

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

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| **Code assigned:** | ***2023.009B*** |  |
| **Short title:** To create a single species genus *Bauervirus* [*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**

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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**

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

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| 2023.009B.N.v1.Bauervirus\_ng.xlsx |

**Abstract**

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| We have created a new genus, *Bauervirus*, for phages belonging to The Actinobacteriophage Database Cluster FN. Currently it contains a single species, *Bauervirus bauer*. |

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| **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]. | |

**Supporting evidence**

**Proposal Data:**

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

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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; Arth = Arthrobacter; Stre = Streptomyces

**A close-up of a graph

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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**.

**Taxonomic Proposals:**

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

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Arthrobacter phage Bauer

**Historical aspects:** This temperate siphophage was isolated against Arthrobacter globiformis B-2979 from soil by Mackenzie Dunn (University of Wisconsin-River Falls, WI USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 11 nt 3’-cohesive termini (CCCCCCGGCAT). The Actinobacteriophage Database considers this phage to be part of Cluster FN.

A close-up of a microscope

Description automatically generated with low confidence

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Bauer (<https://phagesdb.org/phages/Bauer/>). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Bauer | [OP580516.1](https://www.ncbi.nlm.nih.gov/nuccore/OP580516.1) | 50.45 | 62.9 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/120266/1981398|Arthrobacter phage Bauer/viral segment/) | 1 | 100.0 | 100 |

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

**References**

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