

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create a new family, *Lindbergviridae*, for PB1-like phages (Class: *Caudoviricetes*) |
| **Code assigned:** | 2024.020B | |

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| --- | --- | --- | --- |
| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Moraru C | Carl von Ossietzky Universität Oldenburg, Germany | liliana.cristina.moraru@uol.de |  |
| Tolstoy I | National Center for Biotechnology Information, MD, USA | tolstoy@ncbi.nlm.nih.gov |  |
| Kropinski AM | University of Guelph, Ontario, Canada [AMK] | Phage.Canada@gmail.com | **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 |
| **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:** | 27/04/2024 |

**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 | **X** |
| 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| W - Withdrawn |  |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:** |
| Minor correction – ensure taxon names are presented in italics |

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

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| **Response of proposer:** |
| Corrected. |
| **Revision date:** | 30/09/2024 |

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

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| **Name of accompanying Excel module:** |
| 2024.020B.A.v1.Lindbergviridae\_nf.xlsx |

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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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| **Is any taxon name used here derived from that of a living person:** | | **Y/N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  PB1-like phages have been classified into the following genera: *Kylevirus, Tabernariusvirus, Bcepfunavirus, Pbunavirus, Wifcevirus, Myosmarvirus* and *Carpasinavirus.* All these are myoviruses infecting members of the Betaproteobacteria and Gammaproteobacteria.  *Proposed* *taxonomic change(s)*:  A. To create ten new species in the genus *Pbunavirus*  B. To create one new species in the genus *Myosmarvirus*  C. To add six new species to the genus *Wifcevirus*  D. To add one new species to the genus *Carpasinavirus*  E. To create a new single species genus *Gladiolivirus*  F. To create a new single species genus *Irusalimvirus*  G. To create a new single species genus *Plutovirus*  H. To create a new family, *Lindbergviridae*, for the above-mentioned taxa as well as *Kylevirus, Tabernariusvirus*, and *Bcepfunavirus*.  *Justification*:  All our genomic and proteomic analyses reveal that the previously established genera *Kylevirus* (2020.086B.R.Kylevirus), *Tabernariusvirus* (2018.099B.A.v1.Tabernariusvirus), *Bcepfunavirus* (2020.116B.R.Pbunavirus), *Pbunavirus*, *Wifcevirus*, *Myosmarvirus* and *Carpasinavirus* together with the three new genera listed above belong to a new family which we have named in honour of Alf A. Lindberg. The bacteriophages share 12 common proteins. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  PB1-like phages have been classified into the following genera: *Kylevirus, Tabernariusvirus, Bcepfunavirus, Pbunavirus, Wifcevirus, Myosmarvirus* and *Carpasinavirus.* All these are myoviruses infecting members of the Betaproteobacteria and Gammaproteobacteria.  *Proposed* *taxonomic change(s)*:  A. To create ten new species in the genus *Pbunavirus*  B. To create one new species in the genus *Myosmarvirus*  C. To add six new species to the genus *Wifcevirus*  D. To add one new species to the genus *Carpasinavirus*  E. To create a new single species genus *Gladiolivirus*  F. To create a new single species genus *Irusalimvirus*  G. To create a new single species genus *Plutovirus*  H. To create a new family, *Lindbergviridae*, for the above mentioned taxa as well as *Kylevirus, Tabernariusvirus*, and *Bcepfunavirus*.  *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 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]  **Family demarcation criteria:** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (VirClust, ViPTree, GRAViTy dendrogram, vConTACT2 network). Members of the family share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of members of the family). [10]  *Justification*: The criteria for establishing genera and family have been met [10]. |
| **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 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870  2. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.  3. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. http://kronos.icbm.uni-oldenburg.de/viridic/  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. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. https://www.genome.jp/viptree/  5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423  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. doi: 10.1186/1756-0500-6-140. PMID: 23566564.  7. Davis P, Seto D, Mahadevan P. CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. Viruses. 2022 Nov 16;14(11):2534. doi: 10.3390/v14112534. PMID: 36423143; PMCID: PMC9693508.  8. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.  9. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.  10. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.  11. Bin Jang H, Bolduc B, Zablocki O, Kuhn JH, Roux S, Adriaenssens EM, Brister JR, Kropinski AM, Krupovic M, Lavigne R, Turner D, Sullivan MB. Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nat Biotechnol. 2019 Jun;37(6):632-639. doi: 10.1038/s41587-019-0100-8. Epub 2019 May 6. PMID: 31061483.  12. Bolduc B, Jang HB, Doulcier G, You ZQ, Roux S, Sullivan MB. vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect Archaea and Bacteria. PeerJ. 2017 May 3;5:e3243. doi: 10.7717/peerj.3243. PMID: 28480138; PMCID: PMC5419219.  13. Moraru C. VirClust-A Tool for Hierarchical Clustering, Core Protein Detection and Annotation of (Prokaryotic) Viruses. Viruses. 2023 Apr 19;15(4):1007. doi: 10.3390/v15041007. PMID: 37112988; PMCID: PMC10143988.  14. Letunic I, Bork P. Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. Bioinformatics. 2007 Jan 1;23(1):127-8. doi: 10.1093/bioinformatics/btl529. Epub 2006 Oct 18. PMID: 17050570.  15. Zhou T, Xu K, Zhao F, Liu W, Li L, Hua Z, Zhou X. itol.toolkit accelerates working with iTOL (Interactive Tree of Life) by an automated generation of annotation files. Bioinformatics. 2023 Jun 1;39(6):btad339. doi: 10.1093/bioinformatics/btad339. PMID: 37225402; PMCID: PMC10243930.  16. Nguyen LT, Schmidt HA, von Haeseler A, and Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. Molecular Biology and Evolution, 32:268-274. https://doi.org/10.1093/molbev/msu300  17. Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS (2018) UFBoot2: Improving the ultrafast bootstrap approximation. Molecular Biology and Evolution, 35:518–522. <https://doi.org/10.1093/molbev/msx281>  18. Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, and Jermiin JS (2017) ModelFinder: Fast Model Selection for Accurate Phylogenetic Estimates, Nature Methods, 14:587–589. https://doi.org/10.1038/nmeth.4285 |

