

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.083B** |  |
| **Short title:** Create one new genus (*Kozyakovvirus*) including one new species (*Caudovirales*: *Podoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Kropinski AM, Turner D, Adriaenssens EM | [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com);  [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk);  [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk) |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| University of Guelph, Canada [AMK]  University of the West of England, UK [DT]  Quadram Institute Bioscience, UK [EMA] |

**Corresponding author**

|  |
| --- |
| Andrew M. Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

|  |
| --- |
| Bacterial and Archaeal Viruses Subcommittee; *Caudovirales* Study Group |

**ICTV study group comments and response of proposer**

|  |
| --- |
|  |

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair |  |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2020.083B.R.Kozyakovvirus.xlsx |

**Abstract**

|  |
| --- |
| There are currently no viruses specific to the Cyanobacterium *Anabaena* classified by ICTV. This is the first. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | |  | |

**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 Russian scientist S. Ya Koz'yakov who isolated the first virus of this type, Anabaena phage A-4L.

**History:**  Anabaena phage A-4L was “isolated in Leningrad, USSR, by screening about 2000 samples from six regions in the USSR (Koz’yakov, 1977). Among the cyanobacteria tested, only one, a strain of *Anabaena variabilis*, served as host for the nine phages of the A(L) series.” (Hu et al. 1981). “The discovery and properties of cyanophages is reviewed in details (B.V. Gromov. Cyanophages. Ann. Inst. Pasteur. 1983. 134 B, 43-59). Late Dr. S.Ya. Kozyakov originally isolated the first cyanophage of A-(L) series, A-1(L), and descibed its detailed properties in co-authorship with B.V.Gromov and K.A. Mamkaeva in 1970-1975.” (Prof. Alexander V. Pinevich, Head of Microbiology Department, St. Petersburg State University, personal communication).

It was sequenced by a Chinese group (Ou et al. 2015). It shows distinct similarities to T7-like phages (Family, *Autographiviridae*) in possessing direct terminal repeats (810 bp), and DNA primase/helicase, DNA polymerase, tail tubular protein A/B homologs. But, the morphogenesis cassette is oriented in the opposite orientation to that of T7.

**Reference:**

KOZ’YAKOV,S. YA. (1977). Cyanophages of the series A(L) specific for the blue-green alga *Anabaena variabilis*. Eksperimental’naya al’gologiya. Trudi Petergof. Biol. Inst. (Leningrad State Univ.) 25,151-

175.

Hu NT, Thiel T, Giddings TH Jr, Wolk CP. New *Anabaena* and *Nostoc* cyanophages from sewage settling ponds. Virology. 1981 Oct 15;114(1):236-46

Ou T, Liao XY, Gao XC, Xu XD, Zhang QY. Unravelling the genome structure of cyanobacterial podovirus A-4L with long direct terminal repeats. Virus Res. 2015 May 4;203:4-9.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| A-4L | [NC\_024358.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_024358.1) | [KF356198.1](https://www.ncbi.nlm.nih.gov/nuccore/KF356198.1) | 41.75 | 43.4 | 38 | 0 |
|  |  |  |  |  |  |  |

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

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of A-4L 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 text

Description automatically generated

**References**

1. 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.
2. 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.
3. 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.
4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6): doi: 10.1371/journal.pone.0039107. PMID: 22723939.
5. Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.
6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
7. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.
8. 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.
9. 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.