

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

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| **Code assigned:** | ***2023.068B*** |  |
| **Short title:** To create three genera of *Serratia* phages - *Seretavirus, Serbinvirus* and *Otakuvirus* [*Caudoviricetes*] | | |
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**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** |
|  |  |  |  |
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**Authority to use the name of a living person**

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

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

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| --- | --- |
| 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**

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| 2023.068B.N.v1.Caudoviricetes\_Serratia\_3ng.xlsx |

**Abstract**

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| We have created three new genera of Serratia siphoviruses – *Seretavirus, Serbinvirus* and *Otakuvirus* |

**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**

1. **Create a new single species genus, *Seretavirus***
2. **Create a new genus, *Serbinvirus*, with three species**
3. **Create a new genus, *Otakuvirus*, with two species**

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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; vir = virus; Serr = Serratia; Salm = Salmonella; Kleb = Klebsiella

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

1. **Create a new single species genus, *Seretavirus***

**Origin of the name of this taxon:** The name of this taxon is derived from **Ser**ratia phage **Eta**.

**Historical aspects:** This temperate siphophage was isolated in Germany (1966) from supernatant of an overnight culture of Serratia marcescens ES (now lost). While the older scientific literature suggested the presence of a modified guanine residue, none was found on re-examination [Denyes et al. 2014]

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Serratia phage Eta | [KC460990.1](https://www.ncbi.nlm.nih.gov/nuccore/KC460990.1) | 42.72 | 49.9 | [69](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/18300/460112|Serratia phage Eta/viral segment Unknown/) | 100.0 | 100 |

**Conclusion:** A genus comprised of a single species is proposed on the basis of DNA (Fig. 1) and protein (Fig. 2).

**Specific reference:** Denyes JM, Krell PJ, Manderville RA, Ackermann HW, She YM, Kropinski AM. The genome and proteome of Serratia bacteriophage η which forms unstable lysogens. Virol J. 2014 Jan 16;11:6. doi: 10.1186/1743-422X-11-6. PMID: 24433577; PMCID: PMC3918226.

1. **Create a new genus, *Serbinvirus*, with three species**

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Serratia phage Serbin.

**Historical aspects:** Lytic siphophage Serbin was isolated using a Serratia marcescens strain from a pond water sample collected from College Station, Texas (USA) [Williams et al. 2019]. The other two were isolated from raw sewage at Brigham Young University, Provo, UT (USA).

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Serratia phage Serbin | [MK608336.1](https://www.ncbi.nlm.nih.gov/nuccore/MK608336.1) | 42.88 | 51.6 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/80008/559653|Serratia phage Serbin/viral segment/) | 100.0 | 100 |
| Serratia phage vB\_SmaS\_Tlacuache | [OK499995.1](https://www.ncbi.nlm.nih.gov/nuccore/OK499995.1) | 42.68 | 51.6 | [60](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109159/1760424|Serratia phage vB_SmaS_Tlacuache/viral segment/) | 85.8 | 86.4 |
| Serratia phage vB\_SmaS\_Opt-155 | [OL539452.1](https://www.ncbi.nlm.nih.gov/nuccore/OL539452.1) | 42.79 | 51.9 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109273/1760538|Serratia phage vB_SmaS_Opt-155/viral segment/) | 87.7 | 92.4 |

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

**(\*\*) determined using CoreGenes 3.5 [6]**

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive genus.

**Specific reference:** Williams EA, Hopson H, Rodriguez A, Kongari R, Bonasera R, Hernandez-Morales AC, Liu M. Complete Genome Sequence of Serratia marcescens Siphophage Serbin. Microbiol Resour Announc. 2019 May 9;8(19):e00422-19. doi: 10.1128/MRA.00422-19. PMID: 31072887; PMCID: PMC6509536.

1. **Create a new genus, *Otakuvirus*, with two species**

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Serratia phage vB\_SmaM-Otaku.

**Historical aspects:** Lytic Serratia siphophage Tsm2 was isolated from wastewater at Taras Shevchenko National University of Kyiv (Ukraine), while Serratia phage vB\_SmaM-Otaku was isolated from sewage at Georg-August University Goettingen, Germany. Both of these viruses are related to other members of the *Guernseyvirinae* but, at this time, we do not intend to add it to the proposal on updating this taxon.

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Serratia phage vB\_SmaM-Otaku | [ON087563.1](https://www.ncbi.nlm.nih.gov/nuccore/ON087563.1) | 39.86 | 57.4 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/113800/1841938|Serratia phage vB_SmaM-Otaku/viral segment/) | 100.0 | 100 |
| Serratia phage Tsm2 | [MW082583.1](https://www.ncbi.nlm.nih.gov/nuccore/MW082583.1) | 39.8 | 57.0 | [60](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97092/1501070|Serratia phage Tsm2/viral segment/) | 78.3 | 83.9 |

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

**(\*\*) determined using CoreGenes 3.5 [6]**

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive genus.

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