

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

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| **Code assigned:** | ***2023.032B*** |  |
| **Short title:** To create a genus *Halfdanvirus* with a single species [*Caudoviricetes*] | | |
|  | | |

**Author(s) and email address(es)**

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| --- | --- |
| Olsen NS, Turner D, Moraru C, Tolstoy I, Kropinski AM | sno@plen.ku.dk; Dann2.Turner@uwe.ac.uk; liliana.cristina.moraru@uol.de; tolstoy@ncbi.nlm.nih.gov; Phage.Canada@gmail.com |

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

|  |
| --- |
| University of Copenhagen, Frederiksberg, Denmark [NSO]  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**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** |  |

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| **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 | May 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**

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| 2023.032B.N.v1.Halfdanvirus\_ng.xlsx |

**Abstract**

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| The genus *Halfdanvirus* includes a single species *Halfdanvirus halfdan* and exemplar Escherichia phage Halfdan which is a lytic siphovirus. |

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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] | |

**Supporting evidence**

**Proposal Data:**

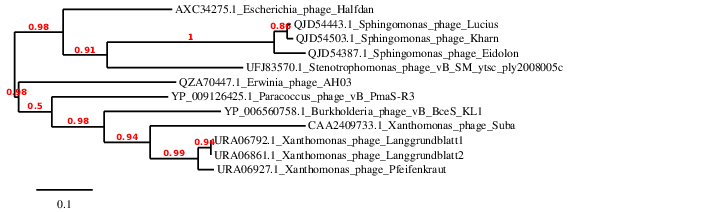
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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Para = Paracoccus; Sphi = Sphingomonas; Xant = Xanthomonas; Esch = Escherichia

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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]. The phages of interest are indicated with **red lines and stars**.

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**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the large subunit terminase proteins 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.”

**Taxonomic Proposal:**

1. **Create a new single species genus, *Halfdanvirus***

**Origin of the name of this taxon:** The name of this taxon is directed derived from that of the first isolate of its type, Escherichia phage Halfdan

**Historical aspects:** This lytic siphophage was isolated from wastewater against Escherichia coli K12 by N.S. Olsen, et al. (Department of Environmental Science, Aarhus University, Roskilde, Denmark; Olsen et al. 2020)

**Electron micrograph:** N/A.

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage Halfdan | [MH362766.1](https://www.ncbi.nlm.nih.gov/nuccore/MH362766.1) | 42.86 | 53.7 | [56](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71187/390963|Escherichia phage Halfdan/viral segment/) | 100 | 100 |

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3) this represents a single species genus.

**Specific reference:**

Olsen NS, Forero-Junco L, Kot W, Hansen LH. Exploring the Remarkable Diversity of Culturable *Escherichia coli* Phages in the Danish Wastewater Environment. Viruses. 2020 Sep 4;12(9):986. doi: 10.3390/v12090986. PMID: 32899836; PMCID: PMC7552041.

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