

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2023.049B*** |  |
| **Short title:** **To create six (6) new genera of *Enterococcus* infecting phages (*Caudoviricetes*)** | | |
|  | | |

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

|  |  |
| --- | --- |
| Wittmann J, Adriaenssens EM, Turner D, Moraru C | [Johannes.Wittmann@dsmz.de](mailto:Johannes.Wittmann@dsmz.de); [Evelien.adriaenssens@quadram.ac.uk](mailto:Evelien.adriaenssens@quadram.ac.uk); [Dann2.Turner@uwe.ac.uk](mailto:Dann2.Turner@uwe.ac.uk); [liliana.cristina.moraru@uol.de](mailto:liliana.cristina.moraru@uol.de) |

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

|  |
| --- |
| Leibniz Institute DSMZ – German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany [JW]  Quadram Institute Bioscience, Norwich Research Park, Norwich, UK [EMA]  Department of Applied Sciences, University of the West of England, Bristol, UK [DM]  Carl von Ossietzky Universität Oldenburg, Germany [CM] |

**Corresponding author**

|  |
| --- |
| J Wittmann |

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

|  |
| --- |
| *Schitoviridae* Study Group, Bacterial Viruses Subcommittee  *Caudoviricetes* Study Group, Bacterial Viruses Subcommittee |

**ICTV Study Group comments and response of proposer**

|  |
| --- |
|  |

**ICTV Study Group votes on proposal**

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

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

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2023 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.049B.N.v1.Caudoviricetes\_Enterococcus\_6ng.xlsx |

**Abstract**

|  |
| --- |
| Here, we propose to create six (6) new genera, *Aramisvirus*, containing two (2) new species; *Efemunavirus*, containing two (2) new species; *Delfunavirus*, containing two (2) new species; *Efemquintavirus*, containing one (1) new species; *Amiranvirus*, containing one (1) new species; and *Thiercelinvirus*, containing one (1) new species, in the group of *Enterococcus* infecting phages in the *Caudoviricetes* class using genome-based comparisons. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | *Amiranvirus*: The name derived from a Georgian mythic hero and titan, Amiran. Enterococcus phage vb\_GEC\_Ef\_S\_9 as the first member of this genus has a genome size of 33,631 bp with 54 CDS. It was isolated from sewage in Georgia.  *Aramisvirus*: The name derived from the first isolated phage of this genus, Enterococcus phage Aramis. The genomes of phages Aramis and dArtagnan consist of 42,697 bp and 42,884 bp, respectively with 72 and 71 CDS, respectively.  *Delfunavirus*: The name derived from the first isolated phage of this genus, Enterococcus phage vB\_EfaS-DELF1 [1]. Phage vB\_EfaS-DELF1 was isolated in Iran. Genome sizes of members of this genus range from of 40,248 bp up to 41,014 bp.  *Efemquintavirus*: The name derived from the first isolated phage of this genus, Enterococcus phage IME-EFm5 was isolated from sewage in China [2]. Its genome consists of 42,265 bp with 70 CDS.  *Efemunavirus*: The name derived from the first isolated phage of this genus, Enterococcus phage IME-EFm1. It was isolated from hospital wastewater and showed morphological features of a siphovirus [3]. Phages IME-EFm1 and have genome sizes of 42,597 bp and 42,236 bp, respectively with 70 and 66 CDS, respectively.  *Thiercelinvirus*: The name derived from microbiologist M. E. Thiercelin who first introduced the term “enterococcus” at the end of the 19th century. The first isolated phage of this genus, Enterococcus phage 9184 was isolated from wastewater in the US [4]. Its genome consists of 44,108 bp with 74 CDS. | |

