

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

|  |  |  |
| --- | --- | --- |
| **Title:** | To create a new subfamily, *Ferrettivirinae*, for *Streptococcus* prophages [Class: *Caudoviricetes*] | |
| **Code assigned:** | 2024.013B |  |

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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 |  |
| Moraru C | Carl von Ossietzky Universität Oldenburg, Germany | liliana.cristina.moraru@uol.de |  |
| 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:** | 07/05/2024 |

**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| W - Withdrawn |  |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:** |
| 2024.013B.A.v1.Ferrettivirinae\_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** |
| *Ferrettivirinae* | Joseph J. Ferretti | 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 in the class *Caudoviricetes*, named in honour of Professor Joseph J. Ferretti, of *Streptococcus* temperate siphoprophages containing three genera: *Spinunavirus, Norfolkplacevirus* and *Hinxtonvirus*.  *Justification*:  Collectively these phages share ≥29.7% DNA sequence similarity and 14 homologous proteins (22.2% in common). |

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| * **Text 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 Joseph J. Ferretti, of *Streptococcus* temperate siphoprophages containing three genera: *Spinunavirus, Norfolkplacevirus* and *Hinxtonvirus*. Collectively these phages share ≥29.7% DNA sequence similarity and 14 homologous proteins (22.2% common).  *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*: These taxa fit within the demarcation criteria outlined above. |

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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. |

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| **Tables, Figures:** |

**Proposals Data:**

1. **Create a new genus,** ***Spinunavirus* with eighteen species**
2. **Create a new genus, *Norfolkplacevirus* with two species**
3. **Create a new genus, *Hinxtonvirus* with three species**
4. **Create a new subfamily, *Ferrettivirinae* for these three genera**



**Figure 1. A. VIRIDIC heat map Subfamily 2:** 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 *Spinunavirus, Norfolkplacevirus* and *Hinxtonvirus*, respectively. The full VIRIDIC heatmap is provided as supplementary material.











**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, *Spinunavirus* with eighteen species**

**Origin of the name of this taxon:** The name of this taxon derives from *Streptococcus* phage Spn1

**Historical aspects:** Temperate siphoviral prophage Spn1 was discovered in*Streptococcus pneumonia* [DeBardeleben et al. 2014] at the University of Pennsylvania (Philadelphia, PA, USA)

**Genome summary:**

|  |  |  |  |
| --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Overall % DNA sequence identity (\*) |
| *Streptococcus* phage Spn1 | KJ417497.1 | 41.3 | 100.0 |
| *Streptococcus* phage IPP61 | KY065497.1 | 50.9 | 79.3 |
| *Streptococcus* phage phiARI0131-1 | KT337341.1 | 42.9 | 86.9 |
| *Streptococcus* phage 040922 | FR671406.1 | 40.1 | 81.3 |
| *Streptococcus* phage IPP9 | KY065451.1 | 41.2 | 82.2 |
| *Streptococcus* phage IPP60 | KY065496.1 | 42.0 | 67.8 |
| *Streptococcus* phage SF39 | OK173051.1 | 41.3 | 74.6 |
| *Streptococcus* phage phiARI0399 | KT337349.1 | 40.6 | 78.7 |
| *Streptococcus* phage IPP10 | KY065452.1 | 40.6 | 74.8 |
| *Streptococcus* phage IPP32 | KY065473.1 | 41.4 | 75.4 |
| *Streptococcus* phage IPP50 | KY065488.1 | 40.3 | 81.9 |
| *Streptococcus* phage phiARI0460-1 | KT337352.1 | 41.8 | 79.5 |
| *Streptococcus* phage IPP8 | KY065450.1 | 40.1 | 81.3 |
| *Streptococcus* phage IPP31 | KY065472.1 | 39.8 | 79.8 |
| *Streptococcus* phage IPP36 | KY065476.1 | 40.8 | 74.5 |
| *Streptococcus* phage IPP37 | KY065477.1 | 39.2 | 76.4 |
| *Streptococcus* phage phiARI0460-2 | KT337353.1 | 42.2 | 75.4 |
| *Streptococcus* phage phiARI0468-2 | KT337356.1 | 42.2 | 80.7 |

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

**Relevant reference for this taxon:**

DeBardeleben HK, Lysenko ES, Dalia AB, Weiser JN. Tolerance of a phage element by *Streptococcus pneumoniae* leads to a fitness defect during colonization. J Bacteriol. 2014 Jul;196(14):2670-80. doi: 10.1128/JB.01556-14. Epub 2014 May 9. PMID: 24816604; PMCID: PMC4097588. [*Streptococcus* phage Spn1]

1. **Create a new genus, *Norfolkplacevirus* with two species**

**Origin of the name of this taxon:** The name of this taxon derives from the address of the Department of Infectious Disease Epidemiology, Imperial College London, Norfolk Place, St. Mary's Campus, London, England where the first virus of its type *Streptococcus* phage phiARI0746 was isolated

**Historical aspects:** These are temperate siphoviruses from *Streptococcus pneumoniae*.

**Genome summary:**

|  |  |  |  |
| --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Overall % DNA sequence identity (\*) |
| *Streptococcus* phage phiARI0746 | KT337365.1 | 33.2 | 100.0 |
| *Streptococcus* phage IPP15 | KY065456.1 | 38.1 | 56.2 |

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

**Relevant reference for this taxon:**

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. [*Streptococcus* phage phiARI0746]

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. [*Streptococcus* phage IPP15]

1. **Create a new genus, *Hinxtonvirus* with eighteen species**

**Origin of the name of this taxon:** The name of this taxon derives from the address of The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, UK.

