

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

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| **Code assigned:** | ***2023.036B*** |  |
| **Short title:** To reassess the classification of *Jedunavirus*, creating eight new genera in the subfamily *Jameshumphriesvirinae* [class *Caudoviricetes*] | | |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Turner D, Moraru C, Tolstoy I, Kropinski AM | [Dann2.Turner@uwe.ac.uk](about:blank); [liliana.cristina.moraru@uol.de](about:blank); [tolstoy@ncbi.nlm.nih.gov](about:blank); [Phage.Canada@gmail.com](about:blank) |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| University of the West of England, Bristol, UK [DT]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  National Center for Biotechnology Information, MD, USA [IT]  University of Guelph, Ontario, Canada [AMK] |

**Corresponding author**

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| Andrew M. Kropinski |

**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)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 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**

|  |
| --- |
| 2023.036B.N.v1.Jameshumphriesvirinae\_8ng.xlsx |

**Abstract**

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| The viral genus, *Jedunavirus*, was proposed in 2018 through Taxonomy Proposal 2018.076B. Since that time numerous other related Klebsiella phage have been deposited in GenBank, and we have been made aware that the current description of this genus is too broad. This proposal corrects this problem, through the creation of a subfamily, *Jameshumphriesvirinae* and eight new genera. |

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

**Overall Rationale:** The viral genus, *Jedunavirus*, was proposed in 2018 through Taxonomy Proposal 2018.076B. Since that time numerous other related Klebsiella phages have been deposited in GenBank, and we have been made aware that the current description of this genus is too broad [10]. This proposal corrects this problem.

**Proposals:**

1. **Cr****eate a genus,** ***Parissaclayvirus*, with a single species.**
2. **Create a** **genus, *Chaoyangvirus,* with a single species.**
3. **Create a genus, *Ringroadvirus*, with a single species.**
4. **Create a genus, *Mascletvirus*, with a single species**
5. **Create a genus, *Geezettvirus*, with a single species.**
6. **Create a genus, *Sircambvirus*, with six species.**
7. **Create a genus, *Bimevirus*, with three species.**
8. **Create a genus, *Zewailvirus*, with two species.**
9. **Create a subfamily, *Jameshumphriesvirinae*, with these eight new genera.**
10. **Transfer *Peatvirus* and *Jedunavirus* to this new subfamily.**

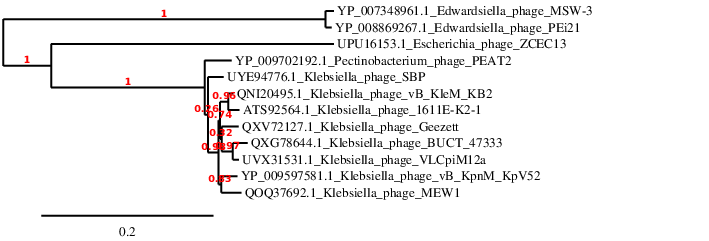
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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to members of a genus, as defined below. Abbreviations: phg = phage; Kleb = Klebsiella; Esch = Escherichia; Pect = Pectobacterium.

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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) Phage Proteomic Tree [5]. With the exception of Pectobacterium PEAT2, Klebsiella phages vB\_KpnM\_KpV79, KpV52 and JD001 the phages of interest are indicated with **red lines and stars**.



**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the DNA polymerases 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.” N.B. some of the phages mentioned in this proposal have not been annotated.

**Taxonomic Proposals:**

1. **Create** **a genus, *Parissaclayvirus*, with a single species.**

**Origin of the name of this taxon:** This taxon is named after Université Paris-Saclay where in the Institute for Integrative Biology of the Cell, Professor C. Pourcel and C. Essoh isolated the first virus of its type, Klebsiella phage vB\_KpnS\_POU148.

**Historical aspects:** Lytic Klebsiella myophage vB\_KpnS\_POU148 was isolated against Klebsiella pneumoniae from Cote d'Ivoire.

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Klebsiella phage vB\_KpnS\_POU148 | [MN689778.1](about:blank) | 49.17 | 48.4 | [72](about:blank#!/proteins/86447/751423|Klebsiella phage vB_KpnM_15-38_KLPPOU148/viral segment/) | 0 |

1. **Create a genus,** ***Chaoyangvirus*, with a single species.**

**Origin of the name of this taxon:** This taxon is named after Chaoyang District, Beijing, (China) where in the College of Life Science and Technology, Beijing University of Chemical Technology where G. Zhang et al. isolated the first virus of its type, Klebsiella phage BUCT\_49532.

