

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

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| **Code assigned:** | **2020.163B** |  |
| **Short title:** Create one new genus (*Teubervirus*) including five new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Adriaenssens EM, Tolstoy I, Moraru C, Turner D, Lueder M, Neve H, Mahony J, Moineau S, Kropinski AM | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  liliana.cristina.moraru@uni-oldenburg.de;  Dann2.Turner@uwe.ac.uk;  matthew.r.lueder.ctr@mail.mil;  Horst.Neve@mri.bund.de;  J.Mahony@ucc.ie; Sylvain.Moineau@bcm.ulaval.ca;  Phage.Canada@gmail.com |

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

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| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  Institute for Chemistry and Biology of the Marine Environment [CM]  University of the West of England, Bristol [DT]  Naval Medical Research Center-Frederick, USA [ML]\* Max Rubner-Institut, Germany [HN]  University College Cork, Ireland [JM]  Université Laval, Canada [SM]  University of Guelph, Canada [AMK] |

“The views expressed in this article reflect the results of research conducted by the author and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, nor the United States Government. This work was supported/funded by work unit number A1417”

**Corresponding author**

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| Andrew M. Kropinski |

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

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| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

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

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Teubervirus* | Professor Dr Michael Teuber | Y |
|  |  |  |
|  |  |  |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | July 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.163B.R.Teubervirus.xlsx |

**Abstract**

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| As part of a major study of the siphoviruses infecting Lactococcus strains we classified phage P087 and its relatives to a new genus Teubervirus. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. | |

**Supporting evidence**

**Source of the name of this taxon:** Named in honour of Professor Dr. Michael Teuber (b. 1937 in Germany; 1962 promotion to Dr. rer.nat. in Botany, Bacteriology and Chemistry at the University of Munich. 1976 – 1990 Director and Professor, Head of the Institute of Microbiology of the Federal Dairy Research Center Kiel (Germany) worked on applied and genetic aspects of dairy starter cultures, President of Commission F Science and Education of the International Dairy Federation Brussels. 1990 – 2002 Professor of Food Microbiology at the Department of Food and Agriculture ETH Zurich, (Switzerland) working on antibiotic resistant bacteria in ready to eat food. 1991 – 2006 Member for Microbiology of the Central Commission for Biological Safety at the Robert-Koch-Institute Berlin, Germany.



(kindly provide by Dr. Horst Neve)

**History:** “Phage P087 was isolated in Germany from a dairy environment in 1978 [Braun V et al., 1989]. Electron microscopy revealed that it belonged to the Siphoviridae family as for the majority of the lactococcal phages. Its noncontractile tail is 163 nm in length and 14–16 nm in width while its isometric capsid is approximately 59 nm in diameter. It differs from other lactococcal phages through its complex baseplate with no terminal fiber.” [Villion M et al., 2009 ] Lactococcus phage LW31 was isolated from Vastedda cheese whey in 2014, while Lactococcus phage AM6 was isolated in 2016 from Caciocavallo cheese whey. Both were isolated in Ireland. There is no record as to whether these are lytic or temperate phages.

**Note of interest:** One of the characteristics of these phages is that none of them have characterized packaging proteins. We identified a potential homolog based upon BLASTP using 949 large subunit terminase; and, verified using HHpred [8] where the following protein exhibited considerable similarity (Probability: 100%; E-value: 1.7e-33) 4IDH - Gene 2 protein; DNA packaging, terminase, ATPase, nuclease; 1.69A {Shigella phage Sf6}

>BBI90336.1 putative uncharacterized protein [Lactococcus phage phiQ1]