**Historical aspects:** These are all temperate siphoviruses from Streptococcus pneumonae

**Genome summary:**

|  |  |  |  |
| --- | --- | --- | --- |
| Phage name | INSDC | Size (kb) | Overall % DNA sequence identity (\*) |
| *Streptococcus* phage K13 | HG799496.1 | 39.4 | 100.0 |
| *Streptococcus* phage 34117 | FR671407.1 | 37.6 | 71.6 |
| *Streptococcus* phage V22 | FR671405.1 | 37.2 | 75.3 |
| *Streptococcus* phage 8140 | FR671410.1 | 35.9 | 76.9 |
| *Streptococcus* phage IPP34 | KY065474.1 | 38.9 | 64.1 |
| *Streptococcus* phage IPP64 | KY065500.1 | 38.7 | 72.7 |
| *Streptococcus* phage 2167 | FR671411.1 | 36.2 | 66.4 |
| *Streptococcus* phage IPP46 | KY065486.1 | 40.2 | 65.6 |
| *Streptococcus* phage IC1 | HG799490.1 | 40.0 | 71.5 |
| *Streptococcus* phage DCC1738 | HG799497.1 | 38.4 | 65.3 |
| *Streptococcus* phage phiARI0462 | KT337354.1 | 40.5 | 64.9 |
| *Streptococcus* phage phiARI0831b | KT337369.1 | 31.1(\*\*) | 49.2 |
| *Streptococcus* phage IPP69 | KY065505.1 | 40.8 | 60.0 |
| *Streptococcus* phage phiARI0004 | KT337339.1 | 41.1 | 67.7 |
| *Streptococcus* phage phiARI0031 | KT337340.1 | 41.9 | 64.5 |
| *Streptococcus* phage phiARI0468-1 | KT337355.1 | 41.1 | 73.6 |
| *Streptococcus* phage phiARI0285-1 | KT337345.1 | 33.4 | 51.9 |
| *Streptococcus* phage phiARI0468b-3 | KT337359.1 | 31.9 (\*\*) | 54.2 |

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

**(\*\*) possibly incomplete**

**Relevant references for this taxon:**

Croucher NJ, Hanage WP, Harris SR, McGee L, van der Linden M, de Lencastre H, Sá-Leão R, Song JH, Ko KS, Beall B, Klugman KP, Parkhill J, Tomasz A, Kristinsson KG, Bentley SD. Variable recombination dynamics during the emergence, transmission and 'disarming' of a multidrug-resistant pneumococcal clone. BMC Biol. 2014 Jun 23;12:49. doi: 10.1186/1741-7007-12-49. PMID: 24957517; PMCID: PMC4094930. [*Streptococcus* phage K13].

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.

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.

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

**Origin of the name of this taxon:** This taxon is named in honour of American microbiologist Joseph J. Ferretti who received a Ph.D. in Biochemistry at the University of Minnesota (1967), was a post-doctoral fellow at The Johns Hopkins University and attended the Cold Spring Harbor Bacterial Virus Course (1967-69). He came to the University of Oklahoma College of Medicine in 1969 and in1983 became Chairman of the Department of Microbiology and Immunology; in 1993 he was the Vice President for Research, and from 1995-2011 served as Senior Vice President and Provost of the University of Oklahoma Health Sciences Center (OUHSC). Over the course of his career, he has authored scientific papers on his specialties of streptococcal infections, antibiotic resistance, and genomics and co- authored six books. He has been a US National Academy of Sciences Visiting Scientist to the German Democratic Republic (1980), a Visiting Professor on sabbatical at the Institut Pasteur, Paris (1982), and a consultant to WHO laboratories in St. Petersburg, Russia (1990) and Beijing, China (1996). He organized ASM International Conferences on Streptococcal Genetics in Sarasota, FL (1986) and Santa Fe, NM (1994). The honors to Dr. Ferretti have been numerous: he was inducted in 1983 into The Johns Hopkins University Society of Scholars; in 1987 he became the George Lynn Cross Research Professor at the University of Oklahoma; a Lecturer at the Deutsche Gesellschaft fur Hygeine und Mikrobiologie Kongress Wissenschafte, Aachen, Germany (2001) an Honorary Member of Akadamie gemeinnütziger Wissenschaften zu Erfurt, Germany (2007) and was awarded an honorary doctorate from the Russian Academy of Medical Sciences in St. Petersburg, Russia (1997).

After 45 years of service, Dr. Ferretti officially retired from the University of Oklahoma College of Medicine in 2014 and is presently a George Lynn Cross Research Professor Emeritus in the Department of Microbiology and Immunology. He is currently the lead Editor of a comprehensive book of 31 chapters, “*Streptococcus pyogenes*; Basic Biology to Clinical Manifestations,” an open access electronic book presently available on the NIH/NCBI bookshelf (https://www.ncbi.nlm.nih.gov/books/NBK587111/. After six years, the website has been visited by over 1.2 million unique Internet Protocol addresses (IPs) with over one million downloads of pages, chapters, and the entire book.



(photo copied from https://www.linkedin.com/in/joseph-ferretti-96b93834/)

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive subfamily. This group share at least 29.7% DNA sequence similarity and 14 homologous proteins [6] including: terminase large subunit, portal, tail tape measure protein, and tail protein.