**Supporting evidence**

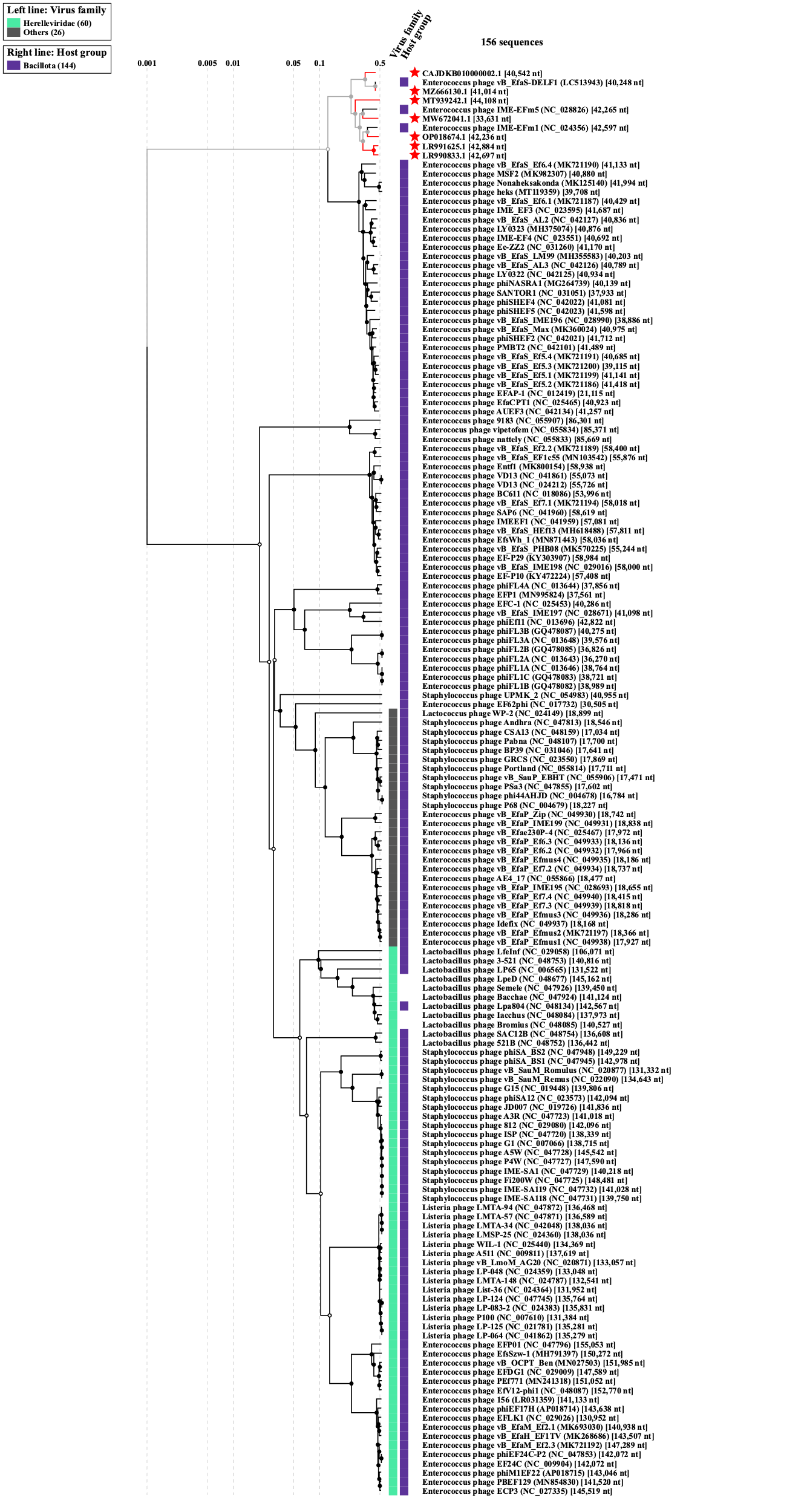
**Electron micrograph:** None available

**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 VIRIDIC [5, 6].

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>) computes pairwise intergenomic distances/similarities amongst phage genomes.



To analyze the similarities or relationship, respectively, between the *Aeromonas* phages and other published phages, we used ViPTree (<https://www.genome.jp/viptree/>; [6]) which is originally based on the Phage Proteomic Tree [7].

****

ViPTree analysis of *Enterococcus* phages of this study with related viruses.

**References**

1. Soleimani-Delfan A, Bouzari M, Wang R. vB\_EfaS-DELF1, a novel Siphoviridae bacteriophage with highly effective lytic activity against vancomycin-resistant Enterococcus faecalis. Virus Res. 2021 Jun;298:198391. doi: 10.1016/j.virusres.2021.198391.
2. Gong P, Cheng M, Li X, Jiang H, Yu C, Kahaer N, Li J, Zhang L, Xia F, Hu L, Sun C, Feng X, Lei L, Han W, Gu J. Characterization of Enterococcus faecium bacteriophage IME-EFm5 and its endolysin LysEFm5. Virology. 2016 May;492:11-20. doi: 10.1016/j.virol.2016.02.006.
3. Wang Y, Wang W, Lv Y, Zheng W, Mi Z, Pei G, An X, Xu X, Han C, Liu J, Zhou C, Tong Y. Characterization and complete genome sequence analysis of novel bacteriophage IME-EFm1 infecting Enterococcus faecium. J Gen Virol. 2014 Nov;95(Pt 11):2565-2575. doi: 10.1099/vir.0.067553-0.
4. Morrisette T, Lev KL, Canfield GS, Duerkop BA, Kebriaei R, Stamper KC, Holger D, Lehman SM, Willcox S, Arias CA, Rybak MJ. Evaluation of Bacteriophage Cocktails Alone and in Combination with Daptomycin against Daptomycin-Nonsusceptible Enterococcus faecium. Antimicrob Agents Chemother. 2022 Jan 18;66(1):e0162321. doi: 10.1128/AAC.01623-21.
5. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>
6. 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
7. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017 Aug 1;33(15):2379-2380. doi: 10.1093/bioinformatics/btx157.
8. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. doi: 10.1128/JB.184.16.4529-4535.2002.