

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

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| **Code assigned:** | **2020.034B** |  |
| **Short title:** Create one new genus (*Chopinvirus*) including one new species (*Caudovirales*: *Podoviridae*) | | |
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**Author(s) and email address(es)**

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“The views expressed in this article reflect the results of research conducted by the author and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, nor the United States Government. This work was supported/funded by work unit number A1417”

**Corresponding author**

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| Andrew M. Kropinski |

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

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| **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)** |
| *Chopinvirus* | Marie-Christine Chopin | Y |
|  |  |  |
|  |  |  |

**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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| --- |
| 2020.034B.R.Chopinvirus.xlsx |

**Abstract**

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| Lactococcus phage KSY1 is an orphan member of the *Podoviridae*. This proposal creates a genus for this 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:** This genus is named in honour of Marie-Christine Chopin (b. 1947, France; PhD (1976). Senior scientist with Institut national de la recherche agronomique (INRA) r. 1985. She contributed significantly to our understanding of lactic acid bacteria and their phages.

**History:** Phage KSYI was obtained from the supernatant of nonropy sour milk (viili). originating from a commercial dairy by Saxelinb and colleagues.“Viili”, is a Finnish fermented ropy milk [A]. This phage possesses has a very distinctive morphology with a bullet-shaped elongated capsid (223 nm long, 45 nm wide), and a short tail (32 nm). KSY1 therefore belongs to the *Podoviridae* family, more precisely to the C3 morphotype.” [A,B]. The sequence of this phage revealed a T7-like RNA polymerase and associated promoters. No large subunit terminase-encoding gene was identified by the authors, but Yury Wolf and Kira Makarova at NCBI, using HHpred, identified ABG21577 (gp35) as possessing structural homology to Bacillus phage φ29 DNA packaging ATPase:



168 residues (45% of gp35) have been modelled with 93.7% confidence by the single highest scoring template (c5hd9A: crystal structure of the n-terminal domain of the dna packaging atpase2 from bacteriophage phi29) using Phyre2.

**Structure of Phi29 DNA encapsidation protein:**



**Structure of KSY1 DNA encapsidation protein:**



This phage appears to be a chimera between a picovirus and a member of the *Autographivirinae*.

**Reference:**

**A:** Saxelin ML, Nurmiaho EL, Korhola MP, Sundman V. Partial characterization of a new C3-type capsule-dissolving phage of Streptococcus cremoris. Can J Microbiol. 1979;25(10):1182-7.

**B:** Chopin A, Deveau H, Ehrlich SD, Moineau S, Chopin MC. KSY1, a lactococcal phage with a T7-like transcription. Virology. 2007 Aug 15;365(1):1-9.

**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| KSY1 | [NC\_009817.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_009817.1) | [DQ535032.1](https://www.ncbi.nlm.nih.gov/nuccore/DQ535032.1) | 79.23 | 35.1 | 130 | 3 |

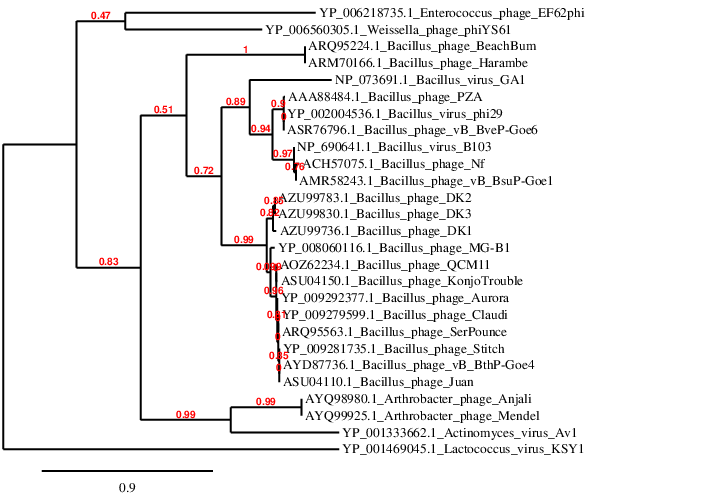
**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:**

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**(derived from: https://reader.elsevier.com/reader/sd/pii/S0042682207002255?token=14994498F0CCF6D84DA9AA167D371A80FFDF040E05D8D5E3A16DD23BBD4E3DC8843B2E09CC646CDBCB311F3C4B45D80D)**

**Phylogeny:** The phylogenetic tree was constructed using the major capsid protein homologs of KSY1 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."



**References**

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3: O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.

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5: Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.

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