

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

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| --- | --- | --- |
| **Code assigned:** | **2021.078B** |  |
| **Short title:** Create eleven new genera including 19 new species (*Caudoviricetes*) | | |
|  | | |

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

|  |  |
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| Andrew M. Kropinski |

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

|  |
| --- |
| Actinobacteriophages Study Group, Bacterial Viruses Subcommittee |

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

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|  |

**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)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

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

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

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| --- |
| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

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

**Name of accompanying Excel module**

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| --- |
| 2021.078B.R.Siphoviridae\_new\_genera |

**Abstract**

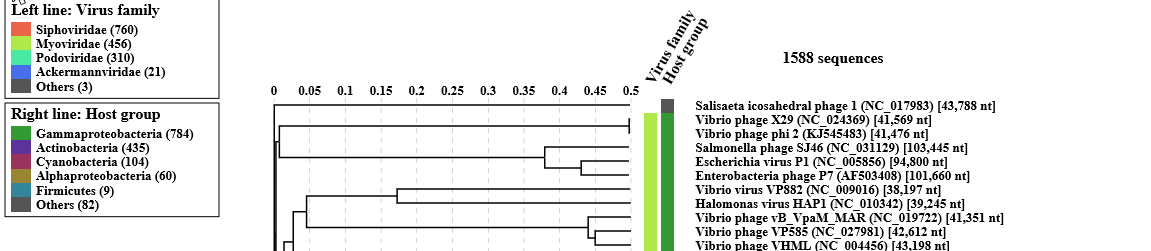
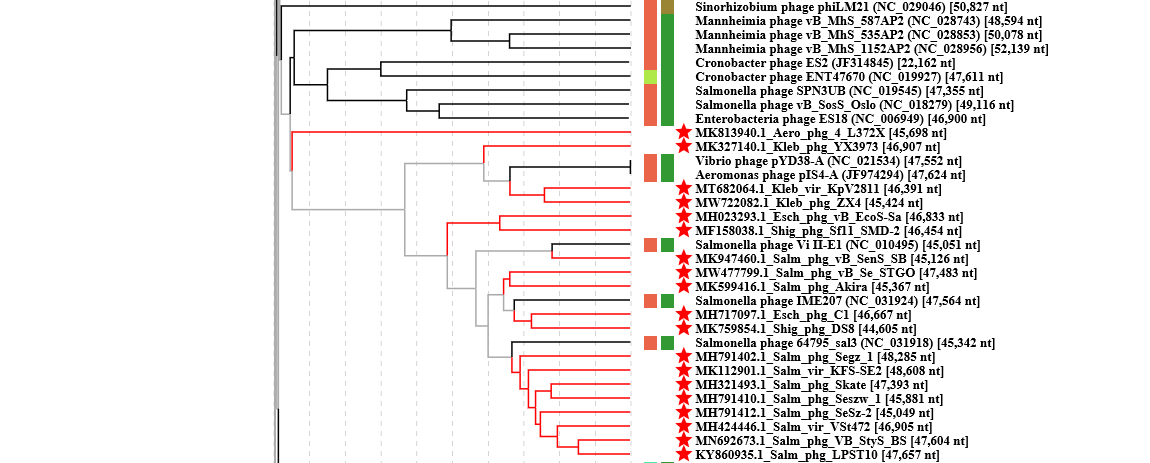
|  |
| --- |
| The following phages are all related to one another, and to a group of Aeromonas, Vibrio and Klebsiella viruses in a complex, and not readily resolvable manner. Rather than propose a subfamily at this time we have decided to generate 11 new genera. The current members possess, on average, genomes of 46.69 kb (46.0 mol%G+C) and encode for 82 proteins and 0.4 (0 - 2) tRNA. Using CoreGenes 5.0 (https://coregenes.ngrok.io/) revealed 18 homologs shared by the current group of phages (22%). These homologs included: tail length tape measure protein, major tail protein, class II holin, portal protein and ATP-dependent helicase. At the DNA level these phages share at least 42.9% DNA similarity. |

