

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

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| **Code assigned:** | **2020.094B** |  |
| **Short title:** Create one new genus (*Seongbukvirus*) including one new species and create four new species of Leuconostoc phages in two existing genera (*Caudovirales*: *Siphoviridae*) | | |
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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 | 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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| 2020.094B.R.Leuconostoc\_siphoviruses.xlsx |

**Abstract**

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| We have reassessed the diversity of *Leuconostoc*-infecting siphoviruses and have created one new genus in the family *Siphoviridae*, and added a further four species to two existing genera in the subfamily *Mccleskeyvirinae,* family *Siphoviridae*. |

**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**

**Overview**

**VIRIDIC analysis:** VIRIDIC (Virus Intergenomic Distance Calculator; [10]) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The gold highlighted names are ICTV recognized species in the genus

**Table

Description automatically generated**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein of the new species exemplars and related phages with phylogeny.fr in “one click” mode [8]. Phage phiMH1 is considered a genomic orphan phage, Lactococcus phage PLgW-1 was used as outlier for the subfamily *Mccleskeyvirinae* phages. "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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**Part A – Create a new genus *Seongbukvirus***

**Source of the name of this taxon:** This genus (*Seongbukvirus*) is named after the Seongbuk District (Seongbuk-gu) which is one of the 25 gu which make up the city of Seoul, South Korea. It was here in the School of Life Science and Biotechnology, Korea University that phage ΦMH1 was isolated [Jang SH et al. 2010]

**History:** This temperate phage was UV-induced from *Leuconostoc pseudomesenteroides*. The GenBank record indicates partial genome, but the publication reveals that it is complete.

**Specific Reference:** Jang SH, Hwang MH, Chang HI. Complete genome sequence of ΦMH1, a Leuconostoc temperate phage. Arch Virol. 2010;155(11):1883-1885. doi:10.1007/s00705-010-0799-5

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Leuconostoc phage phiMH1 |  | [HM596271.1](https://www.ncbi.nlm.nih.gov/nuccore/HM596271.1) | 38.71 | 38.7 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71806/399674|Leuconostoc phage phiMH1/viral segment/) | 0 |

**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:** None available

**Part B – To adjust membership in the *Limdunavirus***

**Part C – To adjust membership in the *Unaquatrovirus***

Based upon the VIRIDIC analysis several species were found to be too related to be considered unique and therefore *Leuconostoc virus LNTR3* (KC013029.1), *Leuconostoc virus Ln8* (KM262191.1), and *Leuconostoc virus LN6B* (KC013024.1) were deleted from their respective taxa, and new species added.

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Leuconostoc phage Ln-7 |  | [KX578042.1](https://www.ncbi.nlm.nih.gov/nuccore/KX578042.1) | 28.09 | 36.3 | [47](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63073/465696|Leuconostoc phage Ln-7/viral segment/) | 0 |
| Leuconostoc phage 1-A4 | [NC\_027987.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_027987.1) | [GQ451696.1](https://www.ncbi.nlm.nih.gov/nuccore/GQ451696.1) | 29.51 | 36.1 | [50](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/40471/461689|Leuconostoc phage 1-A4/viral segment/) | 0 |

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Leuconostoc phage P965 |  | [MN552146.1](https://www.ncbi.nlm.nih.gov/nuccore/MN552146.1) | 26.53 | 36.5 | [38](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85654/744314|Leuconostoc phage P965/viral segment/) | 0 |
| Leuconostoc phage LDG |  | [KX555527.1](https://www.ncbi.nlm.nih.gov/nuccore/KX555527.1) | 26.56 | 36.3 | [40](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63055/465678|Leuconostoc phage LDG/viral segment/) | 0 |

**Strain table**

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| **Phage** | **Accession** | **Belongs to species** |
| Leuconostoc phage LNTR3 | KC013029.1 | *Leuconostoc virus LN34* |
| Leuconostoc phage CHB | KX578043.1 | *Leuconostoc virus LN34* |
| Leuconostoc phage phiLNTR2 | KC013028.1 | *Leuconostoc virus LN34* |
| Leuconostoc phage P974 | MN552147.1 | *Leuconostoc virus LN34* |
| Leuconostoc phage CHA | KX578044 | *Leuconostoc virus LN34* |
| Leuconostoc phage Ln-8 | KM262191.1 | *Leuconostoc virus LN25* |
| Leuconostoc phage LN6B | C013024.1 | *Leuconostoc virus Lmd1* |

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