

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

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| **Code assigned:** | **2020.086B** |  |
| **Short title:** Create one new genus (*Kylevirus*) including one new species(*Caudovirales:* *Myoviridae*) | | |
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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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| *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 | May 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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| 2020.086B.R.Kylevirus.xlsx |

**Abstract**

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| The genus *Kylevirus*, contains of a single species, *Panteoa virus Kyle*. This lytic phage possesses a 73 kb genome and is peripherally related to the *Wifcevirus* and *Myosmarvirus* taxa. |

**Text of proposal**

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**Supporting evidence**

**Proposal:** To create a new genus, *Kylevirus* containing one species.

**Origin of the name of this taxon:** The name is directly derived from that of the first isolate: Panteoa phage Kyle.

**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.

**History:** *Panteoa* phage Kyle was isolated in Richmond, Virginia (USA) from water using an environmental isolate of Panteoa as the host. It is a lytic phage.

**Publications:** None

**BLASTN relationship:** The next closest relative is *Escherichia* phage ECML-117, which shares 21.4% DNA sequence identity with Kyle [1-3]. *Escherichia* phage ECML-117 is a member of the *Wifcevirus* taxon.

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein |
| Panteoa phage Kyle |  | [MN038177.1](https://www.ncbi.nlm.nih.gov/nuccore/MN038177.1) | 73.17 | 49.5 | 113 |

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

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**References**

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