

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.019B** |  |
| **Short title:** Create one new genus (*Badaztecvirus*) including two species in the (*Caudovirales*: *Podoviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Łobocka M, Moraru C, Barylski J, Tong Y, Kropinski AM | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  lobocka@ibb.waw.pl; liliana.cristina.moraru@uol.de;  Jakub.Barylski@gmail.com;  tong.yigang@gmail.com; Phage.Canada@gmail.com |

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

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, Warsaw, Poland [MŁ] Carl von Ossietzky Universität Oldenburg, Germany [CM]  Adam Mickiewicz University, Poland [JB]  Beijing University of Chemical Technology, China [YT]  University of Guelph, Canada [AMK] |

**Corresponding author**

|  |
| --- |
| Andrew Kropinski |

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

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

**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 | June 2020 |
| 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**

|  |
| --- |
| 2020.019B.R.Badaztecvirus.xlsx |

**Abstract**

|  |
| --- |
| 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 actinobacteria from the genus *Bifidobacterium*. This proposal places them in the family *Podoviridae*, though at some point in the future they will be reclassified as a higher order. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **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 Bifidobacterium phage BadAztec

**History:** These two phages are part of the honey bee gut virome and were isolated in Switzerland using *Bifidobacterium asteroides* as the host bacterium.

**Specific Reference:** Bonilla-Rosso G, Steiner T, Wichmann F, Bexkens E, Engel P. Honey bees harbor a diverse gut virome engaging in nested strain-level interactions with the microbiota. Proc Natl Acad Sci U S A. 2020;117(13):7355‐7362. doi:10.1073/pnas.2000228117

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall % DNA sequence identity (\*\*) | Overall % homologous proteins (\*\*\*) |
| BadAztec1 |  | [MT006233.1](about:blank) | 18.64 | 48.8 | 23 | 0 | 100 | 100 |
| BadAargau2 |  | [MT006240.1](about:blank) | 18.9 | 50.4 | 23 | 0 | 74.4 | 95.6 |

**N.BBifidobacterium phages BadAztec 2 [MT006239.1] and BadAztec4 [MT006238.1] should be consider strains of the type species in this genus.**

**(\*) determined using tRNAscan-SE [1]**

**(\*) determined using VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [3]**

**BLASTN homologs:** BLASTN analysis reveals that the closest relative is Bacteriophage sp. isolate 152 [4-6]. It shares 28.4 % DNA sequence identity with BadAztec.

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; 1) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains.



**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Bifidobacterium phage BadAztec1 and related phages with phylogeny.fr in “one click” mode [7]. "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 [8]) 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**

1: 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.

2: Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. [http://kronos.icbm.uni-oldenburg.de/viridic/](about:blank)

3: 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.

4: 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.

5: 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.

6: 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.

7: 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.

8: 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.

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.