

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

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| **Code assigned:** | **2020.165B** |  |
| **Short title:** Create one new subfamily (*Trabyvirinae*) including two new genera (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew M. Kropinski |

**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 | July 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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| 2020.165B.R.Trabyvirinae.xlsx |

**Abstract**

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| We are placing three temperate Listeria phages in a new subfamily *Trabyvirinae*. The genus *Psavirus* is peripherally related to these phages as are several Staphylococcal viruses. |

**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:** These taxa are named after the three clans (*herb*) of Polish nobles (*szlachta*) - Ślepowron, Trąby and Jelita (https://en.wikipedia.org/wiki/Polish\_heraldry)

**History:** These are temperate phages Phage B025 revealed overlapping, single-stranded cohesive genome ends (cos sites; (5′-CGGTGTGGGG-3′). NCBI has tentative lumped these phages in the genus *Psavirus.* We propose based upon genomic analysis that the subfamily (*Trabyvirinae*) consists of two genera *Slepowronvirus* (Listeria phage LP-101, Listeria phage LP-HM00113468) and *Jelitavirus* (Listeria phage B025).

**Specific Reference:** Dorscht J, Klumpp J, Bielmann R, et al. Comparative genome analysis of Listeria bacteriophages reveals extensive mosaicism, programmed translational frameshifting, and a novel prophage insertion site. J Bacteriol. 2009;191(23):7206-7215. doi:10.1128/JB.01041-09 **[B025]**

Denes T, Vongkamjan K, Ackermann HW, Moreno Switt AI, Wiedmann M, den Bakker HC. Comparative genomic and morphological analyses of Listeria phages isolated from farm environments. Appl Environ Microbiol. 2014;80(15):4616-4625. doi:10.1128/AEM.00720-14 **[LP-101]**

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Listeria phage LP-101 | [NC\_024387.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_024387.1) | [KJ094023.1](https://www.ncbi.nlm.nih.gov/nuccore/KJ094023.1) | 43.77 | 35.5 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/33473/460741|Listeria phage LP-101/viral segment/) | 100 | 100 |
| Listeria phage LP-HM00113468 |  | MT500540 | 40.30 | 35.5 | 54 | 68.8 | 55.7 (72.2)# |
|  |  |  |  |  |  |  |  |
| Listeria phage B025 | [NC\_009812.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_009812.1) | [DQ003639.1](https://www.ncbi.nlm.nih.gov/nuccore/DQ003639.1) | 42.65 | 35.1 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/6036/456636|Listeria phage B025/viral segment/) | 56.5 | 62.9 |

**(\*) Determined using VIRIDIC [10]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**# Phage LP-HM00113468 is under-annotated relative to LP-101**

**VIRIDIC analysis:** VIRIDIC (Virus Intergenomic Distance Calculator; [10]) computes pairwise intergenomic distances/similarities amongst phage genomes.



**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of LP-101 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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**References**

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