**Historical aspects:** Lytic Klebsiella myophage BUCT\_49532 was isolated from sewage against Klebsiella pneumoniae

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Klebsiella phage BUCT\_49532 | [MZ374361.1](about:blank) | 49.53 | 48.8 | [81](about:blank#!/proteins/104054/1651777|Klebsiella phage BUCT_49532/viral segment/) | 0 |

1. **Create a genus, *Ringroadvirus*, with a single species.**

**Origin of the name of this taxon:** This taxon is named after the address, 15 North Third Ring Road East where the first virus of its type, Klebsiella phage BUCT\_47333 was isolated.

**Historical aspects:** Lytic Klebsiella myophage BUCT\_47333 was isolated from sewage against Klebsiella pneumoniae by G. Zhang et al. College of Life Science and Technology, Beijing University of Chemical Technology, Beijing, China.

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Klebsiella phage BUCT\_47333 | [MZ398021.1](about:blank) | 47.33 | 49.2 | [73](about:blank#!/proteins/106609/1720268|Klebsiella phage BUCT_47333/viral segment/) | 0 |

1. **Create a genus, *Mascletvirus* with a single species.**

**Origin of the name of this taxon:** The name of this taxon refers to a type of firecracker used in Valencia and called “masclet”, whose shape somewhat resembles the virus.

**Historical aspects:** Lytic Klebsiella myophage VLCpiM12a was isolated from soil against Klebsiella pneumoniae by B. Beamud et al. in Evolution and Health, Institute for Integrative Systems Biology (I2SysBio), Valencia, Spain.

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Klebsiella phage VLCpiM12a | [ON602758.1](about:blank) | 48.83 | 49.6 | [75](about:blank#!/proteins/117852/1931621|Klebsiella phage VLCpiM12a/viral segment/) | 0 |

1. **Create a genus, *Geezettvirus*, with a single species.**

**Origin of the name of this taxon:** This taxon is named directly after the first virus of its type, Klebsiella phage Geezett.

**Historical aspects:** Lytic Klebsiella myophage Geezett was isolated from sewage water obtained from the Sir Run Run Shaw Hospital in Hangzhou, China, using an enrichment culture with the clinical multidrug-resistant Klebsiella pneumoniae strain GZ-1 [11].

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Klebsiella phage Geezett | [MZ504995.1](about:blank) | 50.71 | 48.1 | [79](about:blank#!/proteins/106804/1720522|Klebsiella phage Geezett/viral segment/) | 0 |

1. **Create a genus, *Sircambvirus*, with six species.**

**Origin of the name of this taxon:** This taxon is named after the **S**tate **R**esearch **C**enter for **A**pplied **M**icrobiology and **B**iotechnology (SRC AMB, Obolensk, Moscow reg. 142279, Russian Federation) where the first virus of its type, Klebsiella phage vB\_KpnM\_KpV52, was isolated.

**Historical aspects:** Lytic Klebsiella myophage. Klebsiella phage pKp383 isolated in China, Klebsiella phages vB\_KpnM\_KpV52, vB\_KpnM\_KpV79 and vB\_KpnM\_FZ14 were isolated in Russia; Klebsiella phage vB\_KpnM\_JustaPhage isolated in USA; Klebsiella phage MEW1 isolated in Australia. The phages KpnM\_KpV52, vB\_KpnM\_KpV79 were erroneously assigned to the species *Jedunavirus KpV80*  and *Jedunavirus KvP52* respectively. With this proposal they are moved into the correct genus and their species names are also corrected.

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Klebsiella phage vB\_KpnM\_KpV52 | [NC\_041900.1](about:blank) | [KX237516.1](about:blank) | 47.41 | 49.0 | [75](about:blank#!/proteins/63117/465740|Klebsiella phage vB_KpnM_KpV52/viral segment/) | 100 | 100 |
| Klebsiella phage vB\_KpnM\_KpV79 | [NC\_042041.1](about:blank) | [MF663761.1](about:blank) | 47.76 | 49.0 | [75](about:blank#!/proteins/64175/466583|Klebsiella phage vB_KpnM_KpV79/viral segment/) | 64.3 | 80.0 |
| Klebsiella phage vB\_KpnM\_FZ14 | NC\_071133.1 | [MK521906.1](about:blank) | 49.37 | 48.6 | [85](about:blank#!/proteins/79530/511559|Klebsiella phage vB_KpnM_FZ14/viral segment/)  (\*\*\*) | 79.1 | ND |
| Klebsiella phage vB\_KpnM\_JustaPhage |  | [OK499978.1](about:blank) | 48.13 | 48.6 | [79](about:blank#!/proteins/109180/1760445|Klebsiella phage vB_KpnM_JustaPhage/viral segment/) | 82.7 | 86.7 |
| Klebsiella phage MEW1 |  | [MT894004.1](about:blank) | 47.13 | 49.3 | [67](about:blank#!/proteins/96478/1479965|Klebsiella phage MEW1/viral segment/) | 70.6 | 76.0 |
| Klebsiella phage pKp383 |  | [ON809560.1](about:blank) | 48.84 | 48.5 | [73](about:blank#!/proteins/117881/1931650|Klebsiella phage pKp383/viral segment/) | 64.9 | 77.3 |

