

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

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| **Code assigned:** | **2020.078B** |  |
| **Short title:** Create one new genus (*Jarrellvirus*) including one new species(*Caudovirales: Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Adriaenssens EM, Tolstoy I, Kropinski AM, Barylski J | [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk);  [tolstoy@ncbi.nlm.nih.gov](mailto:tolstoy@ncbi.nlm.nih.gov);  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com);  [Jakub.Barylski@gmail.com](mailto:Jakub.Barylski@gmail.com) |

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

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| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  Adam Mickiewicz University, Poland [JB] |

**Corresponding author**

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| Jakub Barylski |

**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)** |
| Jarrellvirus | Kenneth F. Jarrell | Y |
|  |  |  |
|  |  |  |

**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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| 2020.078B.R.Jarellvirus.xlsx |

**Abstract**

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| The 2018 Master Species List describes only 21 siphoviruses which infect members of the order Bacillales. These fall into nine different genera. Here we propose a new genus *Jarrellvirus*, containing a single species. |

**Text of proposal:**

| additional material in support of this 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.

**Source of the name of this taxon:** This genus is named in honour of Canadian archaeal specialist Dr. Kenneth F. Jarrell (Emeritus professor, Queen’s University, Kingston, Ontario, Canada) in whose laboratory both the host bacterium and phage BCAJ1 were isolated.

**History:** *Bacillus clarkii* JaD is an obligate alkaliphile isolated from alkaline red mud from bauxite processing waste (Agnew et al. 1995). Phage BCAJ1 was isolated from the same source. It has an isometric head (65 nm between opposite apices) and a long (195 nm) noncontractile tail. A clear plaque mutant of bacteriophage BCJA1, BCJA1c, was sequenced as it routinely grew to a higher titer than the wildtype version of the bacteriophage (Jarrell et al. 1997). Sequencing revealed that phage BCAJ1 is temperate and “The integrase gene of this phage is unique in that it contains a ribosomal slippage site. While this type of translational regulation occurs in the synthesis of transposase, this is the first time that it has been observed in a bacteriophage integrase (Kropinski et al. 2005).

**Reference: A.** Agnew MD, Koval SF, Jarrell KF (1995) Isolation and characterization of novel alkaliphiles from bauxite-processing waste and description of *Bacillus vedderi* sp. nov., a new obligate alkaliphile. Syst Appl Microbiol 18:221–230

**B.** Jarrell KF, Vydykhan T, Lee P, Agnew MD, Thomas NA (1997) Isolation and characterization of bacteriophage BCJA1, a novel temperate bacteriophage active against the alkaliphilic bacterium, *Bacillus clarkii*. Extremophiles 1:199–206. DOI: 10.1007/s007920050034

**C.** Kropinski AM, Hayward M, Agnew MD, Jarrell KF. The genome of BCJA1c: a

bacteriophage active against the alkaliphilic bacterium, *Bacillus clarkii*. Extremophiles. 2005;9(2):99-109. DOI: 10.1007/s00792-004-0425-0

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| BCAJ1c | [NC\_006557.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_006557.1) | [AY616446.1](https://www.ncbi.nlm.nih.gov/nuccore/AY616446.1) | 41.09 | 41.7 | 58 | 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 BCAJ1 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."

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**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.