

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, *Vandenendeviridae*, for a group of lytic *Pseudomonas* phages (Class: *Caudoviricetes*) |
| **Code assigned:** | 2024.037B | |

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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 |  |
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| 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 |

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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:** | 25/05/2024 |

**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| W - Withdrawn |  |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:** |
| The proposal describes the creation of genera that appear to be absent from the Excel module (A; *Jayhopvirus, Rybakvirus, Qinghuavirus* and *Chengduvirus).* Check how you want *Chemalvirus* to be spelled as it is entered as *Chemayvirus* in the Excel module. |

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

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| **Response of proposer:** |
| *Jayhopvirus, Rybakvirus, Qinghuavirus* and *Chengduvirus* do not exist in this family. *Chemalvirus* spelling corrected. |

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| **Revision date:** | 30/09/2024 |

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

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| **Name of accompanying Excel module:** |
| 2024.037B.A.v2.Vandenendeviridae\_nf.xlsx |

|  |  |  |  |
| --- | --- | --- | --- |
| **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:** | |  |
| **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*:  Four genera are currently classified; *Baldwinvirus*, *Nankokuvirus, Otagovirus, Flaumdravirus* and *Pakpunavirus.*  *Proposed* *taxonomic change(s):*   1. To create seven new single-species genera: *Weillhallvirus, Omahavirus, Torinovirus, Yunamivirus, Ventosusvirus, Uavernvirus*, and *Chemalvirus* 2. To create a new genus, *Tartuvirus*, with four species 3. To create two new species in the genus *Kremarvirus* 4. To create a new family, *Vandenendviridae*, for these genera and *Balwinvirus*, *Kremarvirus*, *Nankokuvirus, Otagovirus, Flaumdravirus, Pakpunavirus* and *Shenlongvirus*.   *Justification*:  Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Pseudomonas* myoviruses which share ≥12.2% DNA sequence similarity and 15 core proteins. The new family is named in honour of Marius van de Ende of South Africa. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Species, Genus and Family  *Description of current taxonomy*:  Currently phages of this type are recognized in four genera: *Baldwinvirus*, *Nankokuvirus, Otagovirus, Flaumdravirus* and *Pakpunavirus*. These are lytic myoviruses infecting *Pseudomonas* species.  *Proposed* *taxonomic change(s)*:   1. To create seven new single-species genera: *Weillhallvirus, Omahavirus, Torinovirus, Yunamivirus, Ventosusvirus, Uavernvirus*, and *Chemalvirus* 2. To create a new genus, *Tartuvirus*, with four species 3. To create two new species in the genus *Kremarvirus* 4. To create a new family, *Vandenendviridae*, for these genera and *Balwinvirus*, *Kremarvirus*, *Nankokuvirus, Otagovirus, Flaumdravirus, Pakpunavirus* and *Shenlongvirus*.   *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*: Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Pseudomonas* myoviruses which share ≥12.2% DNA sequence similarity and 15 core proteins. The new family is named in honour of Marius van de Ende of South Africa. |

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| **References:** |
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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. 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Epub 2018 Mar 14. PMID: 29541847.  20. van den Ende, Jan. (2009). Marinus van den Ende. SAMJ: South African Medical Journal, 99(1), 29-32. Retrieved May 25, 2024, from http://www.scielo.org.za/scielo.php?script=sci\_arttext&pid=S0256-95742009000100010&lng=en&tlng=en. |

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| **Tables, Figures:** |

<Start here>

Figure 1. Portion of the VIRIDIC heat map of some 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; Pseu = *Pseudomonas*. The gold highlighted accession numbers and phage names in Column A represent ICTV-recognized species, while in Column B in colour are newly proposed genera and current genera(no colour). The complete VIRIDIC heatmap is provided as supplementary material.

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 *Vandenendeviridae* 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 blue green and black line

Description automatically generated with medium confidence

Figure 3. ViPTree [4] hierarchical tree pruned to show the proposed family *Vandenendeviridae* alongside neighbouring clades. The *Vandenendeviridae* (light-green) and proposed *Mktvariviridae* (blue) are shown as collapsed clades.

