

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

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| **Code assigned:** | **2020.181B** |  |
| **Short title:** Create one new genus (*Whiteheadvirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Adriaenssens EM, Tolstoy I, Mahony J, Neve H, Moineau S, Kropinski AM | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  J.Mahony@ucc.ie;  Horst.Neve@mri.bund.de; 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] University College Cork, Ireland [JM]  Max Rubner-Institut, Germany [HN] Université Laval, Canada [SM]  University of Guelph, 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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| *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**

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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 | 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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| 2020.181B.R.Whitehead.xlsx |

**Abstract**

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| As part of a major study of the siphoviruses infecting Lactococcus strains we classified phage 1358 to a new genus, *Whiteheadvirus*. |

**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 Hugh Robinson Whitehead (b. 1899 Hunslet, England, d. 1983 Palmerston North, New Zealand). MSc (1922) from the University of Leeds. He then worked as a biochemist in the College of Medicine of the University of Durham at Newcastle upon Tyne. In 1928, he took up an appointment as chief bacteriologist at the Dairy Research Institute in Palmerston North. He was awarded a DSc by the University of Leeds in 1931. Whitehead became director of the Dairy Research Institute in 1959 and continued to preside over the growing establishment until his retirement in 1964. He was elected a fellow of the Royal Society of New Zealand in 1950, and in 1957 received the gold medal of the Australian Society of Dairy Technology. He was made an OBE in 1964. He and his group contributed to the early recognition of the role of bacteriophages in the dairy industry. (derived from: <https://teara.govt.nz/en/biographies/5w25/whitehead-hugh-robinson>)



**History:** Lytic lactococcal phage 1358 was isolated from a dairy environment in 1981 by the New Zealand Dairy Research Institute [Jarvis, 1984], and fully characterized by Dupuis and Moineau [2010]. Phage 1358 has an icosahedral capsid with a diameter of 54 nm and a noncontractile tail 103 nm in length and 9 nm in width. The sequence of this virus reveals its similarity to Listeria phages, particularly in the packaging and morphogenesis modules.

**Specific Reference:** Jarvis, A. W. 1984. Differentiation of lactic streptococcal phages into phage species by DNA-DNA homology. Appl. Environ. Microbiol. 47:343–349 **[1358]**

Dupuis ME, Moineau S. Genome organization and characterization of the virulent lactococcal phage 1358 and its similarities to Listeria phages. Appl Environ Microbiol. 2010;76(5):1623-1632. doi:10.1128/AEM.02173-09

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Lactococcus phage 1358 | [NC\_027120.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_027120.1) | [GQ403788.1](https://www.ncbi.nlm.nih.gov/nuccore/GQ403788.1) | 36.89 | 51.0 | [43](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/38304/461417|Lactococcus phage 1358/viral segment/) | 0 |
|  |  |  |  |  |  |  |

**BLASTN homologs:** Genomic orphans [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of 1358 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."

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**References**

1. 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.
2. 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.
3. 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.
4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6): doi: 10.1371/journal.pone.0039107. PMID: 22723939.
5. Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.
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. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.
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. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. http://kronos.icbm.uni-oldenburg.de/viridic/