.1016/j.virusres.2011.06.023

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7 Kumar S, Stecher G, and Tamura K (2016) MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol 33:1870-1874. PMID: 27004904 DOI: 10.1093/molbev/msw054