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| **Tables, Figures:** |

<Start here>

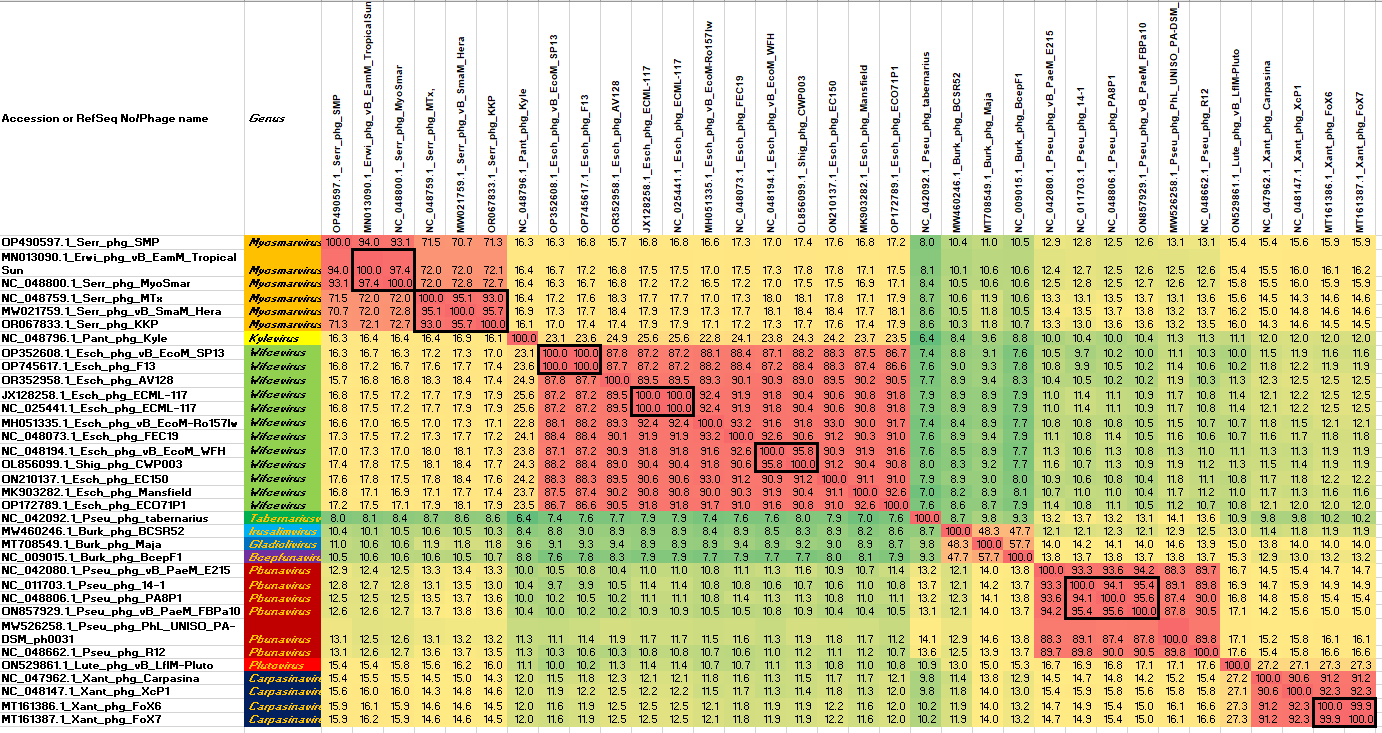


Figure 1. VIRIDIC heat map of a portion of the members of this family: VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Serr = *Serratia*; Erwi = *Erwinia*; Pant = *Pantoea*; Pseu = *Pseudomonas*; Esch = *Escherichia*; Xant = *Xanthomonas*; Burk = *Burkholderia*; Shig = *Shigella*; Lute = *Luteibacter*. In addition, we analyzed a total of 168 members of the *Pbunavirus* and have appended the complete VIRIDIC heatmap (Lindbergviridae\_Pbunavirus\_2024\_VIRIDIC\_heatmap). The coloured accession numbers and phage names in Column A represent ICTV-recognized species.

A circular object with different colored lines

Description automatically generated

Figure 2. ViPTree [4] analysis Proteomic tree of 4,408 bacterial viruses with proposed viral families labeled by the coloured ring. The *Lindbergviridae* are marked with a star symbol. The hierarchical tree was created using ViPTreeGen (version 1.1.2) [4] and annotated using iToL [15-16]. The tree is based on a dissimilarity matrix generated by pairwise tBLASTx scores between each of the genomes.

A screen shot of a black screen

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Figure 3. ViPTree [4] hierarchical tree pruned to show the proposed *Lindbergviridae*. Neighbouring clades are not shown.

and confidence scores for all taxonomic predictions [11,12]. There figure was generated in iTOL, the Interactive Tree Of Life [14, 15]

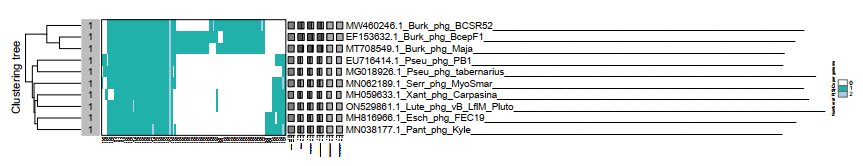


Figure 4. VirClust protein heatmap of representative species of each genus. At the first level, proteins are grouped based on their reciprocal BLASTP similarities into protein clusters, or PCs. At the second level, PCs are grouped based on their Hidden Markov Model (HMM) similarities into protein superclusters, or PSCs. AT the third, still experimental level, PSCs are grouped based on their HMM similarities into protein super-superclusters, or PSSCs [13].

