This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.073B*** | |  |
| **Short title:** Create twenty-four new genera including twenty-six new species and move twelve species to the new genera in the subfamily *Peduovirinae,* family *Myoviridae* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| van Zyl LJ, Lueder MR, Bishop-Lilly KA, Adriaenssens EM, Kropinski AM | | [lvanzyl@uwc.ac.za](mailto:lvanzyl@uwc.ac.za); [matthew.r.lueder.ctr@mail.mil](mailto:matthew.r.lueder.ctr@mail.mil); [kimberly.a.bishop-lilly.civ@mail.mil](mailto:kimberly.a.bishop-lilly.civ@mail.mil); [Evelien.adriaenssens@quadram.ac.uk](mailto:Evelien.adriaenssens@quadram.ac.uk); Phage.Canada@gmail.com | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | | IMBM, C2, Life Science Building, University of the Western Cape, Bellville, South Africa, 7535 [LJ]  Biological Defense Research Directorate, Naval Medical Research Center, Fort Detrick, MD 21702, USA [MR, KA]  Quadram Institute Bioscience, UK [EMA]  Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada [AM] | | | | |
| **Corresponding author** | | | |
| Matthew Lueder matthew.r.lueder.ctr@mail.mil | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | **ICTV Bacterial and Archaeal Viruses Subcommittee**  **Caudovirales Study Group** | |
| |  |  |  | | --- | --- | --- | | **Authority to use the name of a living person:**  Please provide the following information if you propose taxon name(s) which are derived from the name of a living person or persons*.* Please attach documents to verify that permission has been obtained. | | | | **Taxon name** | **Person from whom the name is derived** | **Permission obtained (Y/N)** | | *Eganvirus* | John Barry Egan | Y | |  |  |  | |  |  |  | |  | | |   **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | |  |
| Date of this revision (if different to above): | | |  |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.073B.A.v2.Peduovirinae\_24gen.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |
| **References:** |
| 1. Agren J, Sundström A, Håfström T, Segerman B (2012) Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 7(6):e39107 2. Pryshliak M, Hammerl JA, Reetz J, Strauch E, Hertwig S (2014) *Vibrio vulnificus* Phage PV94 Is Closely Related to Temperate Phages of V. cholerae and Other Vibrio Species. PLoS ONE 9(4): e94707. https://doi.org/10.1371/journal.pone.0094707 3. Beilstein F, Dreiseikelmann B (2008) Temperate bacteriophage ΦO18P from an *Aeromonas* media isolate: Characterization and complete genome sequence. Virology 373: 25-29 4. Campoy S, Aranda J, Àlvarez G, Barbé J, Llagostera M (2006) Isolation and Sequencing of a Temperate Transducing Phage for *Pasteurella multocida*. 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Epub 2008 Apr 19. \*: joint first authors 34. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 2004, Mar;32(5):1792-7. 35. Castresana J. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. Mol Biol Evol. 2000;17(4):540-52. 36. Guindon S., Gascuel O. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst Biol. 2003;52(5):696-704. 37. Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative. Syst Biol. 2006;55(4):539-52. 38. Chevenet F., Brun C., Banuls AL., Jacq B., Chisten R. TreeDyn: towards dynamic graphics and annotations for analyses of trees. BMC Bioinformatics. 2006;7:439. 39. Lavigne R, Seto D, Mahadevan P, Ackermann HW, Kropinski AM. Unifying classical and molecular taxonomic classification: analysis of the Podoviridae using BLASTP-based tools. Res Microbiol. 2008;159(5):406-14.   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 May 6. doi: 10.1038/s41587-019-0100-8. |

**Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in each of genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

**Genus demarcation criterion:** The defining criterion for membership in a genus is that the species display 50-60% DNA sequence identity to one another. The creation of this taxon should also be consistent with the total proteome results and the phylogenic analysis of conserved proteins.

**History:** The subfamily *Peduovirinae*, consisting of two genera *Hp1likevirus* and *P2likevirus*, was created in 2009 (2009.012a-qB) as a result of analysis carried out by Lavigne and colleagues [39]. Subsequently, these two genera were renamed *Hpunavirus* and *Peduovirus* (2018.007B.A.v1.rename137gen6sp). They contain six and 17 species, respectively. Since the first proposal, large numbers of P2-like phages have been deposited in GenBank necessitating a reanalysis of this genus. The References Sequences have all been analyzed using vConTACT 2.0 [40] and fall into two major gene-sharing networks (60\_0; 89\_0) which correspond broadly to the HP1-like phages and P2-like phages (APPENDIX A).

