

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | To create a new subfamily, *Mcshanvirinae*, for *Streptococcus* prophages [Class: *Caudoviricetes*] | |
| **Code assigned:** | 2024.023B |

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| --- | --- | --- | --- |
| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Tolstoy I | National Center for Biotechnology Information, MD, USA | tolstoy@ncbi.nlm.nih.gov |  |
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| Kropinski AM | University of Guelph, Ontario, Canada | 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:** |
| The 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:** | 06/05/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| 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| W - Withdrawn |  |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:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** | DD/MM/YYYY |

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

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| **Name of accompanying Excel module:** |
| 2024.023B.A.v1.Mcshanvirinae\_nsf.xlsx |

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon |  | 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** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
| Mcshanvirinae | W. Michael McShan | 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*:  The viruses classified in this proposal do not have a current taxonomic assignment.  *Proposed* *taxonomic change(s):*  We propose a new subfamily, named in honour of Professor W. Michael McShan, of *Streptococcus* temperate siphoviruses containing three newly established genera: *Adrianbuildvirus, Medawarvirus* and *Phadecavirus*.  *Justification*:  The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  None of these phages have been classified.  *Proposed* *taxonomic change(s)*:  We propose a new subfamily, named in honour of Professor W. Michael McShan, of *Streptococcus* siphoprophages containing three genera: *Adrianbuildvirus, Medawarvirus* and *Phadecavirus*.  *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]. In the case of temperate phages such as these we have allowed some leeway on this cutoff.  **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]  *Justification*:  On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive subfamily. This group share at least 10.7% DNA sequence similarity and 11 homologous proteins [6] including: terminase large subunit, head maturation protease, tail tape measure protein, tail protein, receptor binding protein, endolysin, integrase, anti-repressor, and replication initiation protein. |

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| **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. Furi L, Crawford LA, Rangel-Pineros G, Manso AS, De Ste Croix M, Haigh RD, Kwun MJ, Engelsen Fjelland K, Gilfillan GD, Bentley SD, Croucher NJ, Clokie MR, Oggioni MR. Methylation Warfare: Interaction of Pneumococcal Bacteriophages with Their Host. J Bacteriol. 2019 Sep 6;201(19):e00370-19. doi: 10.1128/JB.00370-19. PMID: 31285240; PMCID: PMC6755750.  12. Brueggemann AB, Harrold CL, Rezaei Javan R, van Tonder AJ, McDonnell AJ, Edwards BA. Pneumococcal prophages are diverse, but not without structure or history. Sci Rep. 2017 Feb 20;7:42976. doi: 10.1038/srep42976. PMID: 28218261; PMCID: PMC5317160.  13. Croucher NJ, Mostowy R, Wymant C, Turner P, Bentley SD, Fraser C. Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. PLoS Biol. 2016 Mar 2;14(3):e1002394. doi: 10.1371/journal.pbio.1002394. PMID: 26934590; PMCID: PMC4774983. |

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| **Tables, Figures:** |

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**Proposals Data:**

1. **Create a new genus,** ***Adrianbuildvirus* with eight species**
2. **Create a new genus, *Medawarvirus* with fourteen species**
3. **Create a new genus, *Phadecavirus* with three species**
4. **Create a new subfamily, *Mcshanvirinae* for these three genera**

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**Figure 1. A. VIRIDIC heat map Subfamily 1:** 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; Stre = *Streptococcus*. The **grey**, **purple** and **green** arrowheads indicate the *Adrianbuildvirus, Medawarvirus* and *Phadecavirus*, respectively. Because of possible difficulty in reading this figure we have attached the original Excel spreadsheet (Mcshanvirinae VIRIDIC heatmap).

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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 **red lines and stars**.

1. **Create a new genus, *Adrianbuildvirus* with eight species**

**Origin of the name of this taxon:** The name of this taxon derives from the Adrian Building at The University of Leicester (UK) where in the Department of Genetics L. Furi, M.R. Clockie, and M.R. Oggioni, isolated Streptococcus phage SpSL1 [11].

**Historical aspects:** *Streptococcus pneumoniae* phage SpSL1 was oral swab samples from healthy adult volunteers. Electron microscopy revealed an isometric capsid (∼50 nm) and long noncontractile tail (∼160 nm) ending in a single tail fiber (∼110 nm). pSL1 possesses a linear genome of 33,756 bp with a GC content of 38.6%. An 11-base single-stranded cohesive end (5′-CGGTGTCAATC-3′), required for genome recircularization, was found at the genome ends. It is temperate possessing an integrase [11]. Other phages of this taxon which have been described in publications include IPP5, IPP41, IPP42, IPP43, IPP44, IPP51 [12], and phiARI0923 [13].