A screenshot of a computer

Description automatically generated

Figure 5. Core genome phylogeny of the proposed *Lindbergviridae* family of bacterial viruses. A partitioned protein ML phylogeny was created from 12 genes present in all species of the proposed family. Alignments were performed using MAFFT in e-insi mode and trimmed using trimAl with a gap threshold of 0.5. The tree was calculated using IQ-Tree2 with 1000 ultrafast (UF) bootstrap replicates and SH-Alrt tests with -m TEST to optimise models for each alignment [16-18]. The tree is rooted at the midpoint and UF bootstrap support ≥ 95% are shown. The coloured strips indicate proposed genera and subfamilies.

Table 1. Signature genes in the proposed *Lindbergviridae* family of bacterial viruses. Genes were identified by clustering with MMSeqs2, with thresholds of 35% sequence similarity and 50% coverage.

|  |  |  |  |
| --- | --- | --- | --- |
| **protein cluster** | **No. of genomes (65 total)** | **Percentage of genomes present in protein cluster** | **Predicted gene function** |
| 1 | 65 | 100% | hypothetical protein |
| 2 | 65 | 100% | DNA polymerase |
| 3 | 65 | 100% | portal vertex protein |
| 4 | 65 | 100% | RecD-like DNA helicase |
| 5 | 65 | 100% | putative structural protein |
| 6 | 65 | 100% | baseplate protein |
| 7 | 65 | 100% | hypothetical protein |
| 8 | 65 | 100% | putative structural protein |
| 9 | 65 | 100% | terminase large subunit |
| 10 | 65 | 100% | DNA helicase |
| 11 | 65 | 100% | DNA primase |
| 12 | 65 | 100% | endolysin |
| 13 | 64 | 98.46% | structural protein |
| 14 | 64 | 98.46% | structural protein |
| 15 | 64 | 98.46% | hypothetical protein |
| 16 | 64 | 98.46% | hypothetical protein |
| 17 | 64 | 98.46% | hypothetical protein |
| 18 | 64 | 98.46% | DNA helicase |
| 19 | 64 | 98.46% | hypothetical protein |
| 20 | 64 | 98.46% | hypothetical protein |
| 21 | 64 | 98.46% | DNA polymerase exonuclease subunit |
| 22 | 64 | 98.46% | hypothetical protein |

**Proposals Data:**

**A. To create ten new species in the genus *Pbunavirus***

**B. To create one new species in the genus *Myosmarvirus***

**C. To add six new species to the genus *Wifcevirus***

**D. To add one new species to the genus *Carpasinavirus***

**E. To create a new single species genus *Gladiolivirus***

**F. To create a new single species genus *Irusalimvirus***

**G. To create a new single species genus *Plutovirus***

**H. To create a new family, *Lindbergviridae*, for the above-mentioned taxa as well as *Kylevirus, Tabernariusvirus*, and *Bcepfunavirus*.**

**Taxonomic Proposals:**

1. **To create ten new species in the genus *Pbunavirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** This taxon was created originally through Taxonomy Proposal . 2009.001a-gB.A.v2.Pb1virus

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Pseudomonas* phage PB1 | NC\_011810.1 | 65.8 | 93 | 100.0 | 100 |
| *Pseudomonas* phage SG1 (partial) | OQ594965.1 | 65.2 | 91 | 91.1 | 92.5 |
| *Pseudomonas* phage 109 | OQ831730.1 | 65.6 | 102 | 93.0 | 88.2 |
| *Pseudomonas* phage vB\_PaeM\_FBPa14 | ON375839.1 | 66.2 | 94 | 85.8 | 94.6 |
| *Pseudomonas* phage Kara-mokiny kep-wari Wadjak\_13 | OP310979.1 | 65.5 | 92 | 89.5 | 94.6 |
| *Pseudomonas* phage TH15 | MW406974.1 | 65.9 | 93 | 87.1 | 89.2 |
| *Pseudomonas* phage PSA09 (partial) | MZ089730.1 | 62.0 | 82 | 87.8 | 86.0 |
| *Pseudomonas* phage PhL\_UNISO\_PA-DSM\_ph0031 | MW526258.1 | 62.5 | 95 | 87.3 | 80.6 |
| *Pseudomonas* phage PSA25 (partial) | MZ089736.1 | 64.3 | 89 | 88.7 | 89.2 |
| *Pseudomonas* phage vB\_PaeM\_FBPa35 | ON857938.1 | 62.3 | 87 | 84.5 | 88.2 |
| *Pseudomonas* phage Victoria | OR805296.1 | 65.7 | 99 | 86.7 | 82.8 |

