

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create a new subfamily (*Cardingvirinae*) with two genera and 18 species (*Caudoviricetes*) |
| **Code assigned:** | 2025.007B.Ac.v3.Cardingvirinae\_1nsf\_2ng\_18ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Andrew M. | Kropinski | Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com |  |
| Cristina | Moraru | Carl von Ossietzky Universität Oldenburg, Germany | liliana.cristina.moraru@uol.de |  |
| Nina | Chanisvili | G. Eliava Institute of Bacteriophages, Microbiology and Virology, Tbilisi, Georgia | nina.chanishvili@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:** <https://ictv.global/sc> |
| 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:** | 15/06/2025 |

**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| W - Withdrawn |  |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:** |
| Please improve the quality of the abstract, there is a lack of phylogenetic tree (not necessary but would improve the proposal). |

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

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| **Response of proposer:** |
| Corrected |

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| **Revision date:** | August 19, 2025 |

<https://ictv.global/taxonomy/templates>

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| **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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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| ***Cardingvirinae*** | **Named in honour of Professor Simon Carding** |
| *Gotuavirus* | Named after the address of the Eliava institute where phage UZM3 was isolated |
| *Kherlenvirus* | Named after the Kherlen River in China |
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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
| Cardingvirinae | Professor Simon Richard Carding | X |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Subfamily, genus, species  *Description of current taxonomy*:  There is no current taxonomy for these lytic phages isolated against *Bacteroides fragilis*  *Proposed* *taxonomic change(s):*  Add two new genera, “*Kherlenvirus*” and “*Gotuavirus*”, and 18 new species to a new subfamily “*Cardingvirinae”*  *Justification*: On the basis of VIRIDIC, CoreGenes and phylogenetic analyses and in keeping with the criteria which we have established for creation of new species, genera and subfamilies these previously unclassified Bacteroides lytic siphoviruses belong to two genera in a new subfamily [8]. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Subfamily, genus, species  *Description of current taxonomy*:  There is no current taxonomy for these lytic phages isolated against *Bacteroides fragilis.*  *Proposed* *taxonomic change(s)*: Add two new genera, “*Kherlenvirus*” and “*Gotuavirus*”, and 18 new species to a new subfamily “*Cardingvirinae”*  *Demarcation criteria*:  Sub-family 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 [8].  Genus demarcation criteria: An intergenomic similarity cut-off of 70%, a combination of average nucleotide identity and alignment fraction, is used to determine genera demarcation. Members of the same genus have >70% intergenomic similarity and cluster tightly in marker gene phylogenies.  Species demarcation criteria: A demarcation value of 95% intergenomic similarity was used to define different species according to intergenomic similarity. Members of the same genus have >95% intergenomic similarity [8].  *Justification*:  On the basis of VIRIDIC, CoreGenes and phylogenetic analyses and in keeping with the criteria which we have established for creation of new species, genera and subfamilies these previously unclassified Bacteroides lytic siphoviruses belong to two genera in a new subfamily [8]. Analysis using CoreGenes 5 [7] revealed that the phages listed in Table 1 share 32 protein homologs, almost all listed as hypothetical proteins, except for thymidylate synthase. This indicates that approximately 50% of the phage-encoded proteins are conserved within the proposed subfamily.  These viruses conform to the criteria established [8] for creating genera and subfamilies |

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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. 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.  Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F, Cohen-Boulakia S, Gascuel O. NGPhylogeny.fr: new generation phylogenetic services for non-specialists. Nucleic Acids Res. 2019 Jul 2;47(W1):W260-W265. doi: 10.1093/nar/gkz303. PMID: 31028399; PMCID: PMC6602494.  9. 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.  10. 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. Bioinformatics. 2023 Jun 1;39(6):btad339. doi: 10.1093/bioinformatics/btad339. PMID: 37225402; PMCID: PMC10243930  11. 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 Jul 1;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797; PMCID: PMC2447785. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.007B.Cardingvirinae\_1nsf\_2ng\_18ns | Data file for this proposal |
| 2025.007B.Cardingvirinae\_VIRIDIC\_heatmap.xlsx | VIRIDIC intergenomic similarity data |
| 2025.007B.Cardingvirinae\_LoA.pdf | Letter of acceptance of Professor Simon Carding |

