

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

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| **Code assigned:** | ***2023.039B*** |  |
| **Short title:** Create a new subfamily, *Jondennisvirinae* containing three genera (*Septimatrevirus*, *Kipunavirus, Kilunavirus*) [class *Caudoviricetes*] | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | Y |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Jondennisvirinae* | Jonathan J. Dennis | Y |
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|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | April 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.039B.N.v1.Jondennisvirinae\_nsf.xlsx |

**Abstract**

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| As a results of new deposits to GenBank and our VIRIDIC and ViPTree clustering algorithms we now realize that two existing genera (*Septimatrevirus, Kilunavirus*) are sufficiently similar in DNA and protein content to be considered to be part of a new subfamily which we have named *Jondennisvirinae* in honour of Professor Jonathan J. Dennis. To this new taxon we have added a third genus, *Kipunavirus*. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **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]. | |

**Supporting evidence**

**Proposals:**

1. **To add eighteen (18) new species to the genus *Septimatrevirus***
2. **To create a new genus, *Kipunavirus*, with a single species**
3. **To create a new subfamily *Jondennisvirinae***
4. **To move the genus, *Kilunavirus*, into this subfamily**

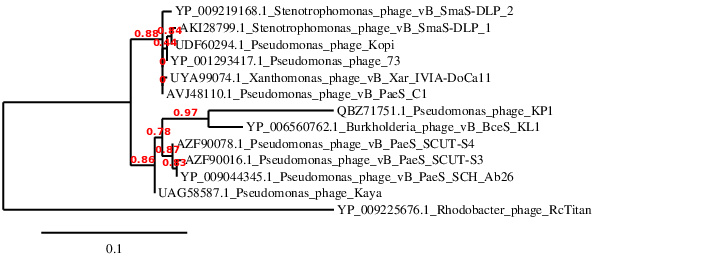
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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Pseudomonas phages PA73, Ab26, Kakheti25 are highlighted in green. Strains within this genus are boxed, while the representatives of the two new genera are highlighted in gold and blue. In the second iteration strains and existing species, except PA73, were removed.

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**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with are indicated with red lines and blue and red arrowheads for the *Kipunavirus* and *Kalunavirus*, respectively.

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**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the MCP proteins from these and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details.”

**Proposal A. To add eighteen (18) new species to the genus *Septimatrevirus***

**Origin of the name of this taxon:** This taxon is named after the first isolated member of this genus, Pseudomonas phage PA73.