**(\*) determined using VIRIDIC [3]**

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

Holger DJ, El Ghali A, Bhutani N, Lev KL, Stamper K, Kebriaei R, Kunz Coyne AJ, Morrisette T, Shah R, Alexander J, Lehman SM, Rojas LJ, Marshall SH, Bonomo RA, Rybak MJ. Phage-antibiotic combinations against multidrug-resistant *Pseudomonas aeruginosa* in *in vitro* static and dynamic biofilm models. Antimicrob Agents Chemother. 2023 Nov 15;67(11):e0057823. doi: 10.1128/aac.00578-23. Epub 2023 Oct 19. PMID: 37855639; PMCID: PMC10648846. [phage 109]

Harada LK, Silva EC, Rossi FP, Cieza B, Oliveira TJ, Pereira C, Tomazetto G, Silva BB, Squina FM, Vila MM, Setubal JC, Ha T, da Silva AM, Balcão VM. Characterization and *in vitro* testing of newly isolated lytic bacteriophages for the biocontrol of *Pseudomonas aeruginosa*. Future Microbiol. 2022 Jan;17:111-141. doi: 10.2217/fmb-2021-0027. Epub 2022 Jan 6. PMID: 34989245. [phage PhL\_UNISO\_PA-DSM\_ph0031]

1. **To create one new species in the genus *Myosmarvirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** This taxon was created through 2020.109B.R.Myosmarvirus

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Serratia* phage MyoSmar | NC\_048800.1 | 68.7 | 105 | 100 | 100 |
| *Serratia* phage SMP | OP490597.1 | 68.4 | 99 | 94.0 | 85.7 |

**(\*) determined using VIRIDIC [3]**

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

**Conclusion:** The DNA sequence similarity value is consistent with membership in the same genus

**C. To add six new species to the genus *Wifcevirus***

**Origin of the name of this taxon:** NA

**Historical aspects:** This genus was created originally through TaxoProp 2019.096B

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Escherichia* phage vB\_EcoM\_WFH | NC\_048194.1 | 71.3 | 105 | 100 | 100 |
| *Escherichia* phage vB\_EcoM\_SP13 | OP352608.1 | 72.4 | 112 | 87.1 | 85.7 |
| *Escherichia* phage AC128 | OR352958.1 | 68.5 | 102 | 90.9 | 88.6 |
| *Escherichia* phage vB\_EcoM-Ro157lw | MH051335.1 | 72.2 | 109 | 91.6 | 88.6 |
| *Escherichia* phage EC150 | ON210137.1 | 68.0 | 94 | 90.9 | 84.8 |
| *Escherichia* phage Mansfield | MK903282.1 | 68.1 | 100 | 91.9 | 89.5 |
| *Escherichia* phage ECO71P1 | OP172789.1 | 68.2 | 96 | 91.6 | 83.8 |

**(\*) determined using VIRIDIC [3]**

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

Vitt AR, Sørensen AN, Bojer MS, Bortolaia V, Sørensen MCH, Brøndsted L. Diverse bacteriophages for biocontrol of ESBL- and AmpC-β-lactamase-producing *E. coli*. iScience. 2024 Jan 17;27(2):108826. doi: 10.1016/j.isci.2024.108826. PMID: 38322997; PMCID: PMC10844046. [phage AC128]

D'Souza GM, Klotz K, Moreland R, Liu M, Ramsey J. Complete Genome Sequence of *Escherichia coli* Myophage Mansfield. Microbiol Resour Announc. 2019 Sep 19;8(38):e01038-19. doi: 10.1128/MRA.01038-19. PMID: 31537679; PMCID: PMC6753283. [Mansfield]

**Conclusion:** The DNA sequence similarity value is consistent with membership in the same genus

**D. To add one new species to the genus *Carpasinavirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** This taxon was created through TaxoProp 2019.070B