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

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

**(\*\*\*) Incomplete annotation; the value presented is from the RefSeq**

1. **Create a genus, *Bimevirus*, with three species.**

**Origin of the name of this taxon:** This taxon is named after the **B**eijing **I**nstitute of **M**icrobiology and **E**pidemiology where the first virus of its type, Klebsiella phage vB\_KpnM\_IME346, was isolated.

**Historical aspects:** Lytic Klebsiella myophage vB\_KpnM\_IME346 was isolated against Klebsiella pneumoniae by M.M. Gao et al. in the State Key Laboratory of Pathogen and

Biosecurity, Beijing Institute of Microbiology and Epidemiology, China). Klebsiella phage 1611E-K2-1 was isolated by T.-L. Lin et al. (Department of Microbiology, National Taiwan University College of Medicine); while Klebsiella phage vB\_KleM\_KB2 was isolated by Q. Peng (College of Life Sciences, Hainan Normal University, Haikou, China). They are all lytic phages active on Klebsiella pneumoniae.

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Klebsiella phage vB\_KpnM\_IME346 |  | [MK685667.1](about:blank) | 49.48 | 49.1 | [79](about:blank#!/proteins/79494/502391|Klebsiella phage vB_KpnM_IME346/viral segment/) | 100 | 100 |
| Klebsiella phage 1611E-K2-1 |  | [MG197810.1](about:blank) | 47.8 | 48.9 | 86 (\*\*\*) | 67.8 | ND |
| Klebsiella phage vB\_KleM\_KB2 | NC\_071139.1 | [MT757392.1](about:blank) | 48.25 | 48.9 | 93 [(\*\*\*)](about:blank#!/proteins/107229/1723939|Klebsiella phage vB_KleM_KB2/viral segment/) | 71.3 | ND |

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

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

**(\*\*\*) underannotated; values from RefSeq**

1. **Create a genus, *Zewailvirus*, with two species.**

**Origin of the name of this taxon:** This taxon is named after in honour of the Zewail City of Science and Technology (6th of October City, Giza, Egypt) where the first virus of its type, Escherichia phage ZCEC13, was isolated.

**Historical aspects:** Lytic Escherichia myophage ZCEC13 was isolated against an Escherichia sp. by S. Ragab et al. Bacteriophage SBP was isolated by M. Asif (University of the Punjab, Lahore, Pakistan) from sewage against Klebsiella pneumoniae.

**Electron micrograph:** NA

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage ZCEC13 | NC\_071140.1 | [ON086804.1](about:blank) | 48.02 | 48.9 | 88 (\*\*\*) | 100 | 100 |
| Klebsiella phage SBP |  | OP114730.1 | 49.37 | 48.7 | 78 | 70.9 | ND |

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

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

**(\*\*\*) overannotated; value from RefSeq**

1. **Create a subfamily, *Jameshumphriesvirinae*, with the above mentioned genera.**

**Origin of the name of this taxon:** This taxon is named in honour of James C. Humphries (b. 1913, Cadiz, Kentucky; d. 2002, Lexington, KY; data kindly provided by archivists of UK Libraries Special Collections Research Center). After obtaining his PhD from Yale University he joining the faculty of the University of Kentucky in 1944. He retired in 1978. He is honoured by this proposal because he is one of the first scientists to isolate a Klebsiella bacteriophage and characterize its capsule depolymerase activity [12].

**Rationale:** Based upon the criteria which we have defined [10] the above listed phages display sufficient similar properties to be included in a single subfamily. Taking one representative from each genus, and using the default setting Bidirectional Best Hit algorithm of CoreGenes5.0 [7] reveals that these viruses share 34 protein homologs. This value and the overall DNA sequence similarity (>53.8%; Figure 1) confirm that these viruses cluster at the subfamily level.

1. **Transfer *Peatvirus* and *Jedunavirus* to this new subfamily.**

**Rationale:** As described above, these established genera are sufficiently similar to the above-described new genera to be included in this subfamily. *Peatvirus* was created through Taxonomy Proposal 2018.084B, and contains a single species. *Jedunavirus* was created through Taxonomy Proposal 2018.076B with three species encompassing Klebsiella phages JD001, vB\_KpnM\_KpV79, and vB\_KpnM\_KpV52. In NCBI KpV79 is listed as KpV80 which will be corrected by this proposal.

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