**Historical aspects:** This genus was created originally through Taxonomy Proposal 2015.054dB. This genus currently consists of three species *Septimatrevirus Ab26, Septimatrevirus kakheti25* and *Septimatrevirus sv73*.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage PA73 | NC\_007806.1 | 43 | 53.6 | [52](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/5716/891150|Pseudomonas phage 73/viral segment Unknown/) | 0 | 100 | 100 |
| Pseudomonas phage Kaya | [MZ927745.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ927745.1) | 43.07 | 54.3 | [58](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/106773/1720491|Pseudomonas phage Kaya/viral segment/) | 1 | 79.8 | 82.7 |
| Pseudomonas phage vB\_PaeS-Yazdi-M | [LC552830.1](https://www.ncbi.nlm.nih.gov/nuccore/LC552830.1) | 42.44 | 54.4 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92342/913303|Pseudomonas phage vB_PaeS-Yazdi-M/viral segment/) | 0 | 71.9 | 82.7 |
| |  | | --- | | Pseudomonas phage Guyu | | [MZ927746.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ927746.1) | 43.14 | 54.8 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/106774/1720492|Pseudomonas phage Guyu/viral segment/) | 1 | 70.3 | 86.5 |
| Xanthomonas phage Samson | [MN062187.1](https://www.ncbi.nlm.nih.gov/nuccore/MN062187.1) | 43.31 | 54.6 | [57](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83777/672168|Xanthomonas phage Samson/viral segment/) | 1 | 70.2 | 82.7 |
| Xanthomonas phage vB\_Xar\_IVIA-DoCa1 | [ON911538.2](https://www.ncbi.nlm.nih.gov/nuccore/ON911538.2) | 43.55 | 54.4 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/119016/1976875|Xanthomonas phage vB_Xar_IVIA-DoCa1/viral segment/) | 1  (\*\*\*) | 69.5 | 80.8 |
| Pseudomonas phage vB\_PaeS\_SCUT-S3 | [MK165657.1](https://www.ncbi.nlm.nih.gov/nuccore/MK165657.1) | 42.62 | 53.5 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/74799/432067|Pseudomonas phage vB_PaeS_SCUT-S3/viral segment/) | 0 | 76.9 | 88.5 |
| Pseudomonas phage Kopi | [OK330455.1](https://www.ncbi.nlm.nih.gov/nuccore/OK330455.1) | 42.82 | 53.5 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/107426/1728967|Pseudomonas phage Kopi/viral segment/) | 0 | 90.7 | 94.2 |
| Pseudomonas phage Epa40 | [MT118304.1](https://www.ncbi.nlm.nih.gov/nuccore/MT118304.1) | 42.79 | 53.2 | [51](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89036/889151|Pseudomonas phage Epa40/viral segment/) | 0 | 90.0 | 84.6 |
| Pseudomonas phage UF\_RH1 | [OQ259603.1](https://www.ncbi.nlm.nih.gov/nuccore/OQ259603.1) | 42.57 | 53.6 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/125386/2115961|Pseudomonas phage UF_RH1/viral segment/) | 0 | 94.2 | 88.5 |
| Pseudomonas phage BUCT-PX-5 | OP422637.1 | 42.8 | 53.6 | 59 | 0 | 94.2 | 92.3 |
| Stenotrophomonas phage vB\_SmaS-DLP\_1 | [KR537872.1](https://www.ncbi.nlm.nih.gov/nuccore/KR537872.1) | 42.89 | 53.7 | [57](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70193/467433|Stenotrophomonas phage vB_SmaS-DLP_1/viral segment/) | 0 | 94.5 | 92.3 |
| Stenotrophomonas phage vB\_SmaS-DLP\_2 | [KR537871.1](https://www.ncbi.nlm.nih.gov/nuccore/KR537871.1) | 42.59 | 53.7 | [58](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70188/467431|Stenotrophomonas phage vB_SmaS-DLP_2/viral segment Unknown/) | 0 | 91.8 | 94.2 |
| Pseudomonas phage vB\_PaeS\_C1 | [MG897800.1](https://www.ncbi.nlm.nih.gov/nuccore/MG897800.1) | 43.13 | 53.6 | [59](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68539/369688|Pseudomonas phage vB_PaeS_C1/viral segment/) | 0 | 93.2 | 92.3 |
| Pseudomonas phage TehO | [OK330456.1](https://www.ncbi.nlm.nih.gov/nuccore/OK330456.1) | 43.02 | 53.7 | [56](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/107427/1728968|Pseudomonas phage TehO/viral segment/) | 0 | 89.9 | 96.1 |
| Pseudomonas phage PSV3 NODE\_3 | OP712474.1 | 40.2 | 53.2 | 71 | 0 | 83.6 | 59.6 |
| Pseudomonas phage PSV3 NODE\_4 | OP712479.1 | 39.0 | 53.3 | 63 | 0 | 87.8 | 53.9 |
| Pseudomonas phage PSV3 NODE\_1 | OP712460.1 | 46.3 | 53.5 | 86 | 0 | 88.7 | 75.0 |
| Pseudomonas phage PSV3 NOD2\_2 | OP712466.1 | 43.3 | 53.3 | 73 | 0 | 86.2 | 63.5 |

**(\*) determined using BLASTn [1,2] or VIRIDIC [3]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**(\*\*\*) determined using tRNAScan-SE [11]**

***Septimatrevirus* References:**

Loh B, Wang X, Hua X, Luo J, Wen T, Zhang L, Ma L, Manohar P, Nachimuthu R, Grainge I, Yu Y, Leptihn S. Complete Genome Sequences of Bacteriophages Kaya, Guyu, Kopi, and TehO, Which Target Clinical Strains of Pseudomonas aeruginosa. Microbiol Resour Announc. 2021 Dec 2;10(48):e0104321. doi: 10.1128/MRA.01043-21. Epub 2021 Dec 2. PMID: 34854702; PMCID: PMC8638596.

