

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

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| **Code assigned:** | ***2023.058B*** |  |
| **Short title:** To create one new genus and two species within family *Salasmaviridae (Caudoviricetes)* | | |
|  | | |

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

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

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| *Salasmaviridae, Rountreeviridae, Guelinviridae* Study Group, Bacterial Viruses Subcommittee |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| *Salasmaviridae, Rountreeviridae, Guelinviridae* Study Group | 2 | 0 | 0 |
|  |  |  |  |

**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)** |
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|  |  |  |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | June 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**

|  |
| --- |
| 2023.058B.N.v1.Salasmaviridae\_ng.xlsx |

**Abstract**

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| --- |
| The family *Salasmaviridae* of the Bacillus phage phi-29-like podoviruses is divided into 3 subfamilies which together inlude 24 species grouped in 7 genera. This proposal expands the *Salasmaviridae* family with an additional single species genus and two species. |

**Text of proposal**

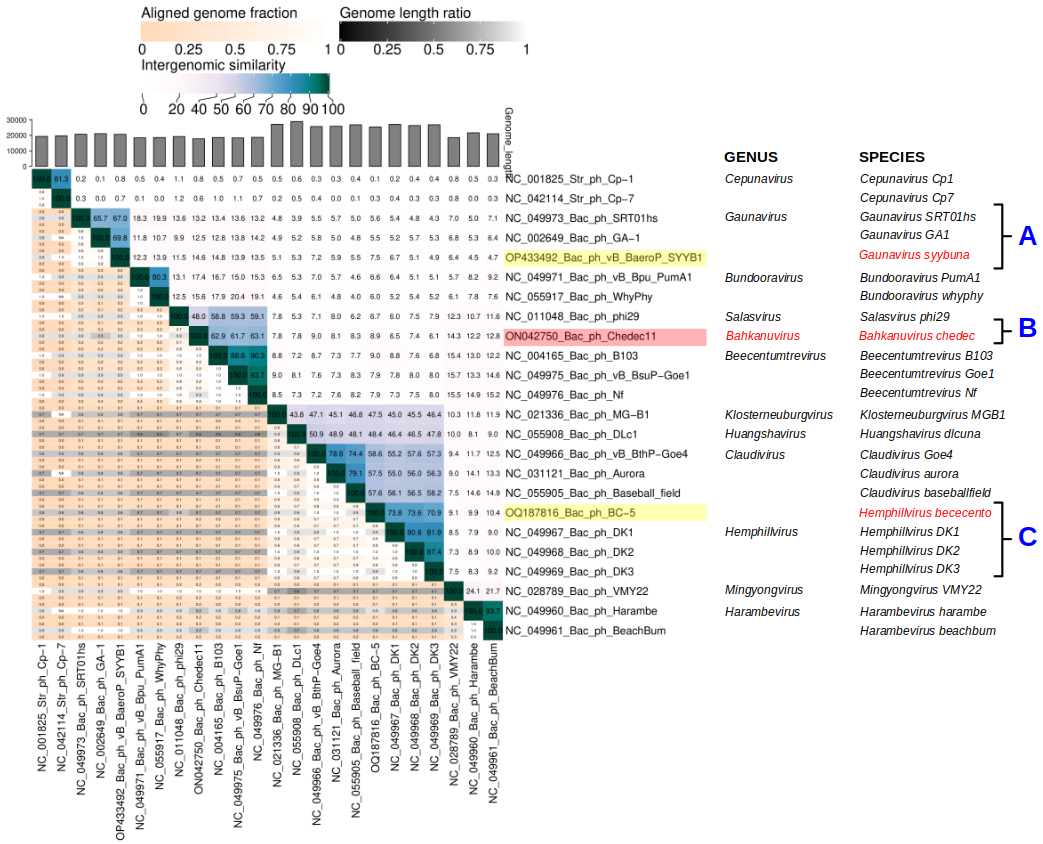
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1,2] – usually calculated using 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]  **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. [10] | |