**Proposal 1:** To remove *Aeromonas virus phiO18P* from genus *Hpunavirus* and assign it to new genus *Bielevirus*.

**Background/History:** The phage was isolated/identified from plaques that formed in a bacterial lawn of a *Aeromonas sp.* (O18) isolate, isolated from a pond in Bielefeld, Germany.

**Source of name of this taxon:** The genus is named for the town the host organism was isolated in, Bielefeld, Germany. Type species: *Aeromonas virus phiO18P*.

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| DQ674738.2 | Aeromonas virus phiO18P | 33,985 | 61.74 | 0 | 53 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 2:** Remove phage F108 from genus *Hpunavirus* and assign it to new genus *Irtavirus*.

**Background/History:** The phage was isolated/identified from a *Pasturella multocida* isolate which was part of the IRTA culture collection.

**Source of name of this taxon:** The genus is named for the research institute it was first isolated at, Institut de Recerca i Tecnologia Agroalimentàries (IRTA). Type species: *Pasteurella virus F108*.

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| DQ114220.1 | Pasteurella virus F108 | 30505 | 42.10 | 0 | 56 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 3:** To create a new genus, *Phitrevirus*, and assign *Pseudomonas virus phi3* to it.

**Background/History:** The phage was identified through sequencing of the genomes of clinical *P. aeruginosa* isolates

**Source of name of this taxon:** The genus is named using the convention of combining the moniker for the type species and the word “virus”. Type species: *Pseudomonas virus phi3*.

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KT887559 | Pseudomonas phage phi3 | 32637 | 63.9 | 1 | 53 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 4:** To create a new genus, *Seongnamvirus*, and assign *Cronobacter virus ESSI2* to it.

**Background/History:** *Cronobacter sakazakii* phage ESSI-2, was isolated from fecal samples from swine in Korea.

**Source of name of this taxon:** This genus is named after Seongnam which is the second largest city in South Korea's Gyeonggi Province, where at Kyungwon University the type virus was isolated. Type species: *Cronobacter virus ESSI2*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| HQ110083.1 | Cronobacter virus ESSI2 | 28765 | 55.17 | 0 | 39 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 5:** To create a new genus, *Catalunyavirus*, and assign *Pseudoalteromonas virus C5a* to it.

**Background/History:** Isolated from Seawater (unpublished)

**Source of name of this taxon:** The genus is named after the province in Spain where at the Departament de Biologia Marina i Oceanografia, Institut de Ciències del Mar-CMIMA, CSIC the type species *Pseudoalteromonas virus C5a*, was isolated.

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KY045851.1 | Pseudoalteromonas virus C5a | 35209 | 42.23 | 0 | 58 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 6:** To create a new genus, *Playavirus*, and assign *Salinivibrio virus SMHB1* to it.

**Background/History:** The phage was isolated/identified from plaques that formed in a bacterial lawn of a *Salinivibrio sp.* (BNH) isolate, isolated from salt playa in the Namib Desert North-East of Swakopmund, Namibia. Sequencing of the bacterial and phage genomes confirmed that the virus lysogenizes this bacterium (unpublished).

**Source of name of this taxon:** The genus is named for the geographic feature that the virus was isolated from. A salt playa in the Namib Desert. Type species: *Salinivibrio virus SMHB1*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KX774374 | Salinivibrio virus SMHB1 | 32,826 | 50.80 | 0 | 55 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 7:** To create a species, *Vibrio virus Canoe* and assign Vibrio phage 1.202.O.\_10N.222.45.E8 to it and to create a new genus, *Canoevirus*, and assign, *Vibrio virus Canoe*

**Background/History:** Vibrio phage 1.202.O.\_10N.222.45.E8 was isolated from Nahant, Canoe Cove, MA (unpublished).

**Source of name of this taxon:** The genus is named using the convention of combining the moniker for the type species and the word “virus”. Type species: *Vibrio virus Canoe*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| MG592573 | Vibrio virus Canoe | 32,014 | 44.56 | 0 | 52 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 8:** To create a new genus, *Vulnificusvirus*, and assign Vibrio phage PV94 to it.

