

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create new genus, *“Lowersilesiavirus”* with six species (class: *Caudoviricetes*) |
| **Code assigned:**  | 2025.038B.Lowersilesiavirus\_1ng\_6ns |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Initials** | **Affiliation** | **Email address** | **Corresponding author(s)**  |
| Michał J. | Wójcicki | Bacteriophage Laboratory, Department of Phage Therapy, Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Wroclaw, Poland | michal.wojcicki@hirszfeld.pl  | X |
| Martyna A. | Cieślik | Bacteriophage Laboratory, Department of Phage Therapy, Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Wroclaw, Poland | martyna.cieslik@hirszfeld.pl  |  |
| Andrzej | Górski | Bacteriophage Laboratory, Department of Phage Therapy, Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Wroclaw, Poland | andrzej.gorski@hirszfeld.pl  |  |
| Ewa M. | Jończyk-Matysiak | Bacteriophage Laboratory, Department of Phage Therapy, Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Wroclaw, Poland | ewa.jonczyk-matysiak@hirszfeld.pl  | X |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | X |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| *Caudoviricetes Study Group* |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** |  24/03/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** |  |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Taxonomic changes proposed:** |
| Establish new taxon | X | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** |
| **Taxon name** | **Etymology of the term** |
| *“Lowersilesiavirus”* | genus name derived from the geographical region - Lower Silesia (Poland) |
| *“Lowersilesiavirus” Acba3* | species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_3 |
| *“Lowersilesiavirus” Acba4* | species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_4 |
| *“Lowersilesiavirus” Acba11* | species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_11 |
| *“Lowersilesiavirus” Acba13* | species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_13 |
| *“Lowersilesiavirus” Acba14* | species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_14 |
| *“Lowersilesiavirus” Acba15* | species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_15 |

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| **Permission for use of names derived from a living person** |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes.**Description of current taxonomy*: *Acinetobacter*-specific temperate phages isolated and sequenced at the Bacteriophage Laboratory of the Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, have not been assigned to any family or genus of bacteriophages within the class *Caudoviricetes*.*Proposed* *taxonomic change(s):* We performed genomic analysis of our six *Acinetobacter*-specific temperate bacteriophages. We propose to create a new genus, *“Lowersilesiavirus”*, with six species.*Justification*:Based on DNA and protein similarity, *“Lowersilesiavirus”* is a cohesive genus. |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes.**Description of current taxonomy*: *Acinetobacter*-specific temperate phages isolated and sequenced at the Bacteriophage Laboratory of the Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, have not been assigned to any known family or genus of bacteriophages within the class *Caudoviricetes*.*Proposed* *taxonomic change(s)*: We performed genomic analysis of our six *Acinetobacter*-specific temperate bacteriophages. We propose to create a new genus, *“Lowersilesiavirus”*, with six species.*Demarcation criteria:***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 several tools, such as BLASTn [1] – usually calculated using the 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 [3].*Justification*: Based on DNA and protein similarity, *“Lowersilesiavirus”* is a cohesive genus. |

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| **References:**  |
| 1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* 2021, 49(D1):D10-D17.
2. Moraru C, Varsani A, Kropinski AM. VIRIDIC - a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. *Viruses* 2020, 12(11):1268.
3. Turner D, Kropinski AM, Adriaenssens EM. A roadmap for genome-based phage taxonomy. *Viruses* 2021, 13(3):506.
4. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. *Bioinformatics* 2017, 33(15):2379-2380.
5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. *J. Bacteriol.* 2002, 184(16):4529-35.
6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. *BMC Res. Notes.* 2013, 6:140.
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| **Accompanying files:** |
| **Filename** | **Description of contents** |
| *Lowersilesiavirus*\_1ng\_6ns.xlsx | To present the proposed taxonomic changes as a comparison of new taxonomic structures. |
| **Tables, Figures:**  |

**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes.



**Figure 2. ViPTree analysis\*:** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phage of interest is indicated with a **red star** and a **blue bar**.



\* The *Autographiviridae* family shown in **Figure 2** (automatically labeled by the software) is outdated. In 2025, the *Autographiviridae* family was elevated to the rank of order and renamed *Autographivirales*.

**Genome summary:**

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| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage Acba\_11 (selected as the reference genome)** | **OQ101254.1** | **OQ101254** | **67,052** | **40.3** | **95** | **100.0** | **100.0** |
| Acinetobacter phage Acba\_3 |  | OQ101248  | 55,181 | 40.1 | 72 | 87.4 | 70.53 |
| Acinetobacter phage Acba\_4 |  | OQ101249  | 57,429 | 40.1 | 77 | 81.9 | 65.26 |
| Acinetobacter phage Acba\_13 |  | OQ101255  | 55,385 | 40.0 | 73 | 87.6 | 70.53 |
| Acinetobacter phage Acba\_14 |  | OQ101256 | 54,941 | 40.0 | 73 | 92.9 | 75.79 |
| Acinetobacter phage Acba\_15 |  | OQ101257 | 60,424 | 40.0 | 81 | 78.6 | 63.16 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

**Rationale:** After examination of our six bacteriophages, on the basis of nucleotide sequence similarity and tblastx distances, we propose the creation of a new cohesive genus, *“Lowersilesiavirus”*. The proposed taxa confirm to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.