

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:** | Create a new family, *Luriaviridae*, with four genera, *Queenastridvirus*, *Wulsvirus*, *Saclayvirus*, and *Dalianvirus*, for a group of *Acinetobacter*-specific phages (class *Caudoviricetes*) |
| **Code assigned:** | 2025.086B.Uc.v3.Luriaviridae\_1nf\_3ng\_1mg\_12ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **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](mailto:michal.wojcicki@hirszfeld.pl) | X |
| Dann | Turner | School of Applied Sciences, University of the West of England, Bristol, UK | [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk) |  |
| Iwona | Gientka | Department of Biotechnology and Food Microbiology, Institute of Food Sciences, Warsaw University of Life Sciences (WULS-SGGW), Warsaw, Poland | [iwona\_gientka@sggw.edu.pl](mailto:iwona_gientka@sggw.edu.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](mailto: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](mailto: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](mailto:ewa.jonczyk-matysiak@hirszfeld.pl) |  |

**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* |

|  |  |  |  |
| --- | --- | --- | --- |
| **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:** | 20/06/2025 |

**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 | **x** |
| 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:** |
| Parts of the proposal do not respect the demarcation criteria (95% for species; 70% for genus). Please also check italics. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| All issues have been corrected in accordance with the comments from the Executive Committee. |

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| **Revision date:** | 17/10/2025 |

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

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | X | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon | X | 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** |
| *Luriaviridae* | family name created in honor of Italian microbiologist - Salvador Edward Luria (b. 1912, d. 1991). Luria researched viruses. Based on images obtained through an electron microscope, he described the structure of bacteriophages and discovered their ability to create mutant replicas. Luria won the Nobel Prize in Physiology or Medicine in 1969, with Max Delbrück and Alfred Hershey, for their discoveries on the replication mechanism and the genetic structure of viruses. |
| *Queenastridvirus* | genus name derived from the Queen Astrid Military Hospital, where the Acinetobacter phage vB\_AbaM\_Acibel004, the only representative of this genus, was isolated |
| *Queenastridvirus Acibel004* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_Acibel004 |
| *Wulsvirus* | genus name derived from Warsaw University of Life Sciences (WULS-SGGW), where the Institute of Food Sciences conducts research on the isolation and characterization of phages with potential use in food biocontrol. |
| *Wulsvirus Acba22* | species name derived from the phage name in the GenBank database –Acinetobacter phage Acba\_22 |
| *Wulsvirus KissB* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_KissB |
| *Wulsvirus Rocket* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_Rocket |
| *Dalianvirus* | genus name derived from the Dalian University of Technology, where the Acinetobacter phage vB\_AbaM\_D22, the one of representatives of this genus, was isolated |
| *Dalianvirus D22* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_D22 |
| *Dalianvirus P1* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_P1 |
| *Saclayvirus Ab121* | species name derived from the phage name in the GenBank database –Acinetobacter phage Ab\_121 |
| *Saclayvirus CP14* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_CP14 |
| *Saclayvirus Liucustia* | species name derived from the phage name in the GenBank database –Acinetobacter phage Liucustia |
| *Saclayvirus phi1092033* | species name derived from the phage name in the GenBank database –Acinetobacter phage phi1\_092033 |
| *Saclayvirus TAC1* | species name derived from the phage name in the GenBank database –Acinetobacter phage TAC1 |
| *Saclayvirus 14CRR8* | species name derived from the phage name in the GenBank database –Acinetobacter phage vB\_AbaM\_14/CRR8 |

