

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

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| **Code assigned:** | **to be assigned by ICTV officers** |  |
| **Short title:** To create two single-species genera, *Athenavirus* and *Theosmithvirus* [*Caudoviricetes*] | | |
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| Andrew M. Kropinski |

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

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| Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

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

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.008B.N.v1.Athenavirus\_Theosmithvirus\_2ng.xlsx |

**Abstract**

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| --- |
| We have created two new genera for novel Bacillus siphoviruses – *Athenavirus* and *Theosmithvirus* |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree [10]. | |

**Supporting evidence**

**Proposals Data:**

1. **To create a single species genus, *Athenavirus***
2. **To create a single species genus, *Theosmithvirus***

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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Baci = Bacillus; Sten = Stenotrophomonas

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**![A screenshot of a computer

Description automatically generated with low confidence]()**

**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red lines and stars**.

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Description automatically generated**

**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the large subunit terminase proteins from these 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.”

**Taxonomic Proposals:**

1. **To create a single species genus, *Athenavirus***

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first isolate of its type, Bacillus phage vB\_BanS\_Athena

**Historical aspects:** Temperate siphophage vB\_BanS\_Athena was isolated from sewage against Bacillus anthracis.

**Genome summary: .**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Bacillus phage vB\_BanS\_Athena | [OK500002.1](https://www.ncbi.nlm.nih.gov/nuccore/OK500002.1) | 37.37 | 35.3 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109261/1760526|Bacillus phage vB_BanS_Athena/viral segment/) | 100 | 100 |

**Conclusion:** A genus comprised of a single species is proposedon the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3).

1. **To create a single species genus, *Theosmithvirus***

**Origin of the name of this taxon:** This taxon was named in honour of American pioneer epidemiologist, bacteriologist, and pathologist, Theobald Smith (b. 1859, Albany, N.Y., d. 1934, New York, N.Y). Received his M.D. from Albany Medical College in 1883. From 1886 - 1895 he taught at what is now George Washington University and created thss university's Department of Bacteriology. In 1895, Smith took up the position of professor of comparative pathology at Harvard University where he remained until 1915. At the end of his illustrious career he was Director of the Department of Animal Pathology at the Rockefeller Institute for Medical Research. We have chosen to honour him because Bacillus phage 0105phi7-2 was isolated from the King Ranch in Kingsville (Texas), the site of Smith's research on Texas fever.

**Historical aspects:** Temperate siphophage 0105phi7-2 was isolated against Bacillus thuringiensis. Phage 0105phi7-2 is diverse in (1) absence of head-assembly scaffolding via either separate protein or classically-sized, head protein-embedded peptide, (2) producing partially condensed, head-expelled DNA, and (3) having a surface relatively poor in AGE-detected net negative charges, which is possibly correlated with observed low murine blood persistence.

**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Bacillus phage 0105phi7-2 | OQ317942.1 | 52.63 | 36.0 | 85 | 100 | 100 |

**Conclusion:** A genus comprised of a single species is proposedon the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3).

**References**

1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870

2. 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.

3. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. http://kronos.icbm.uni-oldenburg.de/viridic/

4. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. https://www.genome.jp/viptree/

5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423

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. Davis P, Seto D, Mahadevan P. CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. Viruses. 2022 Nov 16;14(11):2534. doi: 10.3390/v14112534. PMID: 36423143; PMCID: PMC9693508.

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.

10. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.