**Text of proposal**

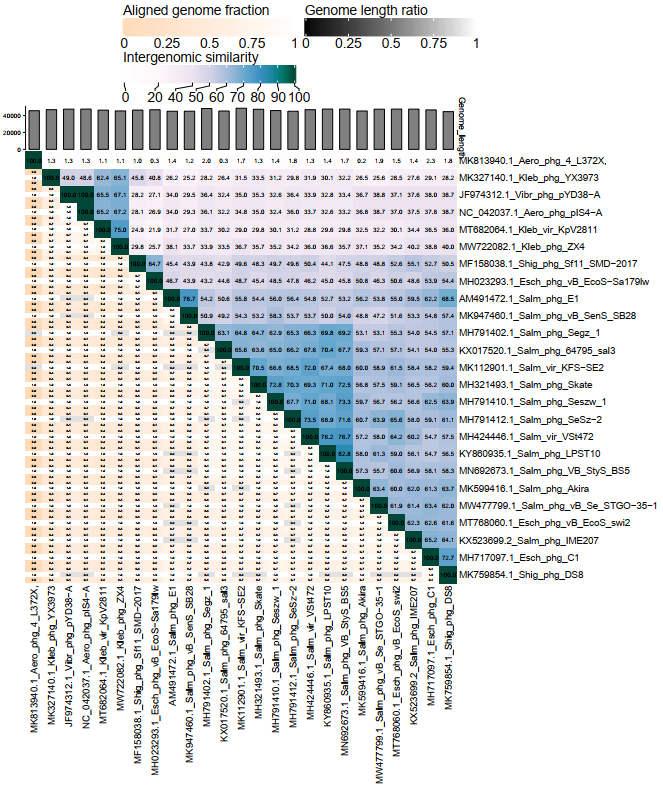
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic 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. [9] | |

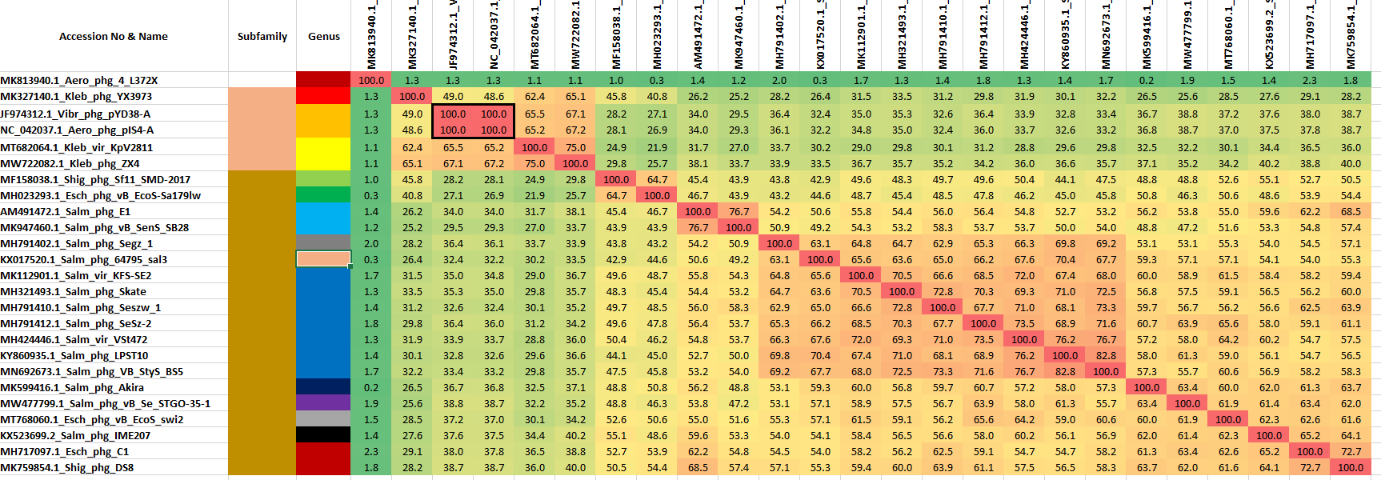
**Supporting evidence**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The phages of interest are indicated with **red lines**. The new subfamily is delineated with a blue bar.

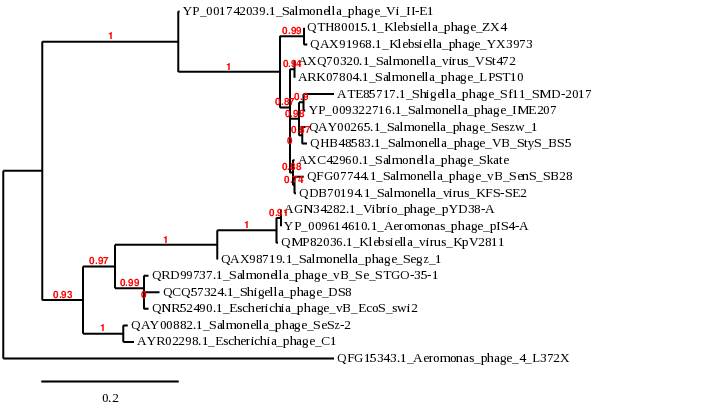
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**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. In the second heat map the strains are indicates in a black box.





**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of these phages with phylogeny.fr in “one click” mode [5]. "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 [6] for details."