**Supporting evidence**

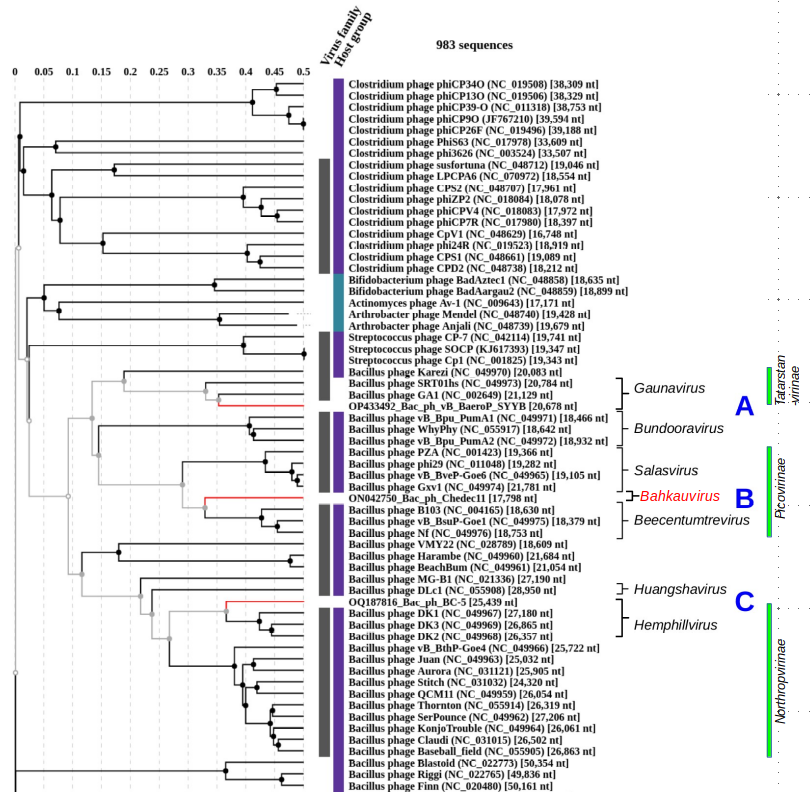
**A. Create a new species *Gaunavirus syybuna* within genus *Gaunavirus***

**B. Create a new genus *Bahkauvirus* with single species *Bahkauvirus chedec***

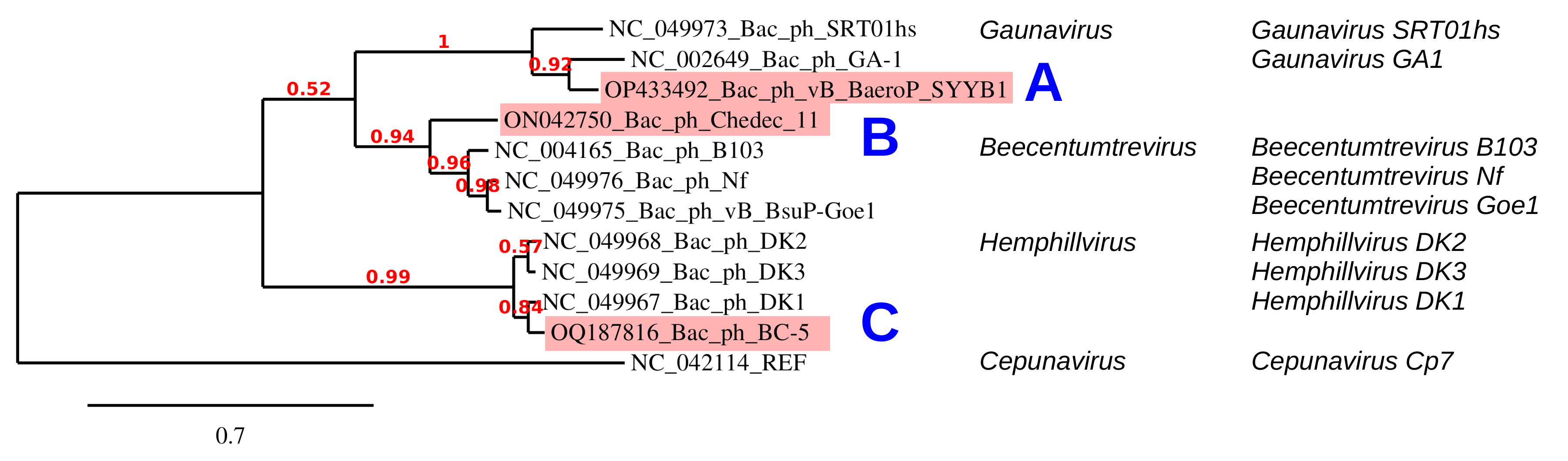
**C. Create a new species *Hemphillvirus bece5* within *Hemphillvirus* genus**

