

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

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| **Code assigned:** | **2020.123B** |  |
| **Short title:** Create one new genus (*Presleyvirus*) including one new species (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| J Wittmann |

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

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| N4-like phages Study Group, Bacterial and Archaeal Viruses Subcommittee |

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

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**Authority to use the name of a living person (not applicable)**

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 6 June 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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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of the new genus “Presleyvirus” comprising one new species, based on genome-based comparisons and phylogenetics of the major coat protein. |

**Text of proposal**

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**Supporting evidence**

**Species demarcation criteria** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm [1-3].

**Source of the name of this taxon:** The name is derived from the name of the isolated phage of this type, Acinetobacterphage Presley.

**History:** Phage Presley is a member of the *Podoviridae* family that infects *Acinetobacter baumannii.* It was isolated from sewage collected in College Station, TX. Its genome consists of 77,181 bp with 94 unique coding sequences (CDSs) and a terminal repeat of 611 bp [4].

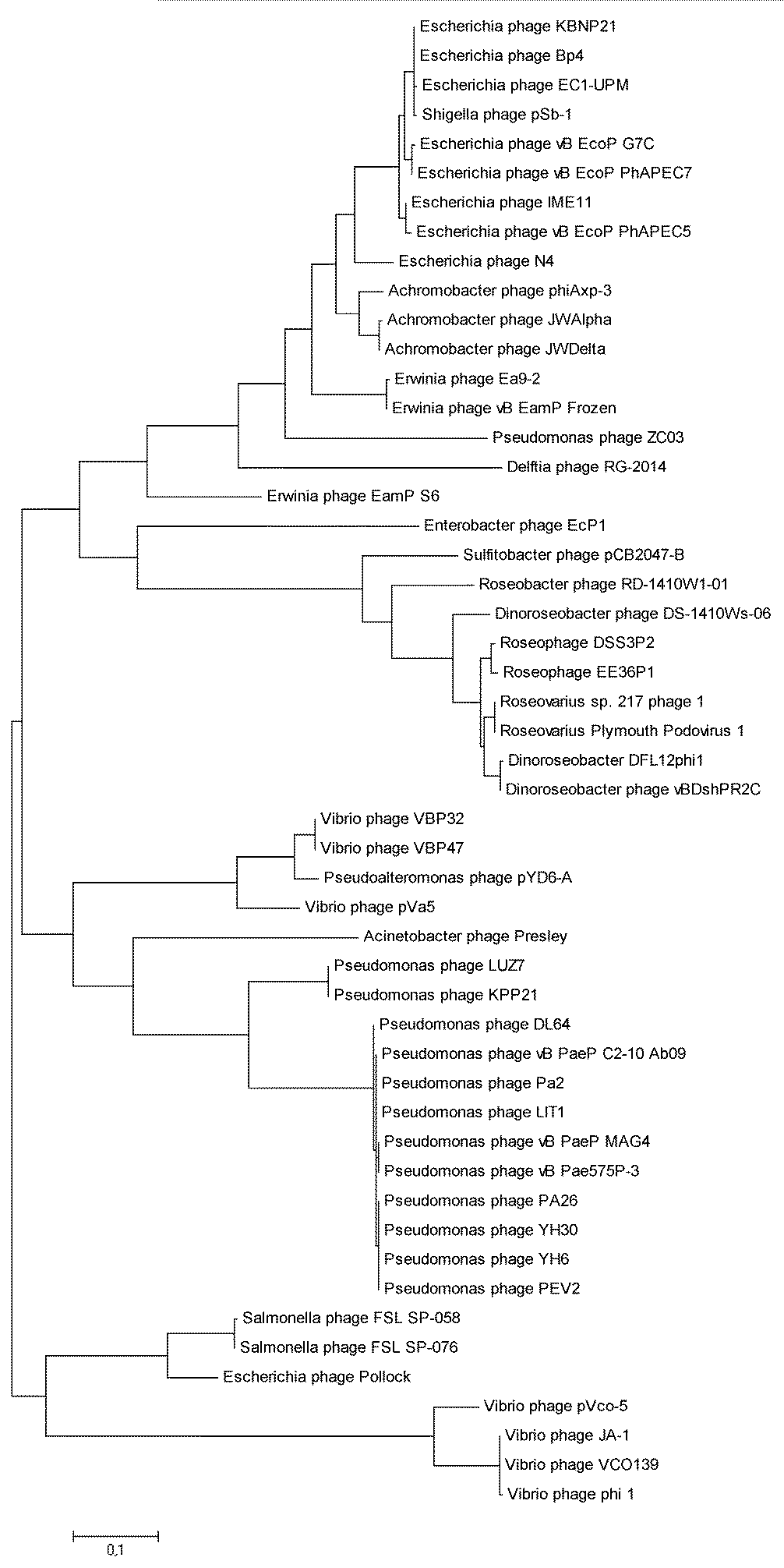
**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Presley | NC\_023581.1 | KF669658 | 77.79 | 37.8 | 94 | 3 |

**BLASTN homologs:** None, genomic orphan/singleton

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed, using MEGA5 [5], using the major coat protein of phage Presley and related N4-like phages.



**References**

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2. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.
3. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID:26553804.
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5. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. [MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods.](http://www.ncbi.nlm.nih.gov/pubmed/21546353) Mol Biol Evol. 2011; 28(10):2731-9. doi: 10.1093/molbev/msr121 PMID: 21546353