MEDRKYTPTYVVPSQMSLNQHKMINRLESLRPYFLHPQLRWLRGYKPMPDWYHRLSLTWKEANDLAIIGYNTVKEETGAE

LYFTQAVLAGLMLESDYRVISCILGTGFGKSFVSSQCNLVRANRGELITAFAPNRELNSIIFKEMVSAVNHSPKLKKVLF

EAESKEEALQRGVSQKRFAFPSGGFVDLTIAKNATGVHSSSYMDEYALLTKEEYNLAEGRAYAYVDKDGNPGKIFKTSNP

HIMNFSYDDMIRTPLPPHEAVLWGDWRLNIGEGKFMELVYSQLDDEHKYLKNKFPLNREERDYLLDQAIQQVIWSPFFND

EDNLRILYLSEFGVNTESAFFTTTPKIDDSPIDWDNSTFYAGNDVAIRGTDACIYALLEHNPNKSYSRIVSFTNVKPQLW

IDHETPKVMAENVIRQLKHDRARLLAIDASGVGEGQFNLLTTDDADTSCPVVPVRFGDGASKWRKDKNAIRSHNKRSELF

LDFKEFVDTDTLRVTSEVWESLEAEMQAVTKMSNDENKRIKIEPKDAIKKRLGGKSTDYLDSSMLALHALILDKLGAVSA

YNKQDDSSFLEFQKELHK

**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 P087 is marked with a **red star**.

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**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The colour code in column 3 indicates the boundary of the proposed genus.



**Strain table:**

|  |  |  |
| --- | --- | --- |
| **Phage name** | **Accession** | **Belongs to species** |
| Lactococcus phage LW32 | KY554763.1 | *Lactococcus virus LW31* |
| Lactococcus phage LW33 | KY554764.1 | *Lactococcus virus LW31* |
| Lactococcus phage LW4 | KY554765.1 | *Lactococcus virus LW31* |
| Lactococcus phage AM7 | KY554767.1 | *Lactococcus virus AM6* |

**Specific Reference:** Mahony J, Moscarelli A, Kelleher P, et al. Phage Biodiversity in Artisanal Cheese Wheys Reflects the Complexity of the Fermentation Process. *Viruses*. 2017;9(3):45. Published 2017 Mar 16. doi:10.3390/v9030045 **[LW31]**

Mahony J, Moscarelli A, Kelleher P, et al. Phage Biodiversity in Artisanal Cheese Wheys Reflects the Complexity of the Fermentation Process. Viruses. 2017;9(3):45. Published 2017 Mar 16. doi:10.3390/v9030045 **[AM6]**

Villion M, Chopin MC, Deveau H, Ehrlich SD, Moineau S, Chopin A. P087, a lactococcal phage with a morphogenesis module similar to an Enterococcus faecalis prophage. Virology. 2009;388(1):49-56. doi:10.1016/j.virol.2009.03.011 **[P087]**

Braun V., Hertwig S., Neve H., Geis A., Teuber M. Taxonomic differentiation of bacteriophages of Lactococcus lactis by electron microscopy, DNA–DNA hybridization, and protein profiles J. Gen. Microbiol., 135 (1989), pp. 2551-2560. **[P087]**

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Lactococcus phage phiQ1 |  | [AP019527.1](about:blank) | 59.83 | 34.4 | [86](about:blank#!/proteins/76493/469190|Lactococcus phage phiQ1/viral segment/) | 5 | 100 | 100 |
| Lactococcus phage LW31 |  | [KY554762.1](about:blank) | 60.55 | 34.3 | [85](about:blank#!/proteins/63416/466037|Lactococcus phage LW31/viral segment/) | 3 | 88.1 | 94.2 |
| Lactococcus phage AM6 |  | [KY554766.1](about:blank) | 62.05 | 34.2 | [90](about:blank#!/proteins/63412/466033|Lactococcus phage AM6/viral segment/) | 4 | 85.5 | 94.2 |
| Lactococcus phage P087 | [NC\_012663.1](about:blank) | [FJ429185.1](about:blank) | 60.07 | 34.4 | [88](about:blank#!/proteins/6461/891425|Lactococcus phage P087/viral segment Unknown/) | 5 | 85.5 | 93.0 |
| Lactococcus phage P596 |  | [MN528768.1](about:blank) | 57.91 | 34.4 | [81](about:blank#!/proteins/85373/740774|Lactococcus phage P596/viral segment/) | 3(\*\*\*) | 86.0 | 90.7 |

**N.B. Lactococcus phages LW32, LW33, LW4 and AM7 should be considered strains in this genus, see strain table.**

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

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

**(\*\*\*) None indicated in NCBI Replicon Info; These found using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](about:blank) **[7]**

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of P087 and 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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**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. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. [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. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
8. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432
9. 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