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| **Tables, Figures:** |

<Start here>**Table 1.** Phages which belong to this subfamily

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| **Accession No.** | **Phage name** | **Taxon** | **Host taxon** |
| OP172666.1 | Bacteroides phage BF486P1 | *Kherlenvirus BF486P1* | *Bacteroides fragilis* |
| OP172680.1 | Bacteroides phage BK649P1 | *Kherlenvirus BK649P1* | Bacteroides fragilis |
| OP172673.1 | Bacteroides phage BF695P2 | *Kherlenvirus BF695P2* | Bacteroides fragilis |
| OP172675.1 | Bacteroides phage BF698P1 | *Kherlenvirus BF698P1* | *Bacteroides fragilis* |
| OP172676.1 | Bacteroides phage BF698P3 | *Kherlenvirus BF698P3* | *Bacteroides fragilis* |
|  |  |  |  |
| NC\_011222.1 | Bacteroides phage B40-8 | *Gotuavirus B408* | *Bacteroides fragilis* |
| OP172663.1 | Bacteroides phage BF10P2 | *Gotuavirus BF10P2* | *Bacteroides fragilis* |
| OP172664.1 | Bacteroides phage BF10P3 | *Gotuavirus BF10P3* | *Bacteroides fragilis* |
| OP172678.1 | Bacteroides phage BF766P1 | *Gotuavirus BF766P1* | *Bacteroides fragilis* |
| MW916539.1 | Bacteroides phage GEC\_vB\_Bfr\_VA7 | *Gotuavirus VA7* | *Bacteroides fragilis* |
| MN078104.1 | Bacteroides phage Barc2635 | *Gotuavirus Barc2635* | *Bacteroides fragilis* |
| MW314138.1 | Bacteroides phage vB\_BfraS\_NCTC | *Gotuavirus NCTC* | *Bacteroides fragilis* |
| OP172665.1 | Bacteroides phage BF344P1 | *Gotuavirus BF344P1* | *Bacteroides fragilis* |
| OP172679.1 | Bacteroides phage BF766P4 | *Gotuavirus BF766P4* | *Bacteroides fragilis* |
| OP172677.1 | Bacteroides phage BF702P1 | *Gotuavirus BF702P1* | *Bacteroides fragilis* |
| HE608841.1 | Bacteroides phage B124-14 | *Gotuavirus B12414* | *Bacteroides fragilis* |
| MT630433.1 | Bacteroides phage vB\_BfrS\_23 | *Gotuavirus gv23* | *Bacteroides fragilis* |
| OQ116603.1 | Bacteroides phage vB\_BfrS\_UZM3 | *Gotuavirus UZM3* | *Bacteroides fragilis* |

Specific reference: Bakuradze N, Makalatia K, Merabishvili M, Togoshvili L, Chanishvili N. SELECTION OF THE ACTIVE PHAGES AGAINST B. FRAGILIS FOR FURTHER STUDY OF THRAPEUTIC PERPECTIVES. Georgian Med News. 2018 Dec;(285):111-116. PMID: 30702082. [Bacteroides phage GEC\_vB\_Bfr\_VA7]; Hawkins SA, Layton AC, Ripp S, Williams D, Sayler GS. Genome sequence of the Bacteroides fragilis phage ATCC 51477-B1. Virol J. 2008 Aug 18;5:97. doi: 10.1186/1743-422X-5-97. PMID: 18710568; PMCID: PMC2535602. [Bacteroides phage B40-8]; Ogilvie LA, Caplin J, Dedi C, Diston D, Cheek E, Bowler L, Taylor H, Ebdon J, Jones BV. Comparative (meta)genomic analysis and ecological profiling of human gut-specific bacteriophage φB124-14. PLoS One. 2012;7(4):e35053. doi: 10.1371/journal.pone.0035053. Epub 2012 Apr 25. PMID: 22558115; PMCID: PMC3338817. [Bacteroides phage B124-14]

A screenshot of a computer

AI-generated content may be incorrect.

**Figure 1.** Partial VIRIDIC heatmap of this group of phages. 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 Bact = *Bacteroides*. The complete VIRIDIC heatmap accompanies this proposal as 2025.007B.Cardingvirinae\_VIRIDIC\_heatmap.xlsx.

A screenshot of a computer

AI-generated content may be incorrect.

**Figure 2.** Phylogenetic tree constructed with major capsid proteins from these and related phages using “One Click” phylogeny.fr at <http://phylogeny.lirmm.fr/phylo_cgi/simple_phylogeny.cgi> [11]

This taxon is named in honour of British immunologist-microbiologist Professor Simon Richard Carding (b. 1958, UK) who completed postgraduate work at the MRC’s Clinical Research Centre studying muscle associated carbohydrate binding proteins in Duchenne Muscular Dystrophy. He then undertook postdoctoral work in the USA at New York University and Yale University in molecular and mucosal immunology prior to becoming a faculty member in the Department of Microbiology and then the Veterinary School of Medicine at the University of Pennsylvania. Returning to the UK and the University of Leeds he developed a programme of research focusing on commensal gut bacteria in health and disease based on *Bacteroides* spp. Now at the Quadram Institute and University of East Anglia his research focuses on understanding how gut bacteria and viruses communicate with their host and the role that *Bacteroides*-generated microvesicles play in this crosstalk within and beyond the gut.

A person in a blue shirt

AI-generated content may be incorrect.

(Photo provided by the honouree)