

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

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| **Code assigned:** | **2021.043B** |  |
| **Short title:** Create one new genus (*Klumppvirus*) including one existing species (*Herelleviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M. Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee |

**ICTV study group comments and response of proposer**

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**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)** | Y |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Klumppvirus* | Jochen Klumpp | Y |
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**Submission dates**

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| Date first submitted to SC Chair | May 2021 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

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

**Name of accompanying Excel module**

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| 2021.043B.A.v1.Klumppvirus.xlsx |

**Abstract**

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| The species *Brochothrix virus A9* was created through Taxonomy Proposal 2018.118B. It is a genomic orphan in the family *Herelleviridae*. With this proposal we finally remove the last orphan species from the bacterial viruses through the creation of a new genus, *Klumppvirus*. |

**Text of proposal**

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| |  | | --- | | **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 – 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. [9] | |

**Supporting evidence**

**Source of the name of this taxon:** This taxon is named in honour of Dr. Jochen Klumpp (b. 1976 Würzburg, Germany). 2005: PhD in Microbiology at Technical University Munich (Germany); 2015: Habilitation thesis and *venia legendi*. 2010-2015: Senior Scientist, Department of Health Sciences and Technology, Swiss Federal Institute of Technology (ETH), Zurich, Switzerland. 2015-present: Private lecturer in Food Microbiology and deputy head of IT, Department of Health Sciences and Technology, ETH. Past Listeria Study Group Chair, Bacterial and Archaeal Viruses Subcommittee of ICTV. He led the group that sequenced phage A9.

**History:** Brochothrix thermosphacta is a nonproteolytic food spoilage organism, adapted to growth in vacuum-packaged meats. Phage A9 was isolated isolation of phages from spoiled retail rib steaks by Dr. G.Gotdon Greer, Agriculture Canada, Lacombe, Alberta, Canada in 1983 [Greer G.G. 1983]. It is a myovirus with an 89-nm capsid diameter and a 171-nm contractile tail [Kilcher S et al. 2010]. The species *Brochothrix virus A9* was created through Taxonomy Proposal 2018.118B. It is a genomic orphan in the family *Herelleviridae*, as detailed in [10].

**Electron micrograph:** None available

**Specific Reference:** Greer, G.G. 1983. Psychrotrophic Brocothrix thermosphacta bacteriophages isolated from beef. Appl. Environ. Microbiol. 46:245-251.

Kilcher S, Loessner MJ, Klumpp J. Brochothrix thermosphacta bacteriophages feature heterogeneous and highly mosaic genomes and utilize unique prophage insertion sites. J Bacteriol. 2010 Oct;192(20):5441-53. doi: 10.1128/JB.00709-10. Epub 2010 Aug 13. PMID: 20709901; PMCID: PMC2950505.

