

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

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| **Code assigned:** | **2020.036P** |  |
| **Short title:** Create one new species in the genus *Aureusvirus* (*Tolivirales*: *Tombusviridae*) | | |
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**Author(s) and email address(es)**

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| Scheets K  on behalf of the *Tombusviridae* Study Group | kay.scheets@okstate.edu |

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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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| 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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| 2020.036P.R.Aureusvirus\_1nsp.xlsx |

**Abstract**

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| A (+) ssRNA virus was identified that has a genome organization found in tombusviruses, aureusviruses, and zeaviruses. Sequence analyses indicates it represents a new aureusvirus species. The GenBank entry identifies it as being a complete genome, but the 5' and 3' UTRs do not have predicted RNA structures and motifs that would indicate that these regions are correct. Therefore, we are listing this as a coding complete genome. |

**Text of proposal**

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| |  | | --- | | A new virus, elderberry latent virus 1, which infects elderberry (*Sambucus nigra* L.) has a (+) ssRNA genome [4]. Its genome organization and encoded proteins are most similar to homologs of recognized aureusviruses, while the CP and replicase are distinct enough to indicate it is a unique species (Table 1). The size ranges of ELV1 encoded proteins are similar to those of recognized aureusviruses, but MG967280, which is identified as having a complete genome, is 4,512 nt, noticeably larger than the 4,293-4,464 nt genome size of current members. Additionally, the 5' and 3' UTRs are longer and do not terminate in the typical 5'AGGA- and -GGCCC3' found on aureusviruses and many other tombusvirids. Therefore, we are indicating this is a coding-complete genome sequence. NCBI Viral Genomes currently has a coat protein sequence of a different isolate listed on the *Tombusviridae* Viral Genomes page (NC\_040713; MG967320), which is confusing, and Viral Genomes has been contacted to replace the CP sequence with MG967280. Note that recombination between tombusvirids has produced species such that the RdRp and CP proteins do not produce similarly branched trees (Figs.1 & 2)  Elderberry latent virus 1 infections were either asymptomatic or showed a mild chlorotic mosaic when it was the only virus present [4]. There is no information about a vector, which would likely be a chytrid fungus. The authors indicated that host range experiments were in progress, but searches via Scopus and PubMed have not found further publications.  Species demarcation criteria in genus *Aureusvirus* are shown below [5].  • Serological specificity (known species are serologically unrelated)  • Extent of sequence identity between relevant gene products  • Less than 60% aa sequence identity of the CP  • Less than 80% aa sequence identity of the polymerase  • Differential cytopathological features  • Transmission by a vector  • Natural host range  • Artificial host range reactions | |

**Supporting evidence**

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| Table 1. Percent identities of aureusvirus RdRps and CPs | | | | | | | | |
|  |  |  |  |  |  |  | |  |
|  |  | **Coat Protein** | | | | | | |
|  |  | **ElAV1** | PoLV | YSV | CLSV | MWLMV | JCSMV | |
| **RdRp** | **ElAV1** | 100 | 55 | 41 | 36 | 41 | | 39 |
| PoLV | 76 | 100 | 43 | 37 | 43 | | 39 |
| YSV | 76 | 79 | 100 | 33 | 32 | | 47 |
| CLSV | 75 | 80 | 86 | 100 | 35 | | 38 |
| MWLMV | 54 | 53 | 56 | 55 | 100 | | 38 |
| JCSMV | 55 | 55 | 55 | 56 | 74 | | 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: 27004904 DOI:10.1093/molbev/msw054.

4. Safarova D, Vavrouskova K, Candresse T, Navratil M (2018) Molecular characterization of a novel aureusvirus infecting elderberry (*Sambucus nigra* L.). PLoS One 13:e0200506. PMID: 30114234 DOI: 10.1371/journal.pone.0200506

5. Scheets K, Rochon D'A. (2015) Create species in genus *Aureusvirus*, family *Tombusviridae*: *Yam spherical virus*. 2015.008aP.A.v1.Aureusvirus\_sp YSV. http://www.ictvonline.org/proposals-15/2015.008aP.A.v1.Aureusvirus\_sp.pdf.

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