Clark S, Le T, Moreland R, Liu M, Gonzalez CF, Gill JJ, Ramsey J. Complete Genome Sequence of Xanthomonas Siphophage Samson. Microbiol Resour Announc. 2019 Oct 17;8(42):e01097-19. doi: 10.1128/MRA.01097-19. PMID: 31624152; PMCID: PMC6797541.

Peters DL, Lynch KH, Stothard P, Dennis JJ. The isolation and characterization of two Stenotrophomonas maltophilia bacteriophages capable of cross-taxonomic order infectivity. BMC Genomics. 2015 Sep 3;16(1):664. doi: 10.1186/s12864-015-1848-y. PMID: 26335566; PMCID: PMC4559383.

1. **To create a new genus, *Kipunavirus*, with a single species**

**Origin of the name of this taxon:** This taxon is named after Pseudomonas phage KP1

**Historical aspects:** This lytic phage was isolated against a Pseudomonas sp from tap water by K. Petrzik et al. (Department of Plant Virology, Biology Centre AS CR, v.v.i., Institute of Plant Molecular Biology, Branisovska 31, Ceske Budejovice, 0 370 05, Czech Republic).

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage KP1 | [MK574078.1](https://www.ncbi.nlm.nih.gov/nuccore/MK574078.1) | 43.47 | 46.6 | [36](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87754/809334|Pseudomonas phage KP1/viral segment/)(\*\*\*) | 0 | 100 | 100 |

**(\*\*\*) Underannotated**

**Conclusion:** A genus comprised of a single species is proposed on the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3) this is a cohesive genus.

1. **To create a new subfamily *Jondennisvirinae***

**Origin of the name of this taxon:** This taxon was named in honour of Professor Jonathan Dennis (b. 1960). Dr. Dennis earned his PhD in Bacterial Genetics, at The University of Calgary in 1995, and after almost five years post-doctoral work at Rutgers, The State

University of New Jersey joined the Biological Sciences Department of the University of Alberta. He is now full professor in that department. He has published extensively on phages of the *Burkholderia cepacia* complex, and *Stenotrophomonas maltophilia*, and isolated Burkholderia phage vB\_BceS\_KL1 the first member of the *Kilunavirus* genus.

**Rationale:** These siphoviruses possess linear double-stranded DNA genomes which are on average 43.0 kb with a mol%G+C content of 49.5. They usually do not encode for tRNAs. At the DNA level all members of this subfamily share ≥41% sequence similarity, which is consistent with them belonging to the same subfamily [10].

1. **To move the genus, *Kilunavirus* into the subfamily *Jondennisvirinae***

**Origin of the name of this taxon:** This taxon was named after Burkholderia phage vB\_BceS\_KL1

**Historical aspects:** This taxon was established through Taxonomy Proposal 2019.002B.A.v1.Kilunavirus.

**Electron micrograph - Figure 4:** Phage KL1 negatively stained with 2% phosphotungstic acid; scale bar: 50 nm. Derived from BMC Genomics; <https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2164-13-223>

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**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Burkholderia phage vB\_BceS\_KL1 | [JF939047.1](https://www.ncbi.nlm.nih.gov/nuccore/JF939047.1) | 42.83 | 54.6 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/14609/459694|Burkholderia phage vB_BceS_KL1/viral segment Unknown/) | 0 | 100 | 100 |

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3) this taxon belongs in the subfamily *Jondennisvirinae*.

**Specific Reference:** Lynch KH, Stothard P, Dennis JJ. Comparative analysis of two phenotypically-similar but genomically-distinct Burkholderia cenocepacia-specific bacteriophages. BMC Genomics. 2012 Jun 7;13:223. doi: 10.1186/1471-2164-13-223. PMID: 22676492; PMCID: PMC3483164.

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