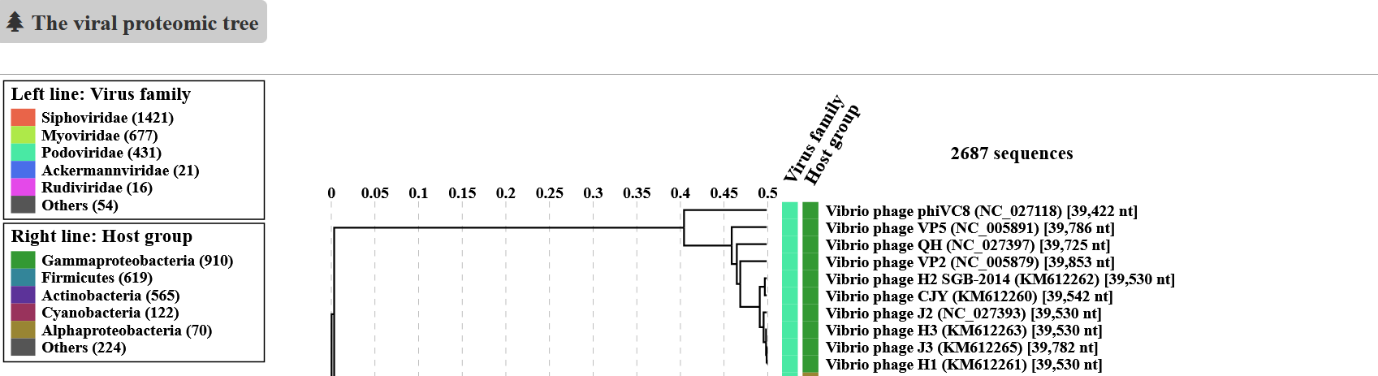
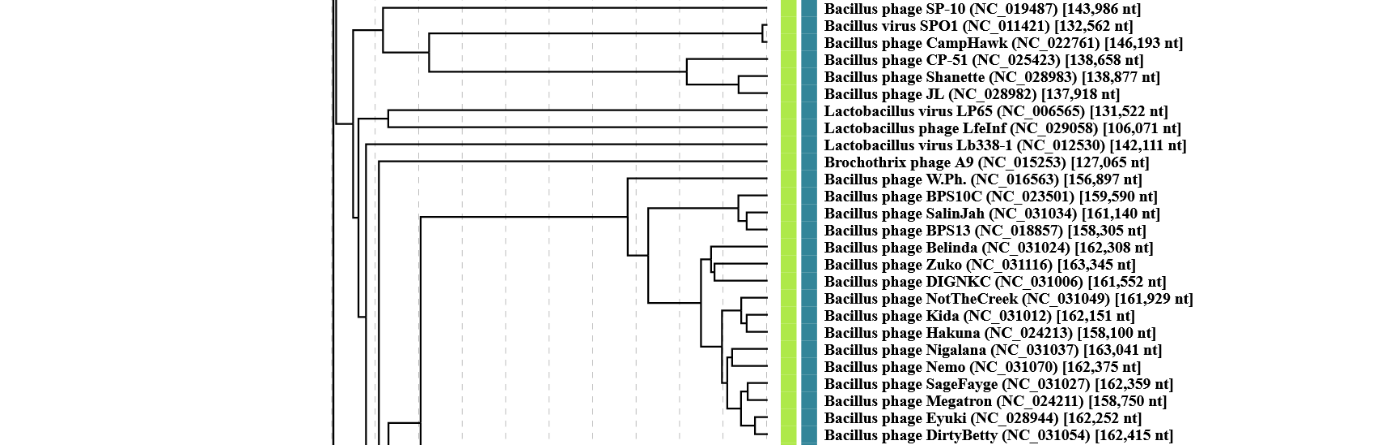
**GenBank Summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Brochothrix phage A9 | HM242243.1 | 127.06 | 41.42 | 199 | 6 | 100 | 100 |

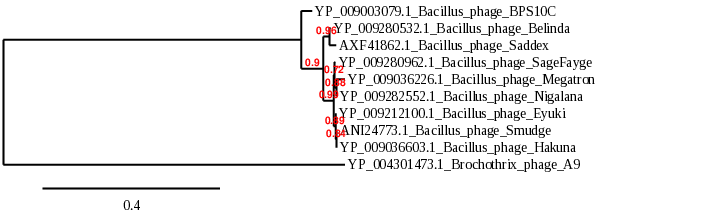
**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](about:blank) **[4]**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. Phage A9 is indicated with a **red arrow**.

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**Phylogeny:** The phylogenetic tree was constructed using the DNA polymerases of related phages with phylogeny.fr in “one click” mode [5]. "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 [6] for details."

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**Phylogeny of concatenated marker genes:** Tree reproduced from reference [10] Barylski et al, in which Brochotrix phage A9 represented an orphan species within the family *Herelleviridae*.

The legend of the figure states [10]: “Maximum-likelihood tree based on concatenated alignment of 10 marker proteins generated using IQ-tree. The scale bar represents the number of substitutions per site, branch support values were calculated from 1000 ultrafast bootstrap (UFBOOT) replicates. The trees were rooted at Brochothrix phage A9 to facilitate comparison. Branches corresponding to genera and subfamilies are delineated with colored squares and circles, respectively.”

**Diagram

Description automatically generated**

**References**

1: 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.

2: 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

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://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)

4: 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.

5: 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.

6: 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.

7: Lowe, T.M. and Chan, P.P. (2016) tRNAscan-SE On-line: Search and Contextual Analysis of Transfer RNA Genes. Nucl. Acids Res. 44: W54-57.

8: Zimmermann L, Stephens A, Nam SZ, et al. A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. J Mol Biol. 2018;430(15):2237-2243. doi:10.1016/j.jmb.2017.12.007

9: Turner D, Kropinski AM, Adriaenssens EM. 2021. A Roadmap for Genome-Based Phage Taxonomy. Viruses 2021, 13, 506. https://doi.org/10.3390/v13030506

10: ﻿1. Barylski J, Enault F, Dutilh BE, et al. 2020. Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. Syst Biol 69:110–123. DOI 10.1093/sysbio/syz036 PMID: 31127947