

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

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| **Code assigned:** | ***2022.012B*** |  |
| **Short title:** **Create a new subfamily (*Beaumontvirinae*) containing three genera (*Bixiavirus, Salvavirus* and *Siaravirus*) (*Caudiviricetes*).** | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee, 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 2022 |
| 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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| 2022.012B.N.v1.Beaumontvirinae\_nsf.xlsx |

**Abstract**

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| Five lytic Stenotrophomonas siphoviruses have been assigned to three genera in a new subfamily. The overall characteristics of this subfamily are: 61.6 kb (56.3 mol%G+C) encoding 100 proteins and 1-3 tRNA. The overall DNA sequence similarity in 41%. |

**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] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **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. [8]  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny. [8] | |

**Supporting evidence**

**Proposal A: To create a new genus, *Salvavirus* with a single species**

**Origin of the name of this taxon:** This taxon is named after Stenotrophomonas phage Salva

**Historical aspects:** This lytic siphophage was isolated against Stenotrophomonas maltophilia from US soil. Its genome contains 3973 bp direct terminal repeats.

**Electron micrograph:** N/A

**Genome summary: N.B. it is closely related to phage Siara, but they are sufficiently different to be considered members of different genera**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Stenotrophomonas phage Salva | [MW393850.1](https://www.ncbi.nlm.nih.gov/nuccore/MW393850.1) | 60.79 | 56.4 | [102](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97924/1542160|Stenotrophomonas phage Salva/viral segment/) | 1 | 100 | 100 |
|  |  |  |  |  |  |  |  |
| Stenotrophomonas phage Siara | [MZ326859.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ326859.1) | 61.43 | 56.5 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/106719/1720378|Stenotrophomonas phage Siara/viral segment/) | 3 | 66.8 | 74.5 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**.

  


**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from Iggy and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of the *Beaumontvirinae* are indicated with a **blue rectangle**.

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**Proposal B: To create a new genus, *Siaravirus* with a single species**

**Origin of the name of this taxon:** This taxon is named after Stenotrophomonas phage Siara

**Historical aspects:** This lytic siphophage was isolated against Stenotrophomonas maltophilia from US soil.

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Stenotrophomonas phage Siara | [MZ326859.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ326859.1) | 61.43 | 56.5 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/106719/1720378|Stenotrophomonas phage Siara/viral segment/) | 3 | 100 | 100 |

**Proposal C: To create a new genus, *Bixiavirus* with three species**

**Origin of the name of this taxon:** This taxon is named after the Chinese goddess of fertility and guardian of children and mothers (<https://mythopedia.com/topics/chinese-gods>).

**Historical aspects:** These lytic siphophages were isolated against Stenotrophomonas maltophilia in China.

**Electron micrograph:** N/A

**Genome summary: N.B. their closest relatives are phages Siara and Salva**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Stenotrophomonas phage vB\_SmaS\_BUCT548 | [MN937349.1](https://www.ncbi.nlm.nih.gov/nuccore/MN937349.1) | 62.35 | 56.3 | [102](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92964/917739|Stenotrophomonas phage vB_SmaS_BUCT548/viral segment/) | 1 | 100 | 100 |
| Stenotrophomonas phage BUCT626 | [MZ398241.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ398241.1) | 61.66 | 56.2 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/104896/1671055|Stenotrophomonas phage BUCT626/viral segment/) | 1 | 88.2 | 89.2 |
| Stenotrophomonas phage BUCT627 | [MZ398240.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ398240.1) | 61.86 | 56.3 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/104897/1671056|Stenotrophomonas phage BUCT627/viral segment/) | 2 | 92.9 | 92.2 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal D: To create a new subfamily, *Beaumontvirinae* with three genera**

**Origin of the name of this taxon:** This taxon is named after Beaumont, Texas (USA) were the first phage of its type was isolated.

**Evidence for subfamily relationship:** Nucleotide sequence identity analysis (> 40% pairwise across the membership) and phylogenetic analysis of the TerL protein showed that the three genera were related at the subfamily level (see figures above).

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