

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create one new genus (*Kronosvirus*) with three species (*Caudoviricetes*). | |
| **Code assigned:** | 2024.018B |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Ely B | University of South Carolina, USA | ely@sc.edu | 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:** |
| *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:** | 27/05/2024 |

**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| W - Withdrawn |  |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:** |
| 2024.018B.A.v1.Kronosvirus\_ng.xlsx |

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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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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached 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)*:  *Caulobacter* bacteriophage Kronos is a unique siphovirus with a 50nm icosahedral head and a long (150nm) flexible tail. There are no close matches of its genome sequence to any other bacteriophage in the GenBank database. We described the phage and deposited its genome sequence in GenBank [14]. Additional phage that are closely related to Kronos can be grouped into 3 distinct species based on the ICTV criteria.  *Justification*:  The creation of the genus *Kronosvirus* complies with current demarcation criteria [10] |

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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)*:  *Caulobacter* bacteriophage Kronos is a unique siphovirus with a 50nm icosahedral head and a long (150nm) flexible tail. There are no close matches of its genome sequence to any other bacteriophage in the GenBank database. We described the phage and deposited its genome sequence in GenBank [14]. Additional phage that are closely related to Kronos can be grouped into 3 distinct species based on the ICTV criteria.  *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].  *Justification*:  In conformity to [10] |

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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. Bin Jang H, Bolduc B, Zablocki O, Kuhn JH, Roux S, Adriaenssens EM, Brister JR, Kropinski AM, Krupovic M, Lavigne R, Turner D, Sullivan MB. Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nat Biotechnol. 2019 Jun;37(6):632-639. doi: 10.1038/s41587-019-0100-8. Epub 2019 May 6. PMID: 31061483.  12. Bolduc B, Jang HB, Doulcier G, You ZQ, Roux S, Sullivan MB. vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect Archaea and Bacteria. PeerJ. 2017 May 3;5:e3243. doi: 10.7717/peerj.3243. PMID: 28480138; PMCID: PMC5419219.  13. Moraru C. VirClust-A Tool for Hierarchical Clustering, Core Protein Detection and Annotation of (Prokaryotic) Viruses. Viruses. 2023 Apr 19;15(4):1007. doi: 10.3390/v15041007. PMID: 37112988; PMCID: PMC10143988.  14. Berrios L, Ely B. The Isolation and Characterization of Kronos, a Novel Caulobacter Rhizosphere Phage that is Similar to Lambdoid Phages. Curr Microbiol. 2019 May;76(5):558-565. doi: 10.1007/s00284-019-01656-1. Epub 2019 Feb 27. Erratum in: Curr Microbiol. 2019 Aug;76(8):964-965. PMID: 30810780; PMCID: PMC6459719. |

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| **Tables, Figures:** |

**Origin of the name of this taxon:** This taxon is named after *Caulobacter* phage Kronos. Species names are taken from the names of towns in rural South Carolina.

**Historical aspects:** This lytic phage was isolated from plant roots anchored on the banks of the Congaree River in Columbia, SC in August of 2017 using rhizosphere *Caulobacter* CBR1 as the host bacterium. It failed to infect *C. crescentus* isolates including CB1, CB2, CB3, CB13, and CB15 as well as members of other *Caulobacter* species such as *C. segnis* and *C. henricii* [4]. The Kronos phage particle consists of a 50 nm icosahedral head with a 150 nm flexible tail. This size and morphology is relatively rare among caulophages, but it is similar to that of Ccr1. TMCBR2 and TMCBR4 were isolated from other locations, but they have a similar size, morphology, and host range (manuscript in preparation).

A close-up of a black circle

Description automatically generated

**Figure 1. Electron micrograph of negatively stained phage Kronos particle**

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**Figure 2. VIRIDIC heat map of *Kronosvirus* genomes:** 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; Caul = *Caulobacter*

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**Figure 3. ViPTree analysis:** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The members are illustrated with a solid blue bar.

**Conclusions:** This genus is very deeply rooted and could be placed in a new family, or possibly order.

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence similarity (\*) | Overall % common proteins (\*\*) |
| *Caulobacter* phage Kronos | MH884648.1 | 42.42 | 66.3 | 60 | 0 | 100 | 100 |
| *Caulobacter* phage TMCBR2 | OQ269668.1 | 42.84 | 66.1 | 61 | 0 | 89.1 | 98.3 |
| *Caulobacter* phage TMCBR4 | OQ330850.1 | 42.28 | 66.1 | 60 | 0 | 91.5 | 93.1 |

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

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

**N.B. *Caulobacter* phagesTMCBR3 and W2 should be considered as strains within this genus.**