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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*:  Family, genus, species  *Description of current taxonomy*:  Currently, the *Saclayvirus* genus includes three species: *Saclayvirus Aci011*, *Saclayvirus* *Aci022*, and *Saclayvirus* *Aci05*.  *Proposed* *taxonomic change(s):*  We performed a genomic analysis of phages deposited in the NCBI database. We propose to create a new family (*Luriaviridae*) with four genera (*Queenastridvirus*, *Wulsvirus*, *Saclayvirus*, and *Dalianvirus*) for a group of *Acinetobacter*-specific phages (realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*).  We performed a genomic analysis of several *Acinetobacter*-specific phages deposited in the NCBI database, all of which have been classified within the genus *Saclayvirus*. Based on our analysis, we propose the creation of a new family for these phages along with four distinct genera.   1. To create a new family, *Luriaviridae*, with four genera. 2. To create a new single species genus, *Queenastridvirus*. 3. To create a new genus, *Wulsvirus*, with three species. 4. To move the genus, *Saclayvirus*, to a new family, *Luriaviridae*. 5. To create six new species in genus *Saclayvirus*. 6. To create a new genus, *Dalianvirus*, with two species.   *Justification*:  After examination of bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Luriaviridae*, to accommodate four genera (*Queenastridvirus*, *Wulsvirus*, *Saclayvirus*, and *Dalianvirus*). The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee. |

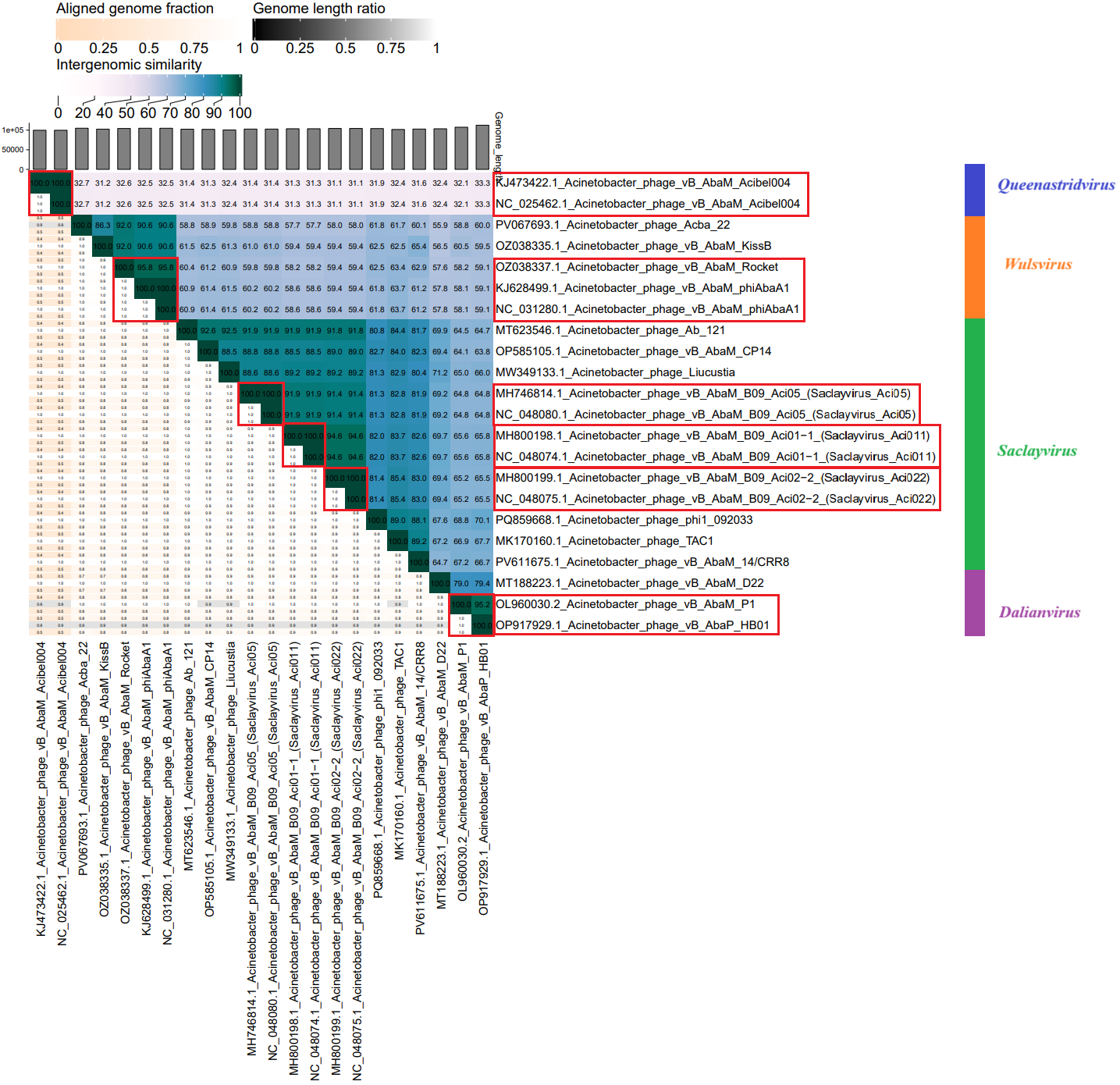
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| --- |
| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Family, genus, species  *Description of current taxonomy*:  Currently, the *Saclayvirus* genus includes three species: *Saclayvirus Aci011*, *Saclayvirus* *Aci022*, and *Saclayvirus* *Aci05*.  *Proposed* *taxonomic change(s)*:  We performed a genomic analysis of phages deposited in the NCBI database. We propose to create a new family (*Luriaviridae*) with four genera (*Queenastridvirus*, *Wulsvirus*, *Saclayvirus*, and *Dalianvirus*) for a group of *Acinetobacter*-specific phages (realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*).  