**Background/History:** The phage was isolated/identified from a human isolate of *Vibrio vulnificus*, strain VN-094.

**Source of name of this taxon:** The genus is named for the bacterial species it was first identified to infect, *Vibrio vulnificus*. Type species: Vibrio phage PV94

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| HG803181 | Vibrio virus PV94 | 33,828 | 48.17 | 0 | 59 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 9:** To create a new genus, *Longwoodvirus* and assign *Vibrio virus K139* to it.

**Background/History:** Isolated as a prophage resident on the genome of *V. cholerae* MO10

**Source of name of this taxon:** The genus is named after Longwood Avenue in Boston, where at the Department of Microbiology and Molecular Genetics, Harvard Medical School the type phage was isolated. Type species: *Vibrio virus K139*

**Genome Summary Table:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Additional  Isolates | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| AF125163 | KF361475, AB374228,  KX058879 | Vibrio virus K139 | 33,106 | 48.90 | 0 | 55 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 10:** To create a new genus, *Baylorvirus* and assign *Mannheimia virus PHL101* and *Mannheimia virus 1127AP1* to it.

**Background/History:** PHL101 was isolated from a bovine pneumonic isolate of *M. haemolytica*, A1, strain PHL101.

1127AP1 was identified in *M. haemolytica* isolates from healthy cattle housed in two commercial feedlots in Alberta, Canada.

**Source of name of this taxon:** The genus is named after the institution where this phage was isolated, Department of Molecular Virology and Microbiology, Baylor College of Medicine, Houston, USA. . Type Species: *Mannheimia virus PHL101*

**Genome Summary Table:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Additional Isolates | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| DQ426904 | KP137438, | Mannheimia virus PHL101 | 34,525 | 41.57 | 0 | 62 | 100% |
| KP137436 | KP137434 | Mannheimia virus 1127AP1 | 36,745 | 41.98 | 0 | 60 | 79.51% |

**N.B. Mannheimia phage vB\_MhM\_1152AP, Bacteriophage phi-MhaA1-BAA410 and Mannheimia phage vB\_MhM\_535AP1 should be considered strains of PHL101**

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 11:** To create a new genus, *Felsduovirus* and assign five (5) species to it.

**Background/History:** RE2010 was identified in genomes of *S. enterica* isolates from several outbreaks. Fels-2 was isolated from *Salmonella typhimurium LT2* (The principal strain for cellular and molecular biology in *Salmonella*). SEN8 was isolated form faeces in the Czech Republic (unpublished). 4 LV-2017 was isolated from the *Klebsiella pneumoniae* outbreak strain ST307 while SopEphi was isolated from *Salmonella enterica* serovar Typhimurium A36.

**Source of name of this taxon:** The name of this genus is derived from that of phage Fels2. Type Species: *Salmonella virus RE2010*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| HM770079 | Salmonella virus RE2010 | 34,117 | 51.02 | 1 | 54 | 100% |
| KY271398 | Klebsiella virus 4LV2017 | 33,540 | 50.40 | 0 | 48 | 62.85% |
| AY319521 | Salmonella virus SopEphi | 35,155 | 51.32 | 1 | 58 | 69.42% |
| KT630647 | Salmonella virus SEN8 | 35,203 | 51.94 | 1 | 53 | 68.5% |
| NC\_010463 | Salmonella virus Fels2 | 33,693 | 52.49 | 0 | 51 | 75.31% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 12:** To create a new genus, *Entnonagintavirus* and assign *Erwinia virus ENT90* to it.

**Background/History:** Identified by Y.D. Lee in Korea (unpublished).

**Source of name of this taxon:** The genus is derived from ENT plus the Latin for 90. Type species: *Erwinia virus ENT90*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| HQ110084 | Erwinia virus ENT90 | 29,564 | 55.81 | 1 | 52 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 13:** To create a new genus, *Eganvirus* and assign four (4) species to it.

**Background/History:** *Salmonella* phage PSP3, was originally derived from a strain of *Salmonella potsdam* isolated from a child with gastroenteritis. From 1999–2005, 40 non-pathogenic strains of *S. enterica* subspecies *salamae*, *arizonae*, *diarizonae*, and *houtenae* (referred as Sen 1–40) were collected in the Czech Republic from human clinical samples and from environmental samples. Phage SEN1 was isolated from one of these strains and EtG was isolated from *Erwinia tracheiphila*-infected cucumber plants.

