

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

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| **Code assigned:** | **2020.045B** |  |
| **Short title:** Create one new genus (*Deurplevirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Annika Gillis |

**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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| 2020.045B.R.Deurplevirus.xlsx |

**Abstract**

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| The 2018 Master Species List describes only 21 siphoviruses which infect members of the order *Bacillales*. These fall into nine different genera. Here we propose a new genus, *Deurplevirus* containing a single species. |

**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 | |

**Supporting evidence**

**Source of the name of this taxon:** The name is directly derived from the name of the phage, Bacillus phage Deep-Purple.

**Type species:** *Bacillus virus DeepPurple*.

**History:** Bacillus phage Deep-Purple was isolated from soil in Belgium using *Bacillus cereus* as the host bacterium. It exhibits a lytic activity against 55% of emetic *Bacillus cereus* and *B. weihenstephanensis* strains.

**Reference:** Hock L, Gillis A, Mahillon J. Complete genome sequence of bacteriophage Deep-Purple, a novel member of the family *Siphoviridae* infecting *Bacillus cereus*. Arch Virol. 2018 Sep;163(9):2555-2559. doi: 10.1007/s00705-018-3865-z. Epub 2018 May 11. PubMed PMID: 29752557.

**Electron micrograph:** None available

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Deep-Purple |  | [MF176161.1](https://www.ncbi.nlm.nih.gov/nuccore/MF176161.1) | 36.28 | 38.4 | 40 | 0 |

**BLASTN relationship:** The next closest relative is Bacillus phage PfIS075, which shares 10.9% DNA sequence identity with Deep-Purple [1-3]. The level of sequence identity that they belong to separate genera.

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Deep-Purple 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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