

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

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| **Code assigned:** | ***2022.046B*** |  |
| **Short title:** Create two new genera of Burkholderia phages (*Magiavirus* and *Bigmanorsvirus)* (*Caudoviricetes*) | | |
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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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| Bacterial Viruses Subcommittee, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **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 2022 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2022.046B.N.v1.Caudoviricetes\_2ng.xlsx |

**Abstract**

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| This proposal formally classifies two Burkholderia phages isolated in USA (*Magiavirus*) and Israel (*Bigmanorsvirus*). Representatives of the former are temperate, while the latter at lytic. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [8] | |

**Supporting evidence – molecular data**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**.



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**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from Magia and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of the *two genera* are indicated with **blue rectangles**.

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**Proposal A. Create a new genus, *Magiavirus*, with a single species**

**Origin of the name of this taxon:** This taxon is named after Burkholderia phage Magia

**Historical aspects:** Magia, a myophage infecting Burkholderia cenocepacia, does not appear to have strong overall similarity to other known phages. The Magia genome encodes a Cro-like transcriptional regulator, a C2-like immunity repressor, and an integrase, suggesting that it is a temperate phage [10]

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Burkholderia phage Magia | [MT701587.1](https://www.ncbi.nlm.nih.gov/nuccore/MT701587.1) | 44.94 | 65.1 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96732/1493957|Burkholderia phage Magia/viral segment/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

The second phage in the phylogenetic tree potentially assigned to this genus, Burkholderia phage Bups\_phi1, does not have a complete genome published, and can therefore not be classified.

**Proposal B. Create a new single-species genus, *Bigmanorsvirus*.**

**Origin of the name of this taxon:** This taxon is named after Burkholderia phage BgManors32

**Historical aspects:** This lytic Burkholderia gladioli myophage was isolated in the Institute of Dental Sciences and School of Dental Medicine, Hebrew University, Hadassah Campus,

Jerusalem (Israel) from sewage.

**Electron micrograph:** N/A

**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Burkholderia phage BgManors32 | [OK665842.1](https://www.ncbi.nlm.nih.gov/nuccore/OK665842.1) | 59.76 | 66.0 | [87](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109200/1760465|Burkholderia phage BgManors32/viral segment/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

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