

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

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| **Code assigned:** | **2020.126B** |  |
| **Short title:** Create one new genus (*Pylasvirus*) including two new species (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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| Johannes Wittmann |

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

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| N4-like phages 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 | 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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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of the genus “Pylasvirus” including two species, Klebsiella phages Pylas and KpCHEMY26 based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analyses of terminase and vRNA polymerase protein sequences. |

**Text of proposal**

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| |  | | --- | | **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 [1-3]. | |

**Supporting evidence**

**Source of the name of this taxon:** The name is derived from the the isolated phage of this type, Klebsiella phage Pylas.

**History:** Phages Pylas and KpCHEMY26 are members of the newly created *Schitoviridae* family and infect strains of *K. pneumoniae*. Bacteriophage Pylas was isolated from a wastewater treatment plant in the US [4], while phage KpCHEMY26 was isolated from sewage in Israel [5].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Pylas |  | MH899585 | 70,48 | 41.2 | 92 | 6 |
| KpCHEMY26 |  | MN163281 | 70,68 | 41.7 | 81 | 11 |

**Electron micrograph:** None available

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [6]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates genus-level.

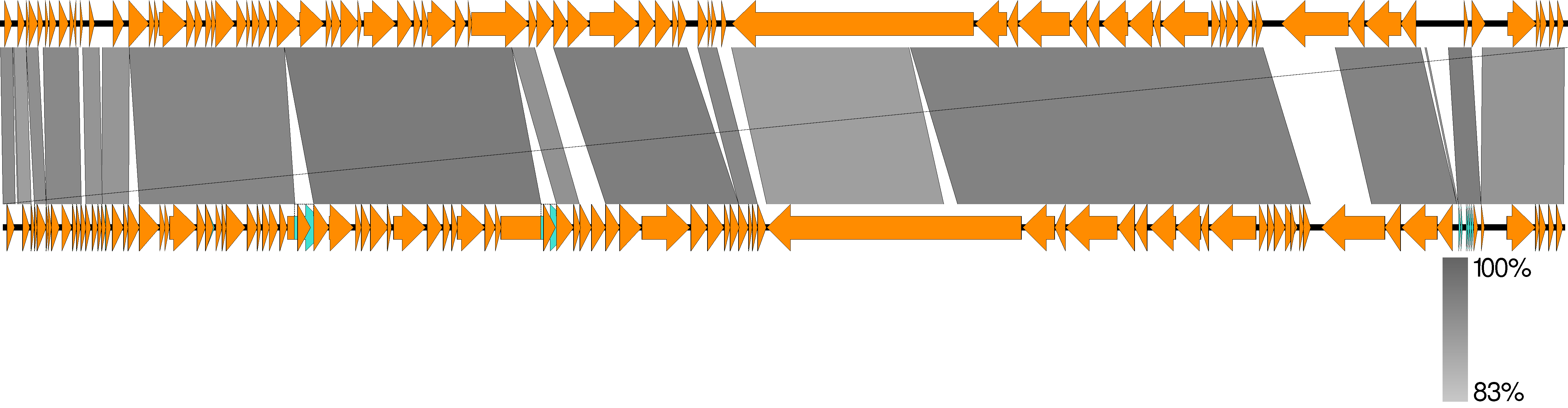


**Synteny plot**

Synteny plot of *Klebsiella* phages KpCHEMY26 and Pylas at nucleotide level. For better visualization, genome direction of phage KpCHEMY26 was reversed. Plot was visualized using EasyFig [7].

KpCHEMY26

Pylas

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**Phylogenetic analysis** using the (A) terminase and (B) vRNA polymerase protein sequences of N4-like phages. The amino acid sequences were compared using MUSCLE with MEGA7 [8]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (100).

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B

A

**References**

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