

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

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| **Code assigned:** | **2020.124B** |  |
| **Short title:** Create one new genus (*Privateervirus*) including two new species (*Caudovirales*: *Podoviridae*) | | |
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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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| *Caudovirales* 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**

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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 | 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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| 2020.124B.R.Privateervirus.xlsx |

**Abstract**

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| The new genus, *Privateervirus* contains C3 morphotype podoviruses infectious for Proteus and Cronobacter strainsidentified in the USA and Iran. |

**Text of proposal**

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| |  | | --- | | **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 | |

**Supporting evidence**

**Source of the name of this taxon:** This genus name is directly derived from that of *Proteus* phage Privateer.

**History:** These are both lytic phages. Phage Privateer was isolated from waste water treatment plant activated sludge sample (Navasota, TX) using *Proteus mirabilis* ATCC 35659 as the host bacterium. *Cronobacter sakazakii* phage vB\_CsaP\_009 was characterized at Abbas Soleimani-Delfan Arak University (Iran).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Privateer | [MT028297.1](about:blank) | 90.71 | 34.5 | [144](about:blank#!/proteins/88377/838838|Proteus phage Privateer/viral segment/) | 4 | 100 | 100 |
| vB\_CsaP\_009 | [LC519601.1](about:blank) | 92.12 | 35.1 | [140](about:blank#!/proteins/86934/759857|Cronobacter phage vB_CsaP_009/viral segment/) | 4(\*) | 82.9 | 88.9 |

**\* None indicated in Replicon Info; discovered using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](about:blank) **[5]**

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**BLASTN homologs:** Genomic orphans [1-3]. The next most closely related phage is *Cronobacter* phage vB\_CsaP\_GAP52 [[JN882286.1](https://www.ncbi.nlm.nih.gov/nucleotide/JN882286.1?report=genbank&log$=nucltop&blast_rank=3&RID=EEEXDE4N016)] which shares 16.2% DNA sequence identity with phage Privateer.

**Electron micrograph:**

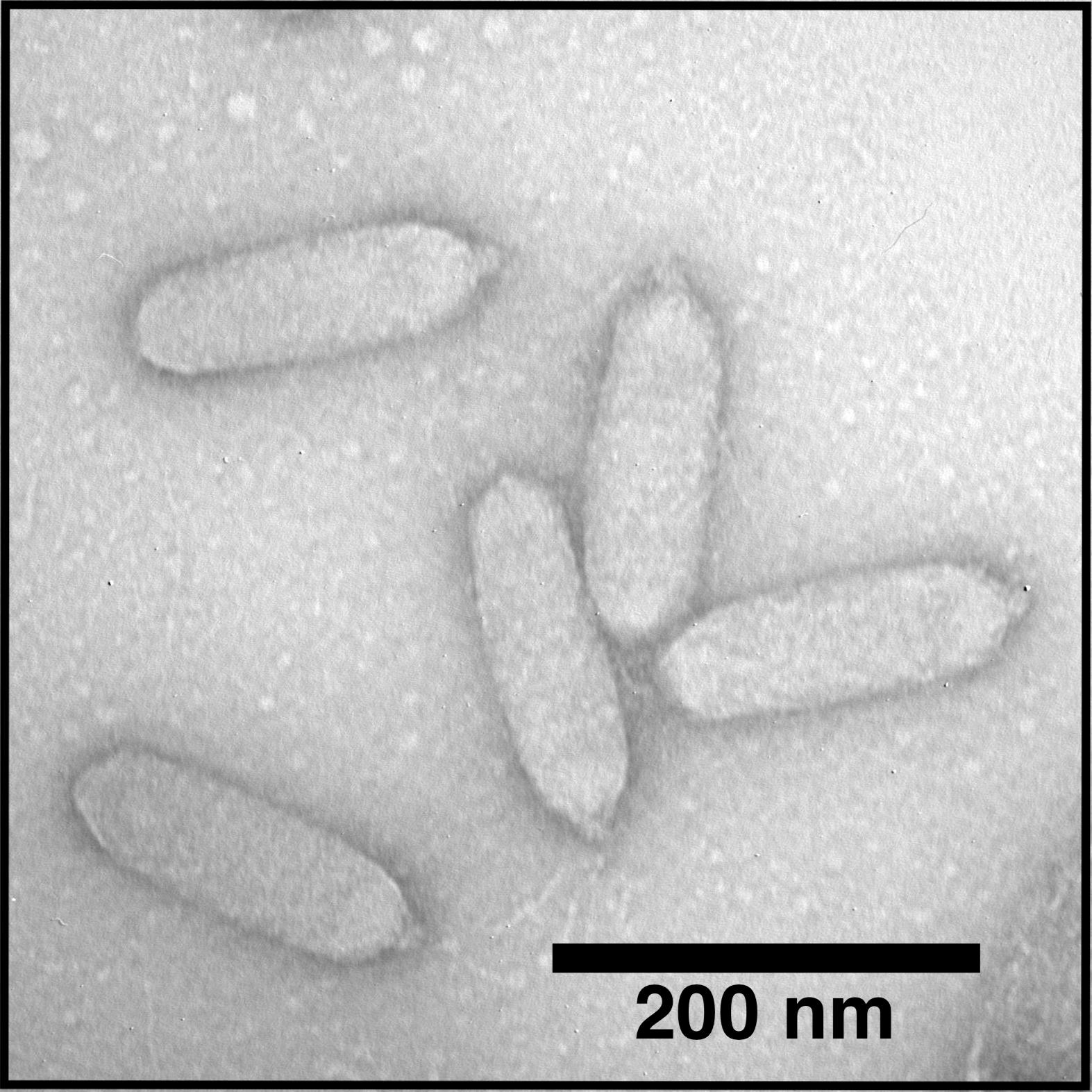
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Image credit: Jolene Ramsey and James Corban

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Privateer and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

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