A white and blue rectangular object with black squares

Description automatically generated with medium confidence

Figure 4. VirClust protein heatmap of the *Vandenendeviridae* group: 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 PSSC [13].

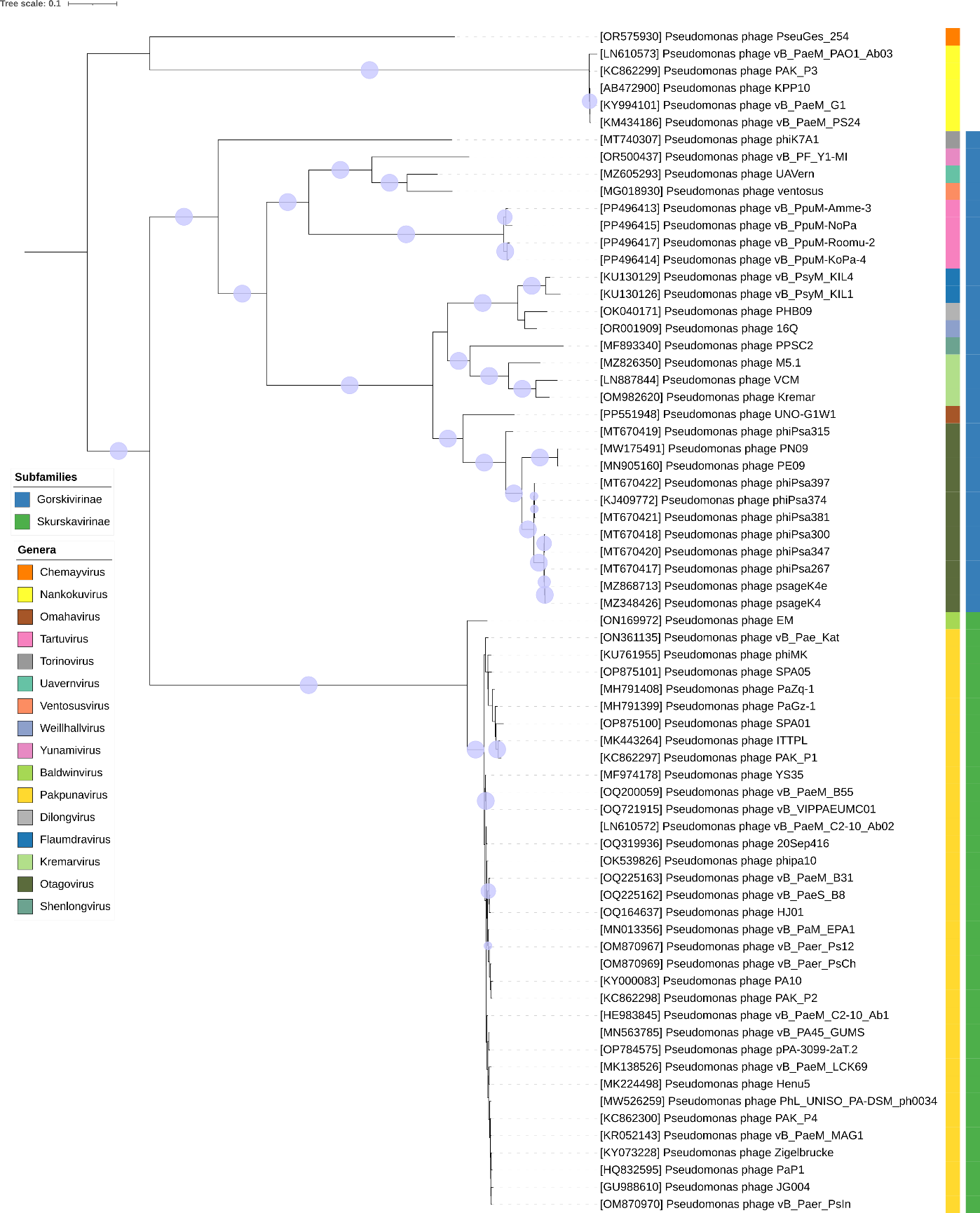


Figure 5. Core genome phylogeny of the proposed *Vandenendeviridae* family of bacterial viruses. A partitioned protein ML phylogeny was created from 27 genes present in all species of the proposed family. Alignments were performed using MAFFT in e-insi mode and trimmed using trimAl with a gap threshold 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.

