

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

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| **Code assigned:** | **2020.046B** |  |
| **Short title:** Create one new genus (*Dibbivirus*) including three new species (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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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)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 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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| 2020.046B.R.Dibbivirus.xlsx |

**Abstract**

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| For a number of years the Georgian isolate *Xanthomonas* phage vB\_XveM\_DBBI has been a genomic outlier. With the isolation of two related *Pantoea* phages in Lithuania, we now propose a genus to encompass the three 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 after the first isolate of its type: Xanthomonas phage vB\_XveM\_DIBBI, which was derived from the institute where it was isolated Durmishidze Institute of Biochemistry and Biotechnology (Tbilisi, Georgia).

**History:** Lytic Xanthomonas phage vB\_XveM\_DBBI was isolated from *Xanthomonas vesicularis*-infected plants in Georgia. The other two lytic phages were isolated, in Lithuania, against *Pantoea agglomerans* strains recovered from *Amelanchier spicata* (low juneberry, thicket shadbush, dwarf serviceberry, or low serviceberry) and *Ribes Jostabeere* (jostaberry (Ribes × nidigrolaria)), respectively. Interestingly phage DIBBI shares 15 genes in common with *Escherichia* phage T1 which is a member of the *Siphoviridae*.

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| vB\_XveM\_DIBBI | [NC\_017981.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_017981.1) | [JN022534.1](https://www.ncbi.nlm.nih.gov/nuccore/JN022534.1) | 49.98 | 52.4 | 81 | 0 | 100 | 100 |
| vB\_PagM\_PSKM |  | [MK798144.1](https://www.ncbi.nlm.nih.gov/nuccore/MK798144.1) | 49.94 | 52.4 | 82 | 0 | 94.0 | 96.3 |
| vB\_PagM\_AAM37 |  | [MK798143.1](https://www.ncbi.nlm.nih.gov/nuccore/MK798143.1) | 49.99 | 52.0 | 86 | 0 | 83.8 | 96.3 |

**\*\* Determined using BLASTn at NCBI [1-3]**

**\*\*\* Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**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.

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

**Electron micrograph:** None available

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

Description automatically generated

**References**

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10: Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>