

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

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| **Code assigned:** | **2021.018P** |  |
| **Short title:** Create one new genus (*Tralespevirus*) and two new species (*Tralespevirus lespedezae* and *Tralespevirus gompholobii*) in the subfamily *Procedovirinae* (*Tolivirales*: *Tombusviridae*) | | |
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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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| A majority of SG members provided input/editing of the proposal, which is reflected in the submitted version. |

**Submission dates**

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| Date first submitted to SC Chair | May 16, 2021 |
| Date of this revision (if different to above) | May 28, 2021 |

**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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| 2021.018P.R.Tombusviridae\_1ng\_2ns |

**Abstract**

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| Two viruses [trailing lespedeza virus 1 (TLV1) and Gompholobium virus A (GomVA)] collected via sampling of natural habitats from opposite sides of the world were sequenced and identified as belonging to the family *Tombusviridae*. The complete sequence or coding complete sequence of the pair indicate that they are more closely related to each other than to other members in the family *Tombusviridae*, and they have a carmovirus-like arrangement of genes. Phylogenetic analysis of their RNA-dependent RNA polymerase (RdRp) indicates that they are most closely related to alphacarmoviruses and pelarspoviruses, and they use a noncanonical start codon for their MP2 (movement protein 2) ORFs. Based on the phylogenetic and sequence analyses, we propose the creation of a new genus *Tralespevirus* within the subfamily *Procedovirinae*, and of two new species, *Tralespevirus lespedezae* and *Tralespevirus gompholobii,* to accommodate TLV1 and GomVA as their exemplar isolates, respectively. |

**Text of proposal**

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| |  | | --- | | Two viruses were identified in many different plant species that were collected from natural habitats, regardless of whether there were any symptoms, using methods allowing to synthesize and sequence cDNAs of any virus containing an RNA genome [1, 2].  The complete sequence of trailing lespedeza virus 1 (TLV1) was obtained from the legume *Lespedeza procumbens* in an Oklahoma tallgrass prairie (2014.008aP.A.v3.Tombusviridae\_sp TLV1) [1, 3]. Based on the sequence and the genome organization, TLV1 was recently assigned to a species, *Trailing lespedeza virus 1*, which was unassigned to any genus in the family *Tombusviridae.* The predicted proteins and RNA sequences/structures suggest that TLV1 makes one subgenomic RNA (sgRNA) and is most closely related both to pelarspoviruses and alphacarmoviruses. The virus genome is predicted to contain open reading frames (ORFs) encoding a 28-kDa replicase-associated protein, an 88.1 kDa RNA-dependent RNA polymerase (RdRp), two movement proteins (MPs), and a 3'-located 37.2 kDa coat protein (CP). TLV1 RNA sequence and structure analyses indicated that the 5' and 3' untranslated regions (UTRs) and internal regions produce structures used by tombusvirids to control replication, sgRNA synthesis, and correctly translate all the viral mRNAs.  Gompholobium virus A (GomVA) was found in *Gompholobium preissii* in southwestern Australia [2]. The sequence assembled for GomVA indicates that it is also related to pelarspoviruses and alphacarmoviruses with a genome organization comparable to that of TLV1, encoding proteins similar to carmovirus-like tombusvirids, including an 88.5 kDa RdRp and a 37.3 kDa CP. But analyses of the 5' and 3' UTRs suggested that the GenBank sequence (KX184304) lacks the expected 5' and 3' UTRs or contains inaccurate terminal sequences. Therefore, the sequence for GomVA will be described as "**coding complete**". GomVA RdRp has the highest sequence identity to TLV1, 46% for RdRP and 37% for CP, thus GomVA should be considered as a representative member of a new species. Phylogenetic analysis of the RdRps of tombusvirids including TLV1 and GomVA RdRps using MEGA7 [4] shows the two sequences cluster together on a branch well-separated from the most similar members in the genera *Alphacarmovirus* and *Pelarspovirus* in the subfamily *Procedovirinae*. Therefore, we propose the following:   * create the new genus *Tralespevirus* in the subfamily *Procedovirinae*; * assign *Trailing lespedeza virus 1*, a hitherto unassigned species in the family *Tombusviridae*, to the new genus *Tralespevirus*; * rename the species *Trailing lespedeza virus 1 Tralespevirus lespedezae* to fulfil the new binomial nomenclature rules for virus species; * and create the novel species *Tralespevirus gompholobii*.     **Species demarcation criteria**:  The species demarcation criteria for similarity of the complete replicase and coat protein for alphacarmoviruses, betacarmoviruses, gammacarmoviruses, pelarspoviruses, and panicoviruses are "less than 75%", and we propose to use the same criteria for genus *Tralespevirus*.  **Origin of names**:  The name of the genus *Tralespevirus* derives from the English name of the host for TLV1 "**tra**iling **lespe**deza". The name of the species *Tralespevirus lespedezae* derives from the host species *Lespedeza procumbens.* The name of the species *Tralespevirus gompholobii* derives from the host species *Gompholobium preissii.* | |  | |

**Supporting evidence**

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Figure 1. Phylogenetic analysis of the RdRps of tombusvirids with one new member and new genus *Tralespevirus*. The alignment was made using MUSCLE while the tree was generated with the Maximum Likelihood (ML) algorithm in MEGA7 [4] using 1000 bootstrap replicates (showing values >50%). All positions with less than 50% site coverage were eliminated. That is, fewer than 50% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were 797 positions in the final dataset. See Table 1 for virus abbreviations and GenBank IDs. Hepatitis C virus (HCV) RdRp (protein AF011751) was used as the outgroup. Bracket marks uncollapsed genus. Monotypic genera names are in colored boxes. Sequence sources and virus names are in Table 1.

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| **Table 1: Abbreviations used in Figure 1** | | | | |
|  |  | **GenBank** | | |
| **Abbr.** | **Species** | | **Genome ID** | |
| TLV1 | Trailing lespedeza virus 1 | | | HM640935 |
| GomVA | Gompholobium virus A | | | KX184304 |
| MCMV | Maize chlorotic mottle virus | | | X14736 |
| GaMV | Galinsoga mosaic virus | | | Y13463 |
| FNSV | Furcraea necrotic streak virus | | | FJ768020 |
| OCSV | Oat chlorotic stunt virus | | | X83964 |
| MNeSV | Maize necrotic streak virus | | | AF266518 |
| CBV | Cucumber Bulgarian latent virus | | | AY163842 |
|  |  | | | **RdRp ID** |
| HCV | Hepatitis C virus H77 | | | AF011751 |

**References**

1 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. DOI 10.1016/j.virusres.2011.06.023. PMID: 21762736

2 Koh SH, Ong JWL, Admiraal R, Sivasithamparam K, Jones MGK, Wylie SJ (2016) A novel member of the *Tombusviridae* from a wild legume, *Gompholobium preissii*. Arch Virol 161: 2893-2898. DOI 10.1007/s00705-016-2992-7. PMID: 27456427

3 Scheets K, Melcher U (2014) ICTV taxonomic proposal 2014.008aP.A.v3.Tombusviridae\_sp. Create 1 new species *Trailing lespedeza virus 1* unassigned in the family *Tombusviridae*.

<https://talk.ictvonline.org/ICTV/proposals/2014.008aP.A.v3.Tombusviridae_sp.pdf>

4 Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol Biol Evol 33:1870-1874.

DOI 10.1093/molbev/msw054. PMID: 27004904