

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

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| **Code assigned:** | **2022.060B** |  |
| **Short title:** Create a new genus (*Paclarkvirus*) with twelve species (*Caudoviricetes*) | | |
|  | | |

**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 |

|  |  |  |
| --- | --- | --- |
| **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 | May 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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| 2022.060B.N.v1.Packlarkvirus\_ng.xlsx |

**Abstract**

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| This genus contains twelve prophages discovered in the genus of Streptococcus pneumoniae strains. This genus was named in honour of Paul and Alice Clark. On average the genomes at 38.0 kb (37.8 mol%G+C) and encode 53 proteins. |

**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:** This taxon is named in honour of Paul Franklin Clark (b. 1882 in Portland, MA, USA - d. 1983 in Livermore, CA, USA) and Alice Edith (nee Schiedt) Clark (1881–1980)). In 1909 he received his Ph.D and 1914 an MD from the Johns Hopkins School of Medicine. In 1914, Paul Franklin Clark accepted a call from the University of Wisconsin School of Medicine and Public Health to an associate professorship of bacteriology, in 1918 he was promoted to full professor, in 1952 he became emeritus. In 1938 he was president of Society of American Bacteriologists. (Reference: https://de.wikipedia.org/wiki/Paul\_Franklin\_Clark)

In 1927 they isolated a phage which Alice C. Evans (Science 80: 40-41, 1934) refers to the "Wisconsin phage." Clark PF & Clark AS. 1927 A bacteriophage active against a virulent hemolytic Streptococcus. Proc. Soc.Exp. Biol. 24: 635-639.

**Historical aspects:** These are all prophages identified in Streptococcus pneumoniae strains [11-14]. MM1 is a siphovirus with an icosahedral head (60 nm in diameter), and a long tail (160 nm in length) [15]. It is not known whether any of the prophages can produce plaques.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptococcus phage MM1 | [NC\_003050.2](https://www.ncbi.nlm.nih.gov/nuccore/NC_003050.2) | [AJ302074.2](https://www.ncbi.nlm.nih.gov/nuccore/AJ302074.2) | 40.25 | 38.4 | [53](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4796/892704|Streptococcus phage MM1/viral segment Unknown/) | 100 | 100 |
| Streptococcus phage IPP65 |  | [KY065501.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065501.1) | 39.05 | 38.5 | [50](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63231/465854|Streptococcus phage IPP65/viral segment/) | 86.3 | 81.1 |
| Streptococcus phage IPP54 |  | [KY065492.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065492.1) | 38.9 | 38.4 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63222/465845|Streptococcus phage IPP54/viral segment/) | 85.0 | 84.9 |
| Streptococcus phage IPP55 |  | [KY065493.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065493.1) | 37.85 | 38.7 | [48](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63223/465846|Streptococcus phage IPP55/viral segment/) | 87.6 | 83.0 |
| Streptococcus phage IPP14 |  | [KY065455.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065455.1) | 37.25 | 38.4 | [49](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63185/465808|Streptococcus phage IPP14/viral segment/) | 88.4 | 86.8 |
| Streptococcus phage IPP39 |  | [KY065479.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065479.1) | 37.76 | 38.4 | [50](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63208/465831|Streptococcus phage IPP39/viral segment/) | 88.5 | 83.0 |
| Streptococcus phage phiBHN167 | [NC\_022791.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_022791.1) | [HF563658.1](https://www.ncbi.nlm.nih.gov/nuccore/HF563658.1) | 37.38 | 38.3 | [49](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/23132/460311|Streptococcus phage phiBHN167/viral segment Unknown/) | 84.4 | 84.9 |
| Streptococcus phage SpGS-1 |  | [KX550065.1](https://www.ncbi.nlm.nih.gov/nuccore/KX550065.1) | 37.63 | 38.3 | [53](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63070/465693|Streptococcus phage SpGS-1/viral segment/) | 84.1 | 88.7 |
| Streptococcus phage IPP48 |  | [KY065487.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065487.1) | 37.85 | 38.5 | [52](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63216/465839|Streptococcus phage IPP48/viral segment/) | 85.9 | 86.8 |
| Streptococcus phage phiARI0468-4 | [NC\_031915.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031915.1) | [KT337358.1](https://www.ncbi.nlm.nih.gov/nuccore/KT337358.1) | 37.39 | 38.1 | [49](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/50429/462912|Streptococcus phage phiARI0468-4/viral segment/) | 85.7 | 79.2 |
| Streptococcus phage IPP52 |  | [KY065490.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065490.1) | 36.81 | 38.1 | [52](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63220/465843|Streptococcus phage IPP52/viral segment/) | 87.5 | 92.4 |
| Streptococcus phage IPP66 |  | [KY065502.1](https://www.ncbi.nlm.nih.gov/nuccore/KY065502.1) | 37.97 | 37.8 | [53](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63232/465855|Streptococcus phage IPP66/viral segment/) | 88.1 | 88.7 |

**(\*) 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.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [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 MM1 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 *Paclarkvirus* are indicated with a **blue rectangle**.

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