

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

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| **Code assigned:** | **2020.017B** |  |
| **Short title:** Create one new genus (*Ayohtrevirus*) including one species (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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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 | 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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| 2020.017B.R.Ayohtrevirus.xlsx |

**Abstract**

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| Proposed single species genus, *Ayohtrevirus,* the sole representative of subcluster AO3 in the Actinobacteriophage Database. |

**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**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [1]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The colour codes in columns 1 indicate ICTV recognized species.

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**History:** Lytic Arthrobacter phage Abba was isolated in 2016 by David Bojorquez (University of California, Los Angeles) as part of Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Program. It was isolated from soil using *Arthrobacter globiformis* B-2979 as the host. The Actinobacteriophage Database states that the genome is Circularly Permuted and places it in Subcluster AO3.

**Source of the name of this taxon:** The name of this genus is derived from the name of The Actinobacteriophage Database to which Arthrobacter phage Abba belongs, AO3.

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Arthrobacter phage Abba | [MT024868.1](https://www.ncbi.nlm.nih.gov/nuccore/MT024868.1) | 46.62 | 65.0 | [71](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/88391/838852|Arthrobacter phage Abba/viral segment/) | 0 |

**VIRIDIC homologs:** The next most related phage is Arthrobacter phage Vibaki which shares 30.9% DNA sequence identity with Abba (see VIRIDIC heatmap). This suggests a subfamily relationship which we do not intend to formally recognize at this time (see also phylogenetic tree).

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Abba and related phages of Actinobacteriophage Database cluster AO (Rhodococcus phage REQ3 as outlier) with phylogeny.fr in “one click” mode [5]. "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 [6] for details."

Diagram

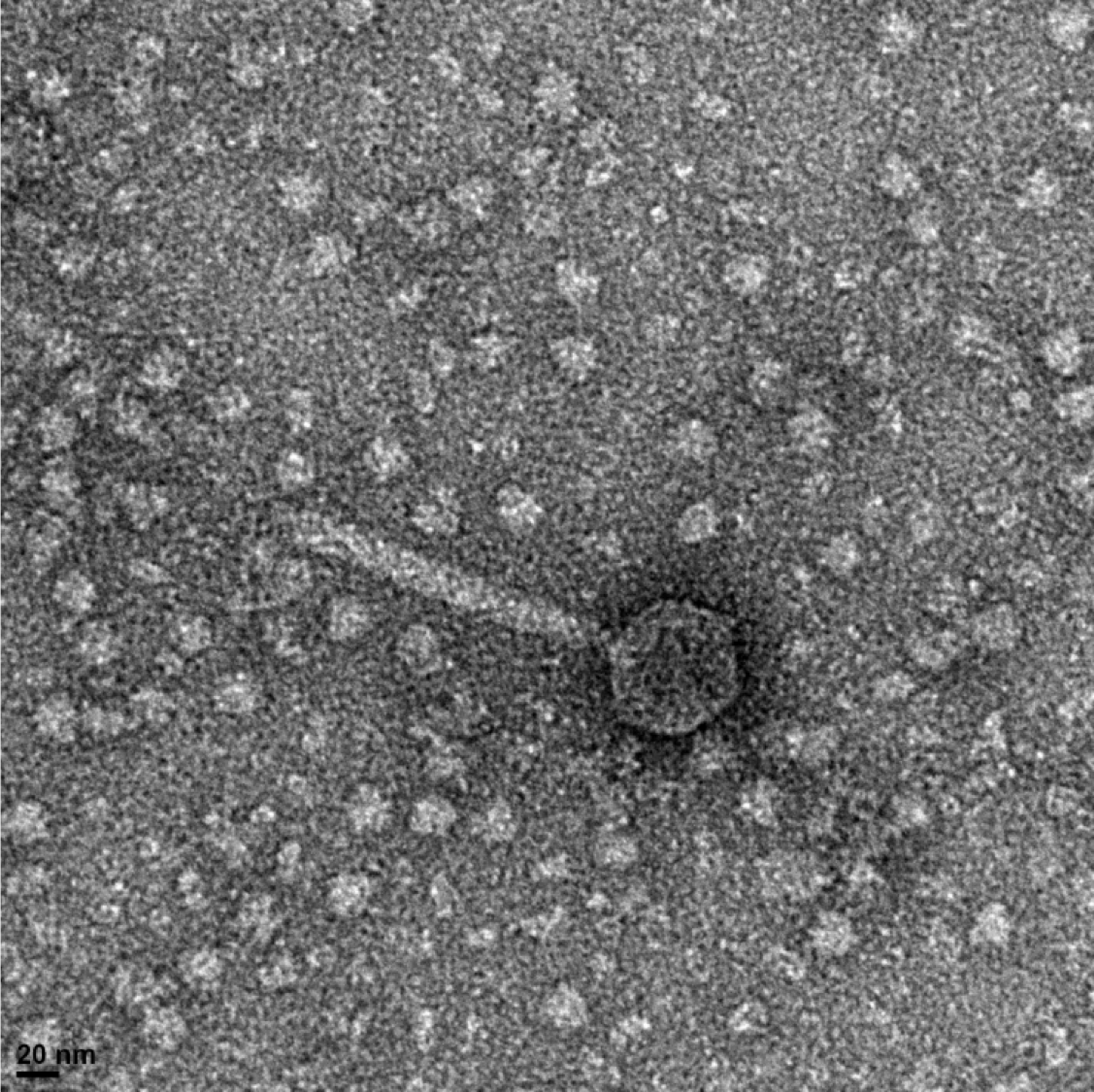
Description automatically generated

**Electron micrograph:** Electron micrograph of negatively stained Arthrobacter phage Abba (https://phagesdb.org/phages/Abba/) - 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

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**References**

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

2: Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.

3: Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432

4: O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804

5: Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.

6: Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.