

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

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| **Code assigned:** | ***2023.021B*** |  |
| **Short title:** To create one genus, *Efunavirus*, containing two species in the class *Caudoviricetes* | | |
|  | | |

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

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| C Buttimer |

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

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**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**

|  |  |
| --- | --- |
| **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)** |
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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**

|  |
| --- |
| 2023.021B.N.v1.Efunavirus\_ng.xlsx |

**Abstract**

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| Here, we propose the creation of a new genus, *Efunavirus*, comprising two new species within the class *Caudoviricetes*. This proposal is based on genomic-based comparisons. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **Source of the names used for taxa:**  ***Efunavirus:*** The name of the genus is derived from the name given to the first example of this phage isolated, namely Enterococcus phage EF1.  **Species demarcation criteria:**  In this proposal, we have chosen 95% DNA sequence identity as the criterion for the demarcation of a species. Each proposed species genome differs by more than 5% in nucleotide identity as determined by the BLASTN algorithm (Table 1). Based on the above criteria, we have classed Enterococcus phage EF5 (accession no. MF001361) as a strain of Enterococcus phage EF1.  **Genus demarcation criteria:**  Phylogenetic analysis indicates that phagesEnterococcus phages EF1 and H1 represent species that form a cohesive and distinct genus within the class *Caudoviricetes* (Table 1, Figures 2-4). Analysis with VIPtree allowed the construction of a proteomic tree utilizing 517 genomes. This analysis shows that EF1-like phages are phylogenetically related to a clade of phages with genomes exceeding 100 kbp and possessing a siphovirus virion morphology, such as found with members of the genus *Audreyjarvisvirus* (figure 2). However, this relationship appears to be distant, as indicated by proteome analysis of these phages using Gegenees (TBLASTX) with low identity values (Figure 3). The position of phage EF1 and H1 within this clade was further confirmed with analysis with VICTOR (Figure 4). Gene synteny can be found between genomes of phage EF1 and H1, with limited gene synteny observed between these phages and those of *Audreyjarvisvirus*. In the latter case, gene synteny appears to be mostly limited to genes with gene products associated with the formation of the phage virion (Figure 5).  Examination of the virions of Enterococcus phage H1 by transmission electron microscopy (TEM) shows they possess a siphovirus morphology with the B1 morphotype [1]. The capsid of the virion is icosahedral (88.98 ± 0.79 nm in diameter) with distinguishable hexagonal outlines with a very long flexible, non-contractile tail (441.26 ± 5.54 nm in length) terminating with a knob-like base plate structure (Figure 1) [2]. | |

**Supporting evidence**

**History:**

Isolation source of the phages forming the proposed genus *Efunavirus*:

* The isolation source of Enterococcus phage EF1 & EF5 is unknown. No details are provided in their GenBank files, and no publication currently exists that describes them.
* Enterococcus phage H1 was isolated from human faeces [2].

**Electron micrograph:**

C:\Users\colinbuttimer\OneDrive - University College Cork\Janssen related work\Organising Andrei's work\Lytic Enterocccus phages\Efaecium phage H1\EfmH1 TEMs\EcC-6-60000x .tifC:\Users\colinbuttimer\OneDrive - University College Cork\Janssen related work\Organising Andrei's work\Lytic Enterocccus phages\Efaecium phage H1\EfmH1 TEMs\EcC-12-160kx .tif

**Figure 1.** Transmission electron micrographs of negatively stained Enterococcus phage H1 using uranyl acetate (0.5%) [2].

**GenBank Summary:**

Table 1. Properties of the two phages representing the species belonging to the genus *Efunavirus*

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **phage** | **INSDC Accession no** | **GC%** | **Genome length (bp)** | **Number of ORFs** | **Number of tRNA genes** | **Nucleotide Identity (%)\*** | **% Common proteins\*\*** |
| Enterococcus phage EF1 | MF001358 | 32 | 141,996 | 172 | 14 | 100 | 100 |
| Enterococcus phage H1 | OP534061 | 32 | 138,084 | 167 | 19 | 86 | 84 |

\* Determined using BLASTN [3]; \*\* Determined using CoreGenes 5 [4]

**Phylogeny:**

