

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

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| **Code assigned:** | ***2022.063B*** |  |
| **Short title:** Create a new genus (*Piorkowskivirus)* with seven species (*Caudoviricetes*) | | |
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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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| Bacterial Viruses Subcommittee, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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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 | February 2022 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2022.063B.N.v1.Piorkowskivirus\_ng.xlsx |

**Abstract**

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| The global LAB (Lactic Acid Bacteriophage) community recognize a group of related phages which are termed the 987-like phages, which infect *Streptococcus thermophilus*. As a result of our multifaceted analyses of these phages who have proposed the creation of a new genus, *Piorkowskivirus*. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [8] | |

**Supporting evidence**

**Origin of the name of this taxon:** The taxon *Piorkowskivirus* is named in honour of G. Piorkowski who was the first to publish an article on Streptococcus phages - Beitrag zur Streptokokkenfrage. Anwendung des d'Herelleschen Phänomens auf Streptokokken, Med. Klin., 1922, xviii, 474.

**Historical aspects:** This lytic phage was isolated against Streptococcus thermophilus from dairy whey from Ireland, The Netherlands, and Denmark. They are recognized as being members of the 987-group of thermophilus phages [**11-14**]. These phages are chimera with one half of the genome derived from/similar to streptococcal *Moineauvirus/Brussowvirus* and the other half of the genome with high sequence similarity to lactococcal P335 phages such as ul36.

**Electron micrograph:** Electron micrography of phage 9871 (kindly provided by Horst Neve, Max Rubner-Institut (retired))

A picture containing tableware

Description automatically generated

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptococcus virus 9871 | NC\_031069.1 | KU678389.1 | 32.73 | 37.1 | 49 | 100 | 100 |
| Streptococcus virus 9872 | NC\_031094.1 | KU678390.1 | 33.11 | 36.8 | 49 | 91.4 | 95.9 |
| Streptococcus phage SW22 |  | MH892369.1 | 31.74 | 37.3 | 45 | 83.7 | 85.7 |
| Streptococcus phage SW16 |  | MH892350.1 | 32.11 | 37.0 | 45 | 83.9 | 83.7 |
| Streptococcus phage CHPC926 |  | KX879642.1 | 30.08 | 37.0 | 44 | 75.6 | 79.6 |
| Streptococcus phage CHPC577 |  | KX879641.1 | 35.13 | 36.8 | 50 | 70.2 | 69.4 |
| Streptococcus virus 9874 | NC\_031023.1 | KU678392.1 | 32.65 | 36.6 | 48 | 74.4 | 77.5 |

**(\*) determined using VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains.

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**ViPTree analysis:** ViPTree analysis (https://www.genome.jp/viptree/; [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**.



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**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from Piorkowskiviruses and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of the *Piorkowskivirus* are indicated with a **blue rectangle**.

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