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

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| **Code assigned:** | ***2022.009B*** |  |
| **Short title:** Create a new genus (*Axeltriavirus*) containing one species in the class *Caudoviricetes* | | |
|  | | |

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

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| McCutcheon JG, Lin A, Dennis JJ | jgmccutc@ualberta.ca; alin3@ualberta.ca; jon.dennis@ualberta.ca |

**Author(s) institutional address(es) (optional)**

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| Department of Biological Sciences, University of Alberta [JGM, AL, JJD] |

**Corresponding author**

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| Jaclyn McCutcheon |

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

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| Caudoviricetes Study Group, Bacterial Viruses subcommittee |

**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**

|  |  |
| --- | --- |
| **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 | April 19 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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| 2022.009B.N.v1.Axeltriavirus\_ng.xlsx |

**Abstract**

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| We recently isolated a novel bacteriophage, vB\_SmaS-AXL\_3, with limited nucleotide sequence identity to known phages. We propose the creation of a new genus, *Axeltriavirus*, containing the new species *Axeltriavirus AXL3*, named after this phage. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | Species demarcation criteria: Two phages are assigned to the same species if they are share at least 95% DNA sequence identity over their genomes. This may be calculated by tools such as BLASTn [1] or VIRIDIC [2].  Genus demarcation criteria: Aligning with the Bacterial Viruses Subcommittee recommendations [3], 70% nucleotide identity along the full length of the genome is required for phages to belong within the same genus, calculated in the same way as for the species cut-off.  Source of the genus name: *Axeltriavirus* is derived from the name of the first phage isolated of its type, Stenotrophomonas phage vB\_SmaS-AXL\_3.  History: Isolated from soil by Andrea Lin and characterized by Jaclyn McCutcheon (University of Alberta, Edmonton, Canada) for its ability to lyse *Stenotrophomonas maltophilia*, phage AXL3 is a siphovirus with a B1 morphotype as shown in transmission electron micrographs. AXL3 has a relatively narrow host range, showing evidence of cell lysis on 5/29 clinical *S. maltophilia* isolates tested. This phage forms small, clear plaques with clear borders approximately 0.78mm in diameter and lifestyle analysis suggests that AXL3 is a virulent phage. A one-step growth curve shows AXL3 produces a burst size of approximately 38 virions per cell at 6.5 h. AXL3 was determined to use the type IV pilus as its receptor for host recognition, requiring a functional pilus capable of retraction for infection. Restriction fragment length polymorphism analysis suggests a genome containing modified G and/or C bases. The AXL3 genome is 47,545 bp in length with a GC content of 63.3% and is predicted to encode 65 putative protein-coding genes. No tRNA genes were identified. Only 26/65 CDSs were assigned putative protein functions. vConTACT2 (v0.9.16) analysis classified AXL3 as an outlier genome sharing little similarity to three viral clusters and other outlier phages.  Electron microscopy: Negative stained particle of *S. maltophilia* bacteriophage AXL3 (provided by the authors)    Specific Reference: McCutcheon JG, Lin A, Dennis JJ. Isolation and Characterization of the Novel Bacteriophage AXL3 against *Stenotrophomonas maltophilia*. Int J Mol Sci. 2020 21, 6338. doi:10.3390/ijms21176338 | |

**Supporting evidence**

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) |
| vB\_SmaS-AXL\_3 | MT536174.2 | 47.55 | 63.3 | 65 | 0 | 100 |
| Pseudoxanthomonas phage PW916 | OL960029.1 | 47.76 | 62.6 | 24 | 0 | 81.562 |

**(\*) Determined using VIRIDIC [2]**

Although phage PW916 appears to belong to this genus as a new species as well, the annotation of its genome is incomplete and lacks all genes encoding hypothetical proteins, therefore it would not be a good exemplar phage for a new species.

**Phylogeny:**

Phylogenetic tree constructed using phylogeny.fr in “one-click” mode [4] of the terminase large subunit proteins of phage vB\_SmaS-AXL\_3 and its top ten relatives determine by BLASTn.

Text

Description automatically generated with low confidence

VipTree (<https://www.genome.jp/viptree/>) [5] analysis of AXL3 and related Pseudoxanthomonas phage PW916 against dsDNA phages. Tree shows a subset of phages with SG scores to AXL3 greater than 0.05.

A screenshot of a computer

Description automatically generated with medium confidence

**References**

1. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. J Mol Biol 215:403-410. <https://doi.org/10.1016/S0022-2836(05)80360-2> PMID:2231712.

2. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC-A novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. Viruses. 12:1268. <https://doi.org/10.3390/v12111268>. PMID: 33172115. <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>

3. Turner D, Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy. Viruses 13:506. <https://doi.org/10.3390/v13030506>

4. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res 36(Web Server issue):W465-469. <https://doi.org/10.1093/nar/gkn180>. PMID:18424797.

5. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S (2017) ViPTree: the viral proteomic tree server. Bioinformatics 33:2379-2380. <https://doi.org/10.1093/bioinformatics/btx157>. PMID: 28379287.