We performed a genomic analysis of several *Acinetobacter*-specific phages deposited in the NCBI database, which have been classified under the genus *Saclayvirus*. Based on our analysis, we propose the creation of a new family for these phages along with four distinct genera.   1. To create a new family, *Luriaviridae*, with four genera. 2. To create a new single species genus, *Queenastridvirus*. 3. To create a new genus, *Wulsvirus*, with three species. 4. To move the genus, *Saclayvirus*, to a new family, *Luriaviridae*. 5. To create six new species in genus *Saclayvirus*. 6. To create a new genus, *Dalianvirus*, with two 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 using several tools, such as BLASTn [1], and are typically determined with 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].  **Family demarcation criteria:** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (e.g. ViPTree, GRAViTy dendrogram, vConTACT2 network). Family members share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of family members) [3].  *Justification*:  Examination of 17 genomes with VIRIDIC resulted in the identification of four cluster of phage genomes with intergenomic nucleotide similarity within the threshold for the establishment of new genera (Figure 1). The genomes formed a single clade in a hierarchically clustered tblastx distance tree (Figure 2). To examine shared proteins between these phages, all genomes were first reannotated using Pharokka with prodigal gene calling to provide a standardised data set. MMSeqs2 was used to perform protein clustering at thresholds of 50% minimum sequence identity and 50% coverage. Protein clusters were extracted as multi-fasta files and converted to matrices of counts and presence/absence by genome (Figures 3 and 4). A total of 44 core proteins were identified and maximum likelihood phylogenetics trees were inferred using IQTree2 (Figure 5). We propose the creation of a new family, *Luriaviridae*, with four genera (*Queenastridvirus*, *Wulsvirus*, *Saclayvirus*, and *Dalianvirus*). |