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**Proposals:**

1. **To create a new genus, *Cedarrivervirus,* with a single species**
2. **To create a new genus, *Buchananvirus*, with a single species**
3. **To create a new genus, *Macdonaldcampvirus,* with two species**
4. **To create a new genus, *Skatevirus*, with seven (7) species**
5. **To create a new genus, *Akiravirus*, with a single species**
6. **To create a new genus, *Caminolopintovirus*, with a single species**
7. **To create a new genus, *Swiduovirus*, with a single species**
8. **To create a new genus, *Shuimuvirus*, with a single species**
9. **To create a new genus, *Deseoctovirus*, with two (2) species**
10. **To create a new genus, *Segzyvirus* with a single species**
11. **To create a new genus, *Saltrevirus* with a single species**
12. **To create a new genus, *Cedarrivervirus,* with a single species**

**Source of the name of this taxon:** This taxon is named after Red Cedar River a tributary of the Grand River in central Michigan in the United States which was the source for Shigella phage Sf11 SMD-2017.

**History:** This lytic siphovirus was isolated from Red Cedar River sediment on Shigella flexneri

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Shigella phage Sf11 SMD-2017 | [MF158038.1](about:blank) | 46.45 | 46.0 | [80](about:blank) | 2 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Buchananvirus*, with a single species**

**Source of the name of this taxon:** This taxon is named after Buchanan Street in Albany, CA where in the Produce Safety and Microbiology, USDA ARS the first phages its type was isolated.

**History:** Lytic siphovirus Escherichia coli phage, vB\_EcoS Sa179lw, was isolated from surface water collected in a produce-growing area.

**Electron micrograph:** None available

**Specific Reference:** Liao YT, Liu F, Sun X, Li RW, Wu VCH. Complete Genome Sequence of Escherichia coli Phage vB\_EcoS Sa179lw, Isolated from Surface Water in a Produce-Growing Area in Northern California. Genome Announc. 2018 Jul 5;6(27):e00337-18. doi: 10.1128/genomeA.00337-18. PMID: 29976601; PMCID: PMC6033975.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Escherichia phage vB\_EcoS Sa179lw | [MH023293.1](about:blank) | 46.83 | 46.0 | [86](about:blank) | 0 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Macdonaldcampvirus,* with two species**

**Source of the name of this taxon:** This taxon is named after the Macdonald Campus of McGill University (QC, Canada) where phage vB\_SenS\_SB28 was isolated.

**History:** This lytic siphovirus was isolated from sewage against Salmonella enterica subsp. enterica serovar Typhi T42 DEF 472.

**Electron micrograph:** None available

**Specific Reference:** Pickard D, Thomson NR, Baker S, Wain J, Pardo M, Goulding D, Hamlin N, Choudhary J, Threfall J, Dougan G. Molecular characterization of the Salmonella enterica serovar Typhi Vi-typing bacteriophage E1. J Bacteriol. 2008 Apr;190(7):2580-7. doi: 10.1128/JB.01654-07. Epub 2008 Jan 11. PMID: 18192390; PMCID: PMC2293211.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage vB\_SenS\_SB28 | [MK947460.1](about:blank) | 45.13 | 46.2 | [73](about:blank) | 0 | 100 | 100 |
| Salmonella phage Vi II-E1 | [AM491472.1](about:blank) | 45.05 | 46.1 | [51](about:blank) | 0 | 76.7 | 58.9 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Skatevirus*, with seven (7) species**

**Source of the name of this taxon:** This taxon is named after Salmonella phage Skate.

**History:** Lytic siphovirus Skate was isolated from soil in the cattle holding pen of a cattle harvesting facility in Michigan in August 2016 using S. Typhimurium strain LT2 [Rohren M et al. 2019]. The bulk of the remaining phages were isolated from China, with additional isolated from Italy, South Korea, and Russia.

**Electron micrograph:** None available

**Specific Reference:** Choi IY, Lee C, Song WK, Jang SJ, Park MK. Lytic KFS-SE2 phage as a novel bio-receptor for Salmonella Enteritidis detection. J Microbiol. 2019 Feb;57(2):170-179. doi: 10.1007/s12275-019-8610-0. Epub 2019 Jan 31. PMID: 30706346.

