

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

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| **Code assigned:** | ***2023.056B*** |  |
| **Short title:** Create two genera of Serratia phages - *Rovertvirus* and *Bonzeevirus* [*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** |
|  |  |  |  |
|  |  |  |  |

**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 |

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

|  |
| --- |
| 2023.056B.N.v1.Caudoviricetes\_Serratia\_2ng.xlsx |

**Abstract**

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| We have created two new genera of lytic Serratia siphoviruses – *Rovertvirus* and *Bonzeevirus* based on comparative genomics and phylogenetic analyses. |

**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, *Rovertvirus***
2. **Create a new genus, *Bonzeevirus*, with four 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; Serr = Serratia; Dick = Dickeya

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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) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red lines and stars**.

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

**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\_SmaS\_Rovert.

**Historical aspects:** This lytic siphophage was isolated from raw sewage against Serratia marcescens by Naomi Marshall (Microbiology and Molecular Biology, Brigham Young University, Provo, UT USA).

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Serratia phage vB\_SmaS\_Rovert | [MW021761.1](https://www.ncbi.nlm.nih.gov/nuccore/MW021761.1) | 38.61 | 42.3 | [58](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97653/1533078|Serratia phage vB_SmaS_Rovert/viral segment/) | 100.0 | 100 |

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

1. **Create a new genus, *Bonzeevirus*, with four 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\_SmaS\_Bonzee.

**Historical aspects:** This lytic siphophage was isolated from raw sewage against Serratia marcescens by Carter Jones (Microbiology and Molecular Biology, Brigham Young University, Provo, UT USA).

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Serratia phage vB\_SmaS\_Bonzee | [OM135608.1](https://www.ncbi.nlm.nih.gov/nuccore/OM135608.1) | 42.05 | 46.1 | [69](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/110789/1791157|Serratia phage vB_SmaS_Bonzee/viral segment/) | 100.0 | 100 |
| Serratia phage vB\_SmaS\_Stoker | [OL539464.1](https://www.ncbi.nlm.nih.gov/nuccore/OL539464.1) | 41.8 | 46.4 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109282/1760547|Serratia phage vB_SmaS_Stoker/viral segment/) | 94.3 | 91.3 |
| Serratia phage vB\_SmaS\_Ulliraptor | [OL539442.1](https://www.ncbi.nlm.nih.gov/nuccore/OL539442.1) | 42.05 | 46.0 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109266/1760531|Serratia phage vB_SmaS_Ulliraptor/viral segment/) | 83.5 | 88.4 |
| Serratia phage vB\_SmaS\_Bigdog | [MW021763.1](https://www.ncbi.nlm.nih.gov/nuccore/MW021763.1) | 42.5 | 45.7 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97654/1533079|Serratia phage vB_SmaS_Bigdog/viral segment/) | 84.2 | 85.5 |

**(\*) 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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