Table1. Signature genes in the proposed *Vandenendeviridae* 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 (69 total)** | **Percentage of genomes present in protein cluster** | **Predicted gene function** |
| 1 | 69 | 100% | hypothetical protein |
| 2 | 69 | 100% | head decoration protein |
| 3 | 69 | 100% | major capsid protein |
| 4 | 69 | 100% | exodeoxyribonuclease |
| 5 | 69 | 100% | baseplate protein |
| 6 | 69 | 100% | tape measure protein |
| 7 | 69 | 100% | hypothetical protein |
| 8 | 69 | 100% | hypothetical protein |
| 9 | 69 | 100% | hypothetical protein |
| 10 | 69 | 100% | hypothetical protein |
| 11 | 69 | 100% | hypothetical protein |
| 12 | 69 | 100% | hypothetical protein |
| 13 | 69 | 100% | DNA ligase |
| 14 | 69 | 100% | hypothetical protein |
| 15 | 69 | 100% | DNA primase/helicase |
| 16 | 68 | 98.55% | hypothetical protein |
| 17 | 68 | 98.55% | head-tail joining protein |
| 18 | 68 | 98.55% | HNH endonuclease |
| 19 | 68 | 98.55% | hypothetical protein |
| 20 | 68 | 98.55% | hypothetical protein |
| 21 | 68 | 98.55% | hypothetical protein |
| 22 | 68 | 98.55% | baseplate protein |
| 23 | 68 | 98.55% | tail fiber protein |
| 24 | 68 | 98.55% | virion structural protein |
| 25 | 68 | 98.55% | hypothetical protein |
| 26 | 68 | 98.55% | thymidylate synthase |
| 27 | 68 | 98.55% | terminase large subunit |

**Proposals Data:**

**A. To create seven new single-species genera: *Weillhallvirus, Omahavirus, Torinovirus, Yunamivirus, Ventosusvirus, Uavernvirus*, and *Chemalvirus***

**B. To** **create a new genus, *Tartuvirus*, with four species**

**C.** **To create two new species in the genus *Kremarvirus***

**D. To create a new family, *Vandenendviridae*, for these genera and** ***Baldwinvirus*, *Nankokuvirus, Otagovirus, Flaumdravirus* and *Pakpunavirus.***

**Taxonomic Proposals:**

1. **To create seven new single-species genera: *Weillhallvirus, Omahavirus, Torinovirus,Yunamivirus, Ventosusvirus, Uavernvirus*, and *Chemalvirus***

**Origin of the name of this taxon:** This taxon was named after the address (Qinghua East Road) of the College of Biological Science and Technology, Beijing Forestry University where this phage was isolated

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage PHB09 | OK040171.1 | 94.8 | 45.3 | 21 | 185 |

**\* Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Origin of the name of this taxon:** This taxon was named after the building (Weill Hall) at the University of California, Berkeley where this phage was isolated.

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage 16Q | OR001909.1 | 94.6 | 45.0 | 21 | 162 |

**\* Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Origin of the name of this taxon:** This taxon was named after the University of Nebraska at Omaha where is the Biology Department this phage was isolated

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage UNO-G1W1 | PP551948.2 | 98.6 | 48.3 | ND | 188 |

**\* tRNAscan-SE 2.0 at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](about:blank) **did not provide any data**

**Origin of the name of this taxon:** This taxon was named after city in Italy, Torino, where at Istituto per la Protezione Sostenibile Delle Piante this phage was isolated

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage phiK7A1 | MT740307.1 | 98.8 | 48.2 | 23 | 174 |

**\* Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Origin of the name of this taxon:** This taxon was named after the first virus of its type, *Pseudomonas* phage vB\_PF\_Y1-MI

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage vB\_PF\_Y1-MI | OR500437.1 | 93.2 | 45.1 | 21 | 174 |

**\* Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Origin of the name of this taxon:** This taxon was named after the first virus of its type *Pseudomonas* phage ventosus

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage ventosus | MG018930.1 | 97.4 | 49.0 | 17 | 172 |

**\* Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Origin of the name of this taxon:** This taxon was named after the first virus of its type *Pseudomonas* phage UAvern

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| *Pseudomonas* phage UAVern | MZ605293.1 | 101.6 | 51.3 | 20 | 176 |

**\* Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Origin of the name of this taxon:** This taxon was named after the river Chemal in the Altay Region of Russia where at the Institute of Chemical Biology and Fundamental Medicine this *Pseudomonas* phage was isolated.

