

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

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| **Code assigned:** | **2020.082B** |  |
| **Short title:** Create one new genus (*Knuthellervirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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**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; *Caudovirales* Study Group** |

**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)** |
| Knuthellervirus | Professor Knut J. Heller | 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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| 2020.082B.R.Knuthellervirus.xlsx |

**Abstract**

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| *Pseudomonas fluorescens* phage PMBT14 is a novel phage which we have placed in a new genus called *Knuthellervirus*. |

**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 after Professor Dr. Knut J. Heller (b. 1948 r. 2014) PhD University of Münster (1977); Former head of the Department of Microbiology and Biotechnology of the Max Rubner-Institut (MRI), Federal Research Institute of Nutrition and Food in Kiel, Germany (1992 – 2014). He was previously also honoured through the creation of *Pseudomonas helleri* sp. *nov*. [von Neubeck M et al. 2016].

A person wearing glasses and smiling at the camera

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(from: https://www.researchgate.net/profile/Knut\_Heller)

**History:** Lytic phage PMBT14 was isolated from a sewage plant near Kiel, Germany, using the *Pseudomonas fluorescens* DSM 50090R derivative as the host bacterium.PMBT14 was assigned to the family Siphoviridaebased on transmission electron microscopy, which revealed an isometric head (diameter: 56.7 nm) and a non-contractile tail (length: 133.0 ± 6.2 nm). A thin central tail fiber (length: 35.8 nm) and a set of three flexible and shorter fibers (length: 22.8 nm) with an enlarged distal end (diameter: 5.0 nm) are present at the conical tail tip of phage PMBT14 [Koberg et al. 2018].

**Reference:**  von Neubeck M, Huptas C, Glück C, et al. *Pseudomonas helleri* sp. nov. and *Pseudomonas weihenstephanensis* sp. nov., isolated from raw cow's milk. Int J Syst Evol Microbiol. 2016;66(3):1163-1173. doi:10.1099/ijsem.0.000852

Koberg S, Gieschler S, Brinks E, Wenning M, Neve H, Franz CMAP. Genome sequence of the novel virulent bacteriophage PMBT14 with lytic activity against *Pseudomonas fluorescens* DSM 50090(R). Arch. Virol. 2018;163(9):2575-2577. doi: 10.1007/s00705-018-3882-y. PubMed PMID: 29786121.

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| PMBT14 |  | [MG596800.2](about:blank) | 47.82 | 54.5 | [76](about:blank#!/proteins/68305/374008|Pseudomonas phage PMBT14/viral segment/) | 0 |

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

**Electron micrograph:**

A picture containing sitting

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Transmission electron micrograph of *Knuthellervirus* *Pseudomonas* virus PMBT14 stained with 2% (w/v) uranyl acetate.

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of PMBT14 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."

**![A screenshot of a cell phone

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**References**

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