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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** |
| 2025.086B.Luriaviridae\_1nf\_3ng\_1mg\_12ns.xlsx | To present the proposed taxonomic changes as a comparison of new taxonomic structures. |
| **Tables, Figures:** | |

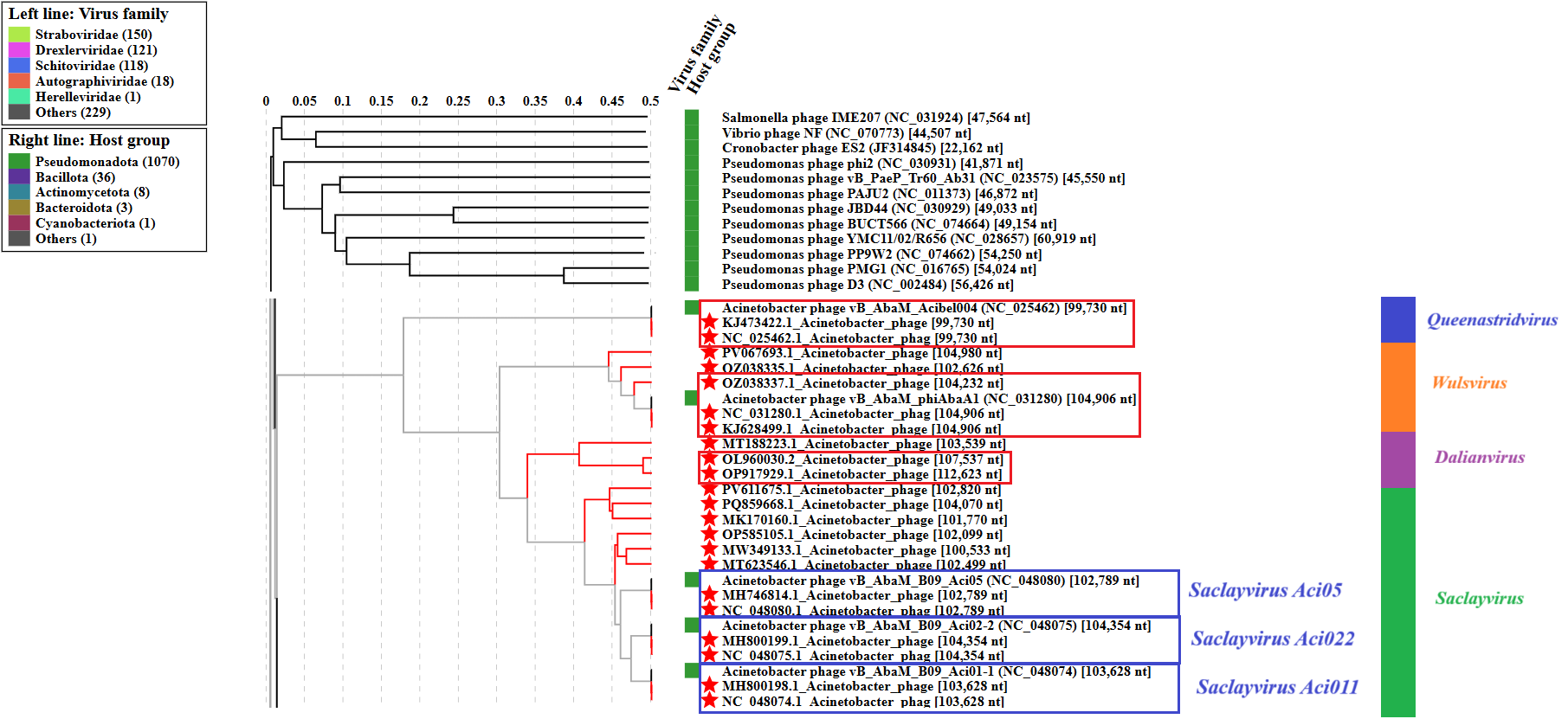
**Proposals data:**

1. **To create a new family, *Luriaviridae*, with four genera.**
2. **To create a new single species genus, *Queenastridvirus*.**
3. **To create a new genus, *Wulsvirus*, with three species.**
4. **To move the genus, *Saclayvirus*, to a new family, *Luriaviridae*.**
5. **To create six new species in genus *Saclayvirus*.**
6. **To create a new genus, *Dalianvirus*, with two species.**



**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. Phages belonging to the same species (nucleotide similarity above 95%) are marked with a **red** frame.

All phages pre-classified in the NCBI database were divided into four groups, based on which we propose the creation of separate genera. Proposed genera names: **blue** – new genus: *Queenastridvirus*, **orange** – new genus: *Wulsvirus*, **green** – genus: *Saclayvirus*, and **purple** – new genus: *Dalianvirus*.



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

Phages belonging to the same species (nucleotide similarity above 95%) are marked with a **red** **frame**.

\* 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*.

All phages pre-classified in the NCBI database were divided into four groups, based on which we propose the creation of separate genera. Proposed genera names: **blue** – new genus: *Queenastridvirus*, **orange** – new genus: *Wulsvirus*, **green** – genus: *Saclayvirus*, and **purple** – new genus: *Dalianvirus*.