**Source of name of this taxon:** The genus is named in honour of John Barry Egan (Research Fellow, University of Adelaide; Member of the Australian Academy of Science) who worked extensively on phage 186. Type Species: *Escherichia virus 186*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| U32222 | Escherichia virus 186 | 30,624 | 53.09 | 0 | 51 | 100% |
| AY135486 | Salmonella virus PsP3 | 30,636 | 52.83 | 0 | 53 | 68.3% |
| KT630644 | Salmonella virus SEN1 | 29,733 | 53.01 | 0 | 50 | 67.5% |
| MF276773 | Erwinia virus  EtG | 30,413 | 54.14 | 0 | 51 | 74.2% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 14:** To create a new genus, *Stockinghallvirus* and assign *Salmonella virus FSLSP004* to it.

**Background/History:** *Salmonella virus FSLSP004* was isolated from dairy farms from New York State (United States).

**Source of name of this taxon:** The genus is named after Stocking Hall at Cornell University (NY, USA) where the type virus was isolated at Cornell University. Type species: *Salmonella virus FSLSP004*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KC139521 | Salmonella virus FSLSP004 | 29,742 | 52.84 | 0 | 51 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 15:** To create a new genus, *Nampongvirus* and assign *Burkholderia virus ST79* to it.

**Background/History:** ST79 was isolated from 30-cm deep soil sample in Nampong District, Khon Kaen Province, Thailand.

**Source of name of this taxon:** The genus is named after the district in Thailand where this phage was discovered. Type species: *Burkholderia virus ST79*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KC462197 | Burkholderia virus ST79 | 35,430 | 62.50 | 0 | 49 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 16:** To create a new genus, *Aresaunavirus* and assign two species to it.

**Background/History:** The exact source of RSA1 is unknown, but was isolated by Fujiwara in 2008 in Japan**.** RSY1 was isolated from soil samples collected from tomato fields in Hiroshima, Japan.

**Source of name of this taxon:** The name of this genus is derived from RSA1. Type species: *Ralstonia virus RSA1*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| AB276040 | Ralstonia virus RSA1 | 38,760 | 65.35 | 0 | 62 | 100% |
| AB981169 | Ralstonia virus RSY1 | 40,002 | 64.82 | 0 | 58 | 55.9% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 17:** To create a new genus, *Kisquattuordecimvirus* and assign *Burkholderia virus KS14* to it.

**Background/History:** KS14 was isolated from an extract of *Dracaena* sp. soil plated on *B. multivorans* C5393

**Source of name of this taxon:** The genus name is derived from K14. Type species: *Burkholderia virus KS14*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| HM461982 | Burkholderia virus KS14 | 32,317 | 62.28 | 0 | 52 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 18:** To create a new genus, *Kisquinquevirus* and assign 2 species to it.

**Background/History:** Seed and Dennis isolated KS5 from an extract of onion soil plated on *B. cenocepacia* K56-2. AP3 was isolated from a natural wastewater treatment plant (irrigated fields) in Wroclaw (Poland).

**Source of name of this taxon:** The genus name is derived from KIS5. Type species: *Burkholderia virus KS5*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| GU911303 | Burkholderia virus KS5 | 37,236 | 63.71 | 0 | 58 | 100% |
| KP966108 | Burkholderia virus AP3 | 36,499 | 64.41 | 1 | 58 | 60.1% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 19:** To create a new genus, *Tigrvirus* and assign 4 species to it.

**Background/History:** The origin of phi52237, phiE122 and phiE202 are unknown. KL3 was isolated from a single plaque on a lawn of *B. cenocepacia* CEP511, an Australian CF epidemic isolate.

**Source of name of this taxon:** The name of the genus is derived from The Institute for Genomic Research,

Rockville, USA where the type virus was isolated. Type species: *Burkholderia virus phi52237*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| DQ087285 | Burkholderia virus phi52237 | 37,639 | 64.82 | 1 | 58 | 100% |
| GU911304 | Burkholderia virus KL3 | 40,555 | 63.23 | 0 | 57 | 53.7% |
| CP000624 | Burkholderia virus phiE122 | 36,690 | 64.62 | 0 | 57 | 62.5% |
| CP000623 | Burkholderia virus phiE202 | 35,741 | 65.43 | 1 | 53 | 85.1% |

**N.B. Burkholderia phage BEK and Burkholderia phage phiX216 are strains of phi52237**

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 20:** To create a new genus, *Simpcentumvirus* and assign *Stenotrophomonas virus Smp131* to it.