Rohren M, Xie Y, O'Leary C, Kongari R, Gill J, Liu M. Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Siphophage Skate. Microbiol Resour Announc. 2019 Jul 3;8(27):e00541-19. doi: 10.1128/MRA.00541-19. PMID: 31270198; PMCID: PMC6606912.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage Skate | [MH321493.1](about:blank) | 47.39 | 45.8 | [90](about:blank) | 1 | 100 | 100 |
| Salmonella virus KFS-SE2 | [MK112901.1](about:blank) | 48.61 | 45.8 | [85](about:blank) | 2 | 70.5 | 74.4 |
| Salmonella phage Seszw\_1 | [MH791410.1](about:blank) | 45.88 | 45.9 | [72](about:blank) | 0 | 72.8 | 71.1 |
| Salmonella phage SeSz-2 | [MH791412.1](about:blank) | 45.05 | 46.0 | [78](about:blank) | 0 | 70.3 | 67.8 |
| Salmonella virus VSt472 | [MH424446.1](about:blank) | 46.91 | 45.6 | [82](about:blank) | 0 | 69.3 | 76.7 |
| Salmonella phage LPST10 | [KY860935.1](about:blank) | 47.66 | 45.5 | [87](about:blank) | 0 | 71.0 | 77.8 |
| Salmonella phage VB\_StyS\_BS5 | [MN692673.1](about:blank) | 47.6 | 45.5 | [83](about:blank) | 0 | 72.5 | 76.7 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Akiravirus*, with a single species**

**Source of the name of this taxon:** This taxon is named after the first phage of its type, Salmonella phage Akira

**History:** This lytic siphovirus was isolated from wastewater against Salmonella enterica subsp. enterica servar Enteritidis PT1

**Electron micrograph:** None available

**Specific Reference:** Olsen,N.S., Hendriksen,N.B., Hansen,L.H. and Kot,W. A New High-Throughput Screening Method for Phages: Enabling Crude Isolation and Fast Identification of Diverse Phages with Therapeutic Potential. Phage (New Rochelle) 1 (3), 137-148 (2020)

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage Akira | [MK599416.1](about:blank) | 45.37 | 46.0 | [85](about:blank) | 1 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Caminolopintovirus*, with a single species**

**Source of the name of this taxon:** This taxon is named after the street address of the Universidad Andres Bello where the first phage of its type, Salmonella phage vB\_Se\_STGO-35-1, was isolated.

**History:** This lytic siphovirus was isolated from fecal material against Salmonella enterica subsp. enterica serovar Enteritidis.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage vB\_Se\_STGO-35-1 | [MW477799.1](about:blank) | 47.48 | 46.5 | [88](about:blank) | 1 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Swiduovirus*, with a single species**

**Source of the name of this taxon:** This taxon’s name is derived from that of the phage’s name Escherichia phage vB\_EcoS\_swi2.

**History:** This lytic siphovirus was isolated in the College of Veterinary Medicine, Qingdao Agricultural University, China.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Escherichia phage vB\_EcoS\_swi2 | [MT768060.1](about:blank) | 47.61 | 46.3 | [88](about:blank) | 1 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

**8. To create a new genus, *Shuimuvirus*, with a single species**

**Source of the name of this taxon:** This taxon is named after Shuimu, is a water demon, spirit or witch of Buddhist and Taoist origin in Chinese mythology [Wiki].

**History:** This lytic siphovirus was isolated from sewage.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage IME207 | [KX523699.2](about:blank) | 47.56 | 46.4 | [94](about:blank) | 0 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Deseoctovirus*, with two (2) species**

**Source of the name of this taxon:** This name of this taxon is derived from Shigella phage DS8

**History:** This lytic siphovirus was isolated at Kunming University Of Science And Technology, China against Shigella flexneri strain ATCC 29903.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Shigella phage DS8 | [MK759854.1](about:blank) | 44.61 | 46.5 | [79](about:blank) | 0 | 100 | 100 |
| Escherichia phage C1 | [MH717097.1](about:blank) | 46.67 | 46.6 | [76](about:blank) | 0 | 72.7 | 74.7 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Segzyvirus* with a single species**

**Source of the name of this taxon:** This taxon’s name is derived from that of Salmonella phage Segz\_1

**History:** This lytic siphovirus was isolated from seawater by the staff at Institute of Synthetic Biology, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, Shenzhen, China

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage Segz\_1 | [MH791402.1](https://www.ncbi.nlm.nih.gov/nuccore/MH791402.1) | 48.29 | 46.4 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75892/446550%7CSalmonella%20phage%20Segz_1/viral%20segment/) | 0 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

1. **To create a new genus, *Saltrevirus* with a single species**

**Source of the name of this taxon:** This taxon’s name is derived from that of Salmonella phage 64795\_sal3

**History:** This lytic siphovirus was isolated from Capua (Italy) water buffalo faeces on Salmonella enterica subsp. Typhimurium by the staff of the Animal Health, Istituto Zooprofilattico Sperimentale del Mezzogiorno, Portici, Italy in 2014.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage 64795\_sal3 | [KX017520.1](https://www.ncbi.nlm.nih.gov/nuccore/KX017520.1) | 45.34 | 45.6 | [74](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/50468/462932%7CSalmonella%20phage%2064795_sal3/viral%20segment/) | 0 | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

**References:**

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2: 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

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://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)

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5: 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.

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