**A blue and white rectangles

AI-generated content may be incorrect.**

**Figure 3.** Presence-absence matrix of protein clusters by genome. Rows and columns were heirarchically clustered using the complete method. Rows represent individual genomes with columns representing protein clusters. Vertical blue bars denote the presence of protein clusters in each genome.

**A red square with black lines

AI-generated content may be incorrect.**

**Figure 4.** Heatmap of Jaccard similarity calculated from the percentage of shared protein clusters between genomes.

**A black background with white text

AI-generated content may be incorrect.**

**Figure 5.** Co-phylogeny of partitioned maximum likelihood phylogeny of 42 proteins (left) and portal vertex protein (right). The protein clusters corresponding to a DNA polymerase and HNH homing endonuclease were omitted from the partition tree.

**A. To create a new family, *Luriaviridae*, with four genera.**

After examination of bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Luriaviridae*, with four genera (*Queenastridvirus*, *Wulsvirus*, *Saclayvirus*, and *Dalianvirus*).

**B. To create a new single species genus, *Queenastridvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_AbaM\_Acibel004 | KJ473422 = NC\_025462 | KJ473422 | 99,730 | 37.3 | 156 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

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

**C. To create a new genus, *Wulsvirus*, with three species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage Acba\_22 (selected as the reference genome)** | **PV067693.1** | **PV067693** | **104,980** | **37.9** | **162** | **100.0** | **100.00** |
| Acinetobacter phage vB\_AbaM\_KissB |  | OZ038335 | 102,626 | 37.7 | 190 | 86.3 | 91.36 |
| Acinetobacter phage vB\_AbaM\_Rocket |  | OZ038337 | 104,232 | 37.8 | 189 | 92.0 | 95.06 |

(\*) determined using VIRIDIC [2]

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

**D. To move the genus, *Saclayvirus,* to a new family, *Luriaviridae*.**

After examining bacteriophages based on nucleotide sequence similarity, tblastx distance, and core gene phylogeny, we proposed to include the genus *Saclayvirus* in a newly proposed family, *Luriaviridae.*

**E. To create six new species in genus *Saclayvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage vB\_AbaM\_B09\_Aci01-1 (*Saclayvirus Aci011;* reference genome)** | **MH800198 = NC\_048074** | **MH800198** | **103,628** | **37.2** | **163** | **100.0** | **100.00** |
| Acinetobacter phage vB\_AbaM\_B09\_Aci02-2 (*Saclayvirus Aci022*) | MH800199 = NC\_048075 | MH800199 | 104,354 | 37.2 | 171 | 94.6 | 96.93 |
| Acinetobacter phage vB\_AbaM\_B09\_Aci05 (*Saclayvirus Aci05*) | MH746814 = NC\_048080 | MH746814 | 102,789 | 37.2 | 160 | 91.9 | 92.02 |
| Acinetobacter phage Ab\_121 |  | MT623546 | 102,499 | 37.2 | 159 | 91.9 | 88.34 |
| Acinetobacter phage vB\_AbaM\_CP14 |  | OP585105 | 102,099 | 37.4 | 169 | 88.5 | 90.80 |
| Acinetobacter phage Liucustia |  | MW349133 | 100,533 | 37.1 | 157 | 89.2 | 90.18 |
| Acinetobacter phage phi1\_092033 |  | PQ859668 | 104,070 | 37.6 | 188 | 82.0 | 90.18 |
| Acinetobacter phage TAC1 |  | MK170160 | 101,770 | 37.5 | 163 | 83.7 | 92.64 |
| Acinetobacter phage vB\_AbaM\_14/CRR8 |  | PV611675 | 102,820 | 37.6 | 164 | 82.6 | 86.50 |

(\*) determined using VIRIDIC [2]

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

**F. To create a new genus, *Dalianvirus*, with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage vB\_AbaM\_D22 (selected as the reference genome)** | **MT188223.1** | **MT188223** | **103,539** | **37.4** | **159** | **100.0** | **100.00** |
| Acinetobacter phage vB\_AbaM\_P1 |  | OL960030 | 107,537 | 37.7 | 183 | 79.4 | 91.19 |

(\*) determined using VIRIDIC [2]

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