**Background/History:** Smp131 was isolated by spotting culture supernatants from 86 clinical isolates of *S. maltophilia* onto lawns formed separately by all other isolates. The culture supernatant from *S. maltophilia* strain T13 was observed to cause clearing zones on 3 of the samples. Following 3 rounds of single plaque isolation, Smp131 was obtained.

**Source of name of this taxon:** The name of this genus was derived from Smp plus 100. Type species: *Stenotrophomonas virus Smp131*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| JQ809663 | Stenotrophomonas virus Smp131 | 33,525 | 65.02 | 1 | 59 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 21:** To create a new genus, *Citexvirus* and assign 2 species to it.

**Background/History:** phiCTX is a temperate phage isolated from a Pseudomonas aeruginosa strain that produces a pore‐forming toxin, called cytotoxin while Dobby is a temperate phage isolated from a strain of *Pseudomonas aeruginosa* cultured from a kidney stone.

**Source of name of this taxon:** The name of this genus was derived from CTX. Type species: *Pseudomonas virus phiCTX*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| AB008550 | Pseudomonas virus phiCTX | 35,580 | 62.62 | 0 | 55 | 100% |
| MK034952 | Pseudomonas virus dobby | 37,152 | 62.21 | 1 | 58 | 71.1% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 22:** To create a new genus, *Senquatrovirus* and assign *Salmonella virus SEN4* to it.

**Background/History:** SEN4 was isolated from non-pathogenic *S. enterica* strain isolated from human faeces in the Czech Republic.

**Source of name of this taxon:** The name of this virus was derived from SEN4. Type species: *Salmonella virus SEN4*

**Genome Summary Table:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Additional Isolates | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KT630645 | KT630646 | Salmonella virus SEN4 | 33,509 | 53.36 | 0 | 56 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 23:** To create a new genus, *Xuanwuvirus* and assign *Escherichia virus P88* to it.

**Background/History:** P88 was isolated on *Escherichia coli* strain K88 which came from a swine source in China.

**Source of name of this taxon:** This genus is named after the district in Nanjing City where at Nanjing Agricultural

University the type phage was isolated. Type species: *Escherichia virus P88*

**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KP063541 | Escherichia virus P88 | 35,814 | 52.87 | 0 | 63 | 100% |

*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

**Proposal 24:** To create a new genus, *Reginaelenavirus* and assign *Klebsiella virus 3LV2017* to it.

**Background/History:** 3 LV-2017 was isolated from the *Klebsiella pneumoniae* outbreak strain ST307.

**Source of name of this taxon:** The name of this genus comes from Via Regina Elena in Rome, where at Istituto Superiore di Sanita the type phage was isolated. Type species: *Klebsiella virus 3LV2017*

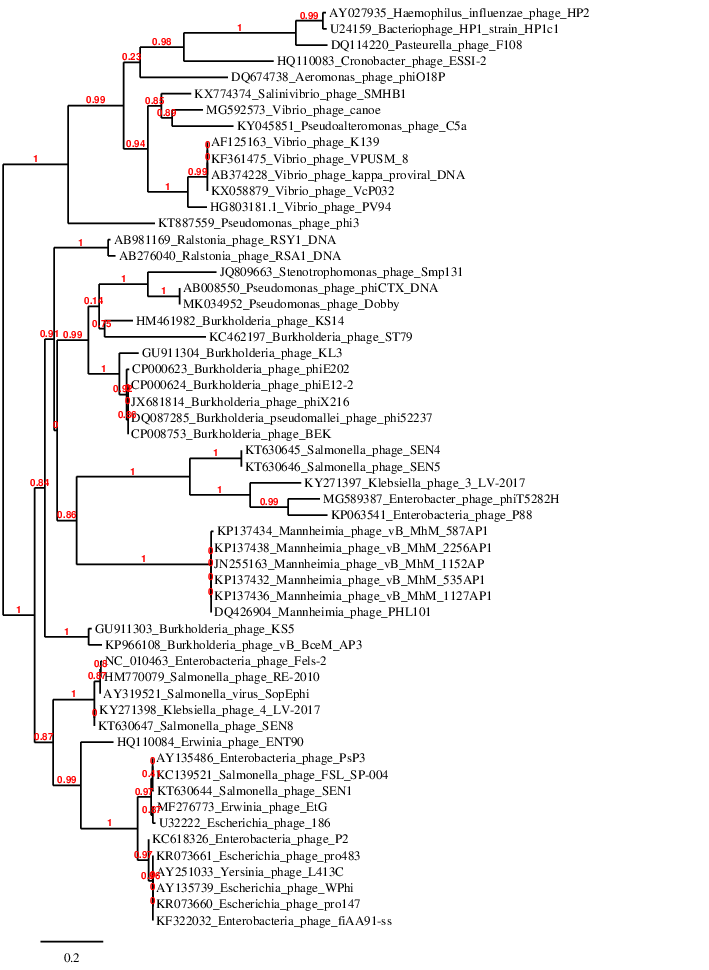
**Genome Summary Table:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenBank Accession No. | Species Name | Genome Length (bp) | Mol% G+C | Number of tRNAs\* | Number of ORFs\*\* | Percent Identity\*\*\* |
| KY271397 | Klebsiella virus 3LV2017 | 35,100 | 54.43 | 0 | 54 | 100% |