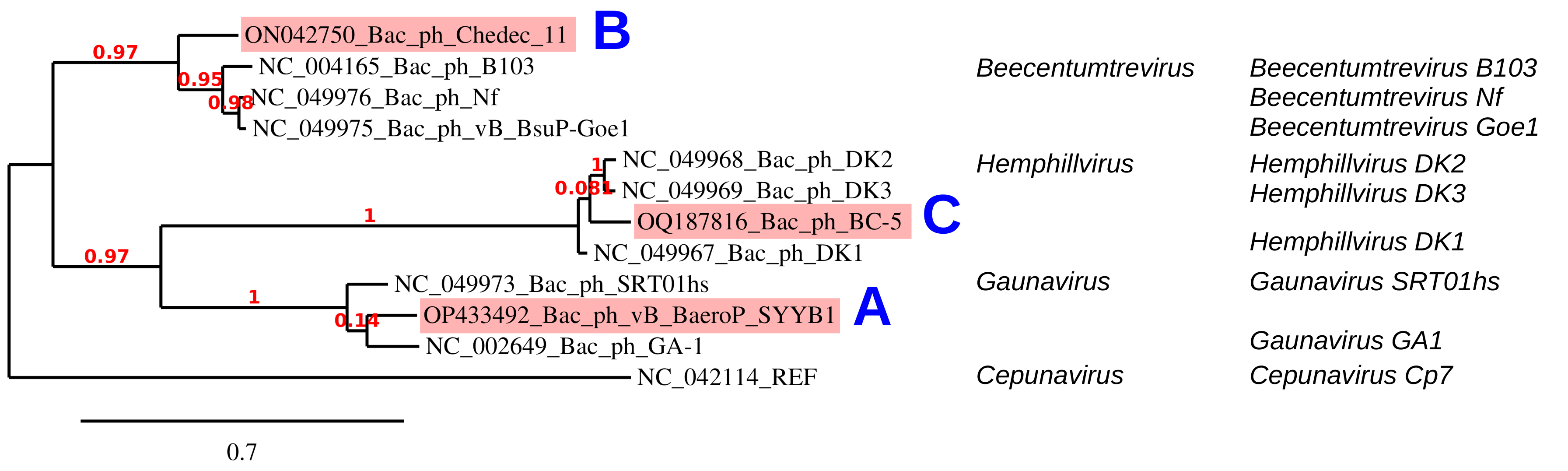
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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The reference strains listed with NCBI Accessions starting with "NC\_" contain additional information about their genera and species. Proposal data concerning expansion of a given genus are marked with capital A, B and C letters shown in blue, phages of new species are highlighted in yellow while phages of new genera are highlited in red. Proposed names of new taxons are in red.

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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.** Relevant genera and subfamilies are indicated on the right to the tree.Proposed name of the new genus is in red.





**Figure 3. Phylogeny:** The phylogenetic trees were constructed using the major capsid (upper) and DNA polymerase (lower) proteins of the new 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. A. Create new species *Gaunavirus* *syybuna* within the *Gaunavirus* genus of subfamily *Tatarstanvirinae*

**Origin of the name of this taxon:** The name of this species was derived from the name of its only phage isolate Bacillus phage vB\_BaeroP\_SYYB1

**Historical aspects:** The *Gaunavirus* was established within the Taxonomy Proposal *2020.143B.R.Salasmaviridae*

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Bacillus phage vB\_BaeroP\_SYYB1 | OP433492.1 | 20.68 | 35.1 | 33 | 69.8 | 81.8 |

(\*) determined using VIRIDIC [3], (\*\*) determined using CoreGenes 3.5 [6]

and compared with the most similar known phage *Gaunavirus GA1* (NC\_002649.1)

1. B. Create new genus *Bahkauvirus* with single species *Bahkauvirus chedec* within subfamily *Picovirinae*

**Origin of the name of this taxon:** The Bacillus phage Chedec 11 phage was isolated from *Bacillus subtilis* extracted from a sewage sample. Bahkau is a german folklore monster known to lurk near fountains, streams and sewers (https://en.wikipedia.org/wiki/Bahkauv).

**Historical aspects:** The subfamily *Picovirinae* was initially established within the Taxonomy Proposal *2008.011a-gB.V3.Picovirinae* as a part of family *Podoviridae*. It was transferred, with only one of its initial genera (*Salasvirus*) and one new genus *Beecentumtrevirus* to new family *Salasmaviridae* based on Taxonomy Proposal *2020.143B.R.Salasmaviridae*. Here we propose to add one single species genus to this subfamily.

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Bacillus phage Chedec 11 | ON042750.1 | 17.8 | 38.4 | 20 | 63.1 | 95 |

(\*) determined using VIRIDIC [3], (\*\*) determined using CoreGenes 3.5 [6]

and compared with the most similar known phage *Beecentumtrevirus Nf* (NC\_049976.1)

1. C. Create new species *Hemphillvirus bece5* within *Hemphillvirus* genus of *Northropvirinae* subfamily

**Origin of the name of this taxon:** The name of this species is derived from the name of single representative of this genus, Bacillus phage BC-5.

**Historical aspects:** The *Hemphillvirus* genus was established within the Taxonomy Proposal *2020.143B.R.Salasmaviridae* and assigned in the same proposal to the subfamily *Northropvirinae*

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Bacillus phage BC-5 | OQ187816.1 | 25.4 | 30.6 | 41 | 73.8 | 92.7 |

(\*) determined using VIRIDIC [3], (\*\*) determined using CoreGenes 3.5 [6]

and compared with the most similar known phage *Hemphillvirus DK1* (NC\_049967.1)

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