

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

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| **Code assigned:** | **2020.010B** |  |
| **Short title:** Create one new genus (*Anjalivirus*) including two species (C*audovirales*: *Podoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew Kropinski |

**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 |  |
| 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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| 2020.010B.R.Anjalivirus |

**Abstract**

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| As part of an extensive analysis of phages which are described as Phi29-like and tentatively assigned to the subfamily *Picovirinae*, family *Podoviridae* we discovered a group of related viruses which infect the Gram-positive bacterium Arthrobacter. These were recognized by The Actinobacteriophage Database as belonging to Cluster FD. |

**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:** This genus is named after Arthobacter phage Anjali

**History:** Lytic phage Anjali was isolated in 2017 by Gabrielle Giglietti (University of Pittsburgh) using Arthrobacter globiformis B-2979 as the host bacterium as part of the Phage Hunters Integrating Research and Education (<https://phagesdb.org/phages/Anjali/>). Assumed to possess terminal proteins.

**Specific Reference:** None

**GenBank Summary:**

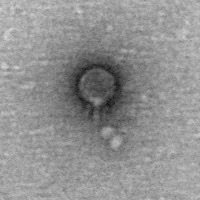
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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name |  | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall % DNA sequence identity with the type species (\*) | Overall % homologous proteins with the type species (\*\*) |
| Anjali |  | [MK016490.1](https://www.ncbi.nlm.nih.gov/nuccore/MK016490.1) | 19.68 | 59.4 | [27](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73795/418493|Arthrobacter phage Anjali/viral segment/) | 0 | 100 | 100 |
| Mendel |  | [MK016500.1](https://www.ncbi.nlm.nih.gov/nuccore/MK016500.1) | 19.43 | 59.8 | [28](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73804/418502|Arthrobacter phage Mendel/viral segment/) | 0 | 72.6 | 85.2 |

**(\*) determined using VIRIDIC [1]**

**(\*\*) determined using CoreGenes 3.5 [4]**

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

**Electron micrograph:** Electron micrograph of negatively stained Arthobacter phage Anjali (<https://phagesdb.org/phages/Anjali/>) - Limited permission was granted by The Actinobacteriophages Database, funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.



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



**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/>