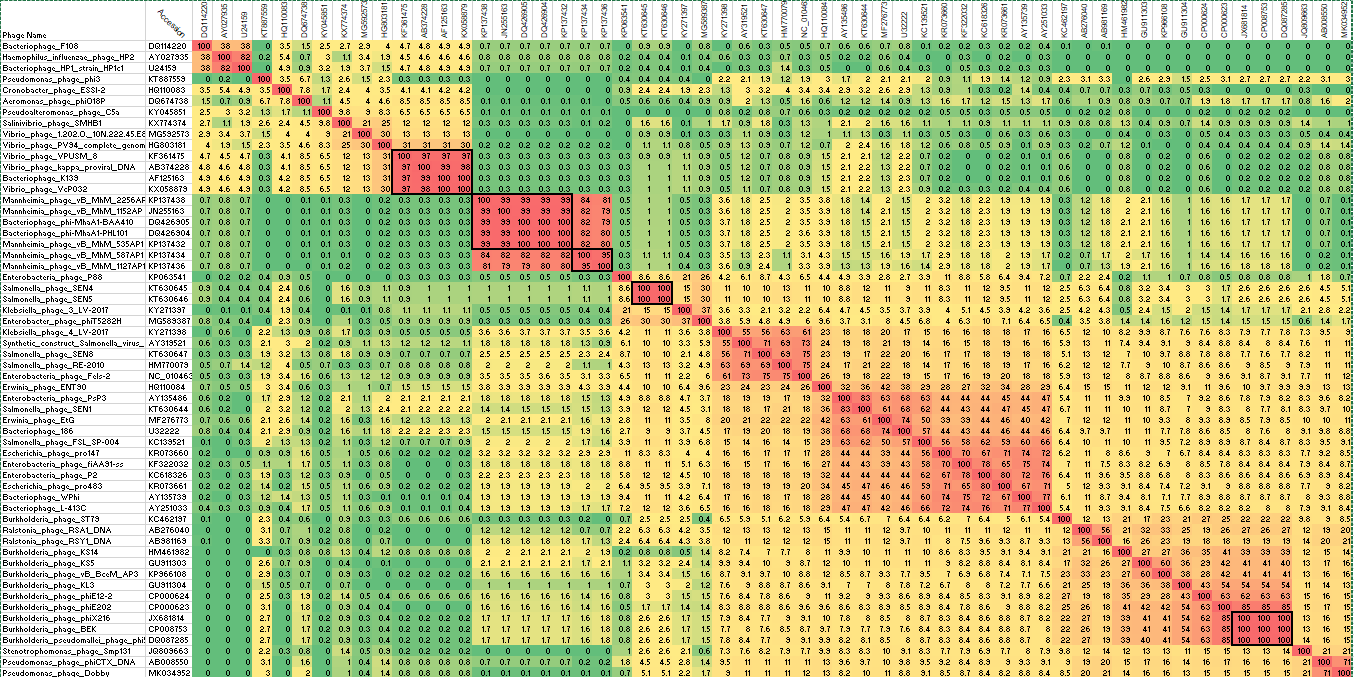
*\* Determined using tRNAscan-SE*

*\*\* Determined using PHANOTATE*

*\*\*\* Determined using BLASTn*

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**Figure 1. Phylogenetic tree constructed with large terminase proteins from phages within *Peduovirinae*, using ‘one-click mode’ on phylogeny.fr [32-38]**



**Figure 2. A similarity matrix showing pairwise nucleotide identity for phages within *Peduovirinae* (Supplementary file 1). Phages belonging to the same species are boxed.**