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Xanthomonas phage Carpasina | NC\_047962.1 | 61.9 | 86 | 100 | 100 |
| Xanthomonas phage FoX6 | MT161386.1 | 61.1 | 99 | 91.2 | 94.2 |

**(\*) determined using VIRIDIC [3]**

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

Holtappels D, Fortuna KJ, Moons L, Broeckaert N, Bäcker LE, Venneman S, Rombouts S, Lippens L, Baeyen S, Pollet S, Noben JP, Oechslin F, Vallino M, Aertsen A, Maes M, Van Vaerenbergh J, Lavigne R, Wagemans J. The potential of bacteriophages to control *Xanthomonas campestris* pv. *campestris* at different stages of disease development. Microb Biotechnol. 2022 Jun;15(6):1762-1782. doi: 10.1111/1751-7915.14004. Epub 2022 Jan 27. PMID: 35084112; PMCID: PMC9151335. [phage FoX6]

**E. To create a new single species genus *Gladiolivirus***

**Origin of the name of this taxon:** The name of this taxon derived from the species of its bacterial host, *Burkholderia gladioli*

**Historical aspects:** This phage was isolated from Houston, TX soil and sequenced by Z. Yu et al. (Center for Phage Technology, TAMU, College Station, TX, USA)

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Burkholderia* phage Maja | MT708549.1 | 68.39 | 114 | 100 | 100 |

**F. To create a new single species genus *Irusalimvirus***

**Origin of the name of this taxon:** This taxon is named after the city where *Burkholderia* phage BCSR52 was isolated.

**Historical aspects:** This phage was isolated from sewage by C. Rakov et al. in the Institute of Dental Sciences and School of Dental Medicine, Hebrew University, Hadassah Campus, Jerusalem, Israel.

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Burkholderia* phage BCSR52 | MW460246.1 | 70.04 | 116 | 100 | 100 |

**G. To create a new single species genus *Plutovirus***

**Origin of the name of this taxon:** The name of this taxon derives from that of the first isolate of its type, *Luteibacter* phage vB\_LflM-Pluto

**Historical aspects:** *Luteibacter* is a genus of the Gammaproteobacteria in the family *Rhodanobacteraceae.* This phage was isolated from sewage against *Luteibacter* sp. EIF3 by I. Friedrich et al. Genomic and Applied Microbiology, Georg-August University Goettingen, Lower Saxony, Germany.

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Luteibacter* phage vB\_LflM-Pluto | ON529861.1 | 67.53 | 99 | 100 | 100 |

**H. To create a new family, *Lindbergviridae*, for the above-mentioned taxa as well as *Kylevirus, Tabernariusvirus*, and *Bcepfunavirus*.**

**Origin of the name of this taxon:** This taxon is named in honour of Alf Erik Anton Lindberg (b.1939 Växjö; d. 2021 in Stockholm), who was a Swedish physician scientist. He received his doctorate in 1971 at the Karolinska Institute with a thesis entitled "Bacteriophage attachment and inactivation in relation to chemical composition of *Salmonella* lipopolysaccharides" and was professor of clinical bacteriology at Huddinge Hospital. Alf Lindberg also had extensive experience in vaccine development and for several years was head of research for Wyeth Vaccines and Sanofi Pasteur. Since 1989 he was a member of the Swedish Academy of Sciences since 1989. From 1991–1992 he was the secretary of the Karolinska Institute's Nobel Committee. (<https://sv.wikipedia.org/wiki/Alf_A._Lindberg>



(photograph reprinted from: <https://lakartidningen.se/aktuellt/minnesord/2021/06/till-minne-av-alf-lindberg/>

**Conclusion:** All our genomic and proteomic analyses reveal that the previously established genera *Kylevirus* (2020.086B.R.Kylevirus), *Tabernariusvirus* (2018.099B.A.v1.Tabernariusvirus), *Bcepfunavirus* (2020.116B.R.Pbunavirus), *Pbunavirus, Wifcevirus, Myosmarvirus* and *Carpasinavirus* together with the three new genera listed above belong to a new family which we have named in honour of Alf A. Lindberg.