

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

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| **Code assigned:** | **2020.157B** |  |
| **Short title:** Create one new genus (*Spizizenvirus*) including one new species (Caudovirales: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Jakub Barylski |

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

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| Bacterial and Archaeal Viruses Subcommittee; *Caudovirales* Study Group |

**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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| 2020.157B.R.Spizizenvirus.xlsx |

**Abstract**

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| The 2018 Master Species List describes only 21 siphoviruses which infect members of the order *Bacillales*. These fall into nine different genera. Here we propose a new genus, *Spizizenvirus*, containing a single species. |

**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.

**Source of the name of this taxon:** The taxon is named in honour of American microbial geneticist John Spizizen (1927 - 2010) who worked at the Scripps Clinic and Research Foundation (1965 - 1979) prior to being head of the Department of Microbiology at the University of Arizona Medical School (1979 - 1988). He worked on phage Phi105 in 1969.

**History:** This temperate *Bacillus subtilis* phage is inducible with mitomycin C. “The phage has an icosohedral head with a diameter of about 52 nm and a flexible, noncontractile tail about 225 nm long with about 50 rows of subunits. The base plate has a central hole surrounded by six appendages.” [Birdsell et at., 1969]. Its genome has 7-bp cohesive ends. It was sequenced in 1999 by Kazuo Kobayashi et al. (AB016282.1) and again in 2013 [Zeigler, 2013]

**Reference:** Birdsell DC, Hathaway GM, Rutberg L. 1969. Characterization of temperate *Bacillus* bacteriophage φ105. J. Virol. 4:264–270.

Zeigler DR. Complete Genome Sequence of *Bacillus subtilis* Phage φ105. Genome Announc. 2013 Sep 5;1(5). pii: e00641-13. doi: 10.1128/genomeA.00641-13. PubMed PMID: 24009114

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein |
| Phi105 |  | HM072038 | 39.32 | 42.7 | 52 |

**BLASTN relationship:** The next closest relative is *Bacillus* phage BM5, which shares 8.8% DNA sequence identity with *Bacillus* phage phi105 [1-3].

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of phi105 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."

**![A screenshot of a cell phone

Description automatically generated]()**

**References**

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