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Streptococcus* phage SpSL1 | KM882824.1 | 33.8 | 50 | 100.0 | 100 |
| *Streptococcus* phage IPP5 | KY065449.1 | 33.5 | 47 | 52.0 | 44.0 |
| *Streptococcus* phage IPP44 | KY065484.1 | 30.6 | 45 | 58.6 | 58.0 |
| *Streptococcus* phage IPP42 | KY065482.1 | 35.1 | 43 | 64.1 | 54.0 |
| *Streptococcus* phage IPP51 | KY065489.1 | 32.8 | 48 | 64.7 | 54.0 |
| *Streptococcus* phage phiARI0923 | KT337370.1 | 33.5 | 35(\*\*\*) | 65.1 | 50.0 |
| *Streptococcus* phage IPP41 | KY065481.1 | 34.9 | 46 | 65.3 | 56.0 |
| *Streptococcus* phage IPP43 | KY065483.1 | 33.0 | 47 | 66.0 | 56.0 |

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

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

**(\*\*\*) probably underannotated**

1. **Create a new genus, *Medawarvirus* with fourteen species**

**Origin of the name of this taxon:** The name of this taxon derives from Peter Medawar Building for Pathogen Research, Nuffield Department of Medicine, University of Oxford (UK) where many of these phages were characterized [12].

**Historical aspects:** The IPP series of temperate *Streptococcus pneumoniae* siphoviruses were all isolated at Oxford [11], while *Streptococcus* phage phiARI0131-2 was isolated at Imperial College London from Streptococcus pneumoniae 10B01058 [13].

**Genome summary: .**

|  |  |  |  |
| --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | Overall % DNA sequence identity (\*) |
| *Streptococcus* phage IPP12 | KY065454.1 | 34.4 | 100.0 |
| *Streptococcus* phage IPP22 | KY065463.1 | 36.3 | 81.1 |
| *Streptococcus* phage IPP18 | KY065459.1 | 34.2 | 80.9 |
| *Streptococcus* phage IPP57 | KY065494.1 | 33.1 | 79.3 |
| *Streptococcus* phage IPP20 | KY065461.1 | 37.4 | 83.7 |
| *Streptococcus* phage IPP21 | KY065462.1 | 37.1 | 79.8 |
| *Streptococcus* phage IPP30 | KY065471.1 | 36.8 | 82.7 |
| *Streptococcus* phage IPP11 | KY065453.1 | 37.5 | 78.7 |
| *Streptococcus* phage IPP29 | KY065470.1 | 33.9 | 80.5 |
| *Streptococcus* phage IPP19 | KY065460.1 | 33.9 | 82.7 |
| *Streptococcus* phage phiARI0131-2 | KT337342.1 | 34.6 | 77.6 |
| *Streptococcus* phage IPP63 | KY065499.1 | 34.3 | 72.8 |
| *Streptococcus* phage IPP17 | KY065458.1 | 34.9 | 79.7 |
| *Streptococcus* phage IPP28 | KY065469.1 | 33.0 | 77.6 |
|  |  |  |  |

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

***Streptococcus* phage IPP58 (KY065495.1) is a strain of IPP57**

1. **Create a new genus, *Phadecavirus* with three species**

**Origin of the name of this taxon:** The name of this taxon derives from Streptococcus phage PH10 (**Ph** a plus **deca**).

**Historical aspects:** These temperate siphoviruses infect *Streptococcus infantis* (phage 23TH) and *Streptococcus oralis* (PH10 & OlisA1) which were isolated in Ireland, Switzerland and the UK, respectively.

**Genome summary: .**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Streptococcus* phage PH10 | FN391954.1 | 31.3 | 54 | 100 | 100 |
| *Streptococcus* phage 23TH | MT900487.1 | 32.3 | 49 | 58.9 | 61.1 |
| *Streptococcus* phage OlisA1 | OL774868.1 | 30.2 | 49 | 65.1 | 72.2 |

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

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

1. **Create a new subfamily, *Mcshanvirinae* for these three genera**

**Origin of the name of this taxon:** This taxon is named in honour of American microbiologist Dr. W. Michael McShan (b. 1953). He did his doctorate with Richard Hull at Baylor College of Medicine on Neisseria gonorrhoeae. This was followed by post-doctoral studies at the VA Medical Center (Houston, Texas) with Roger Rossen (infectious disease) and the University of Oklahoma Health Sciences Center with Joseph Ferretti (genetics and genomics of Streptococcus pyogenes). From there he joined the Department of Pharmaceutical Sciences at the University of Oklahoma College of Pharmacy until his retirement in 2023. His laboratory was involved in a number of investigations involving bacteriophages of S. pyogenes including the discovery and characterization of the phage-like chromosomal islands that mediate a mutator phenotype (DOI: 10.1128/JB.01569-07) and the lysogen origin of the lytic transducing phage A25 (DOI: 10.1128/JB.00358-18).



(photo copied from https://pharmacy.ouhsc.edu/directory/michael-mcshan-ph-d)

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive subfamily. This group share at least 10.7% DNA sequence similarity and 11 homologous proteins [6] including: terminase large subunit, head maturation protease, tail tape measure protein, tail protein, receptor binding protein, endolysin, integrase, anti-repressor, and replication initiation protein.