**Genomic characterization:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %GC | tRNA(\*) | Protein |
| Pseudomonas phage PseuGes\_254 | OR575930.1 | 95.1 | 44.1 | 21 | 182 |

**\*** **Determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

**B. To create a new genus, *Tartuvirus*, with four species**

**Origin of the name of this taxon:** This taxon was named after the University of Tartu, Estonia where these phages were isolated.

**Genomic characterization:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %G+C | tRNA  (\*\*\*) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Pseudomonas* phage vB\_PpuM-Amme-3 | PP496413.1 | 96.7 | 47.2 | 20 | 172 | 100 | 100 |
| *Pseudomonas* phage vB\_PpuM-NoPa | PP496415.1 | 95.7 | 47.2 | 20 | 170 | 93.4 | 91.3 |
| *Pseudomonas* phage vB\_PpuM-KoPa-4 | PP496414.1 | 97.4 | 47.3 | 21 | 171 | 89.3 | 89.5 |
| *Pseudomonas* phage vB\_PpuM-Roomu-2 | PP496417.1 | 96.0 | 47.2 | 21 | 176 | 91.5 | 94.2 |

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

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

**(\*\*\*) determined using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/**

1. **To create two new species in the genus *Kremarvirus***

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

**Historical aspects:** This genus was created through Taxonomy Proposal 2023.027B.Gorskivirinae\_nsf

**Genomic characterization:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | %G+C | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Pseudomonas* phage Kremar | OM982620.1 | 97.6 | 48.6 | 173 | 100 | 100 |
| *Pseudomonas* phage REC | MZ826353.1 | 98.4 | 49.0 | 174 | 73.8 | 86.7 |
| *Pseudomonas* phage Psxphi15 | PP203289.1 | 96.0 | 48.3 | 201 (#) | 81.9 | 85.0 |

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

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

**(#) probably over annotated**

1. **To create a new family, *Vandenendeviridae*, for these genera and *Baldwinvirus*, *Dilongvirus*, *Kremarvirus*, *Nankokuvirus, Otagovirus, Flaumdravirus, Pakpunavirus* and *Shenlongvirus.***

**Origin of the name of this taxon:** This taxon is named in honour of South African medical scientist and virologist (b. 1912, Potgietersrust [now Mokopane], Bosveld, Limpopo, South Africa; d. 1957, Cape Town, Western Cape, South Africa). He studied medicine at the University of Cape Town graduating with a MB ChB in 1933. “In 1935 he joined the Pathology Department at UCT Medical School, under Professor B J Ryrie, as a junior assistant in Pathology and Forensic Pathology.” In 1937 with a scholarship he “proceeded to Cambridge University, where he was awarded a PhD in Pathology in 1940.” During WWII is worked at the National Institute for Medical Research NIMR) on ‘air hygiene’ and rickettsial infections. In 1946 he was appointed to the Chair of

Bacteriology at UCT and in 1948 he was appointed the first director of the Virus Research Unit. “Many papers were published from the Unit, including work on bacteriophages, influenza virus, poliomyelitis, Rift Valley fever, rabies and blue tongue, plus physical and chemical studies on viruses and general methods of virus research.” [20]. In 1953 he was diagnosed with Hodgkin’s disease. Despite this life-limiting illness he devoted his life to research, teaching and administration as Dean of the Faculty.

****

(Photo reproduced from Marinus van den Ende. 9th February 1912-4th June 1957

Evans, D. G. Journal of pathology and bacteriology, 1958-07, Vol.76 (1), p.314-319).

**Rationale:** Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Pseudomonas* myoviruses which share ≥6.9% DNA sequence similarity and possess 15 core genes.