

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.159B** |  |
| **Short title:** Create four new species in the genus *Samwavirus* (*Caudovirales*: *Siphoviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Turner D, Kropinski AM | [evelien.adriaenssens@quadram.ac.uk](about:blank);  [tolstoy@ncbi.nlm.nih.gov](about:blank);  [dann2.turner@uwe.ac.uk](about:blank);  [Phage.Canada@gmail.com](about:blank) |

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

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

**Corresponding author**

|  |
| --- |
| Andrew M. 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**

|  |
| --- |
| 2020.159B.R.Samwavirus\_new species.xlsx |

**Abstract**

|  |
| --- |
| Here, we add four new species to the *Corynebacterium*-infecting phage genus *Samwavirus*. |

**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 first isolated phage of this type, Corynebacterium phage SamW.

**History:**  The genus *Samwavirus* was established by Taxonomy Proposal 2019.027B.A.v1.Samwavirus

**Reference:** 2019.027B.A.v1.Samwavirus

**VIRIDIC analysis:** isolates boxed in black are to be considered strains

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage Name** | **Coryne\_phg\_IME1320\_01** | **Coryne\_phg\_Bran** | **Coryne\_phg\_StAB** | **Coryne\_phg\_Stiles** | **Coryne\_phg\_Adelaide** | **Coryne\_phg\_Dina** | **Coryne\_phg\_Lederberg** | **Coryne\_phg\_SamW** | **Coryne\_phg\_Troy** |  |
| **Coryne\_phg\_IME1320\_01** | 100.0 | 3.7 | 15.1 | 17.6 | 15.9 | 15.7 | 15.8 | 15.9 | 15.9 |  |
| **Coryne\_phg\_Bran** | 3.7 | 100.0 | 54.1 | 55.4 | 67.4 | 68.1 | 60.3 | 61.7 | 61.6 |  |
| **Coryne\_phg\_StAB** | 15.1 | 54.1 | 100.0 | 81.1 | 74.4 | 75.9 | 78.0 | 78.0 | 78.0 |  |
| **Coryne\_phg\_Stiles** | 17.6 | 55.4 | 81.1 | 100.0 | 75.8 | 73.2 | 75.0 | 75.5 | 75.5 |  |
| **Coryne\_phg\_Adelaide** | 15.9 | 67.4 | 74.4 | 75.8 | 100.0 | 83.8 | 80.9 | 81.6 | 81.6 |  |
| **Coryne\_phg\_Dina** | 15.7 | 68.1 | 75.9 | 73.2 | 83.8 | 100.0 | 87.3 | 89.4 | 89.4 |  |
| **Coryne\_phg\_Lederberg** | 15.8 | 60.3 | 78.0 | 75.0 | 80.9 | 87.3 | 100.0 | 97.4 | 97.4 |  |
| **Coryne\_phg\_SamW** | 15.9 | 61.7 | 78.0 | 75.5 | 81.6 | 89.4 | 97.4 | 100.0 | 100.0 |  |
| **Coryne\_phg\_Troy** | 15.9 | 61.6 | 78.0 | 75.5 | 81.6 | 89.4 | 97.4 | 100.0 | 100.0 |  |
|  |  |  |  |  |  |  |  |  |  |  |

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| SamW | [NC\_048069.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048069.1) | [MH727560.1](https://www.ncbi.nlm.nih.gov/nuccore/MH727560.1) | 44.61 | 68.1 | [60](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72679/408807|Corynebacterium phage SamW/viral segment/) | 1 | 100 | 100 |
| Stiles | NC\_048789.1 | [MK977710.1](about:blank) | 42.85 | 67.7 | 54 | 1 | 75.5 | 75.0 |
| StAB | [NC\_048780.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048780.1) | [MK937613.1](about:blank) | 45.75 | 67.9 | 61 | 1 | 78.0 | 75.0 |
| Dina | NC\_048787.1 | [MK977706.1](about:blank) | 44.38 | 68.0 | 63 | 1 | 89.4 | 85.0 |
| Adelaide | NC\_048791.1 | [MK977715.1](about:blank) | 44.1 | 68.0 | 57 | 1 | 81.6 | 81.7 |

**\*\* Determined using VIRIDIC [10]**

**\*\*\* Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[6]**

**N.B. Corynebacterium phages Troy [**[MH926061.1](about:blank)] **and Lederberg [**[MK977712.1](about:blank)] **should be considered strains of *Corynebacterium virus SamW*.**

**BLASTN homologs:** The next closely related phage to SamW is *Corynebacterium* phage Bran [1-3]. They share 61.7% overall genome sequence identity (intergenomic distance). While this is sufficient to crease a subfamily, we do not choose to do so at this time. Please note that the Actinobacteriophage Database lumps all these phages into Cluster EP.

**Electron micrograph:** Electron micrograph of negatively stained *Corynebacterium* phage Stiles ([https://phagesdb.org/phages/Stiles/](about:blank)). 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.

**A picture containing sitting, person, holding, person

Description automatically generated**

**Phylogeny:** The phylogenetic tree was constructed using the terminase protein of SamW 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."

1. **TerL protein  
     
   ![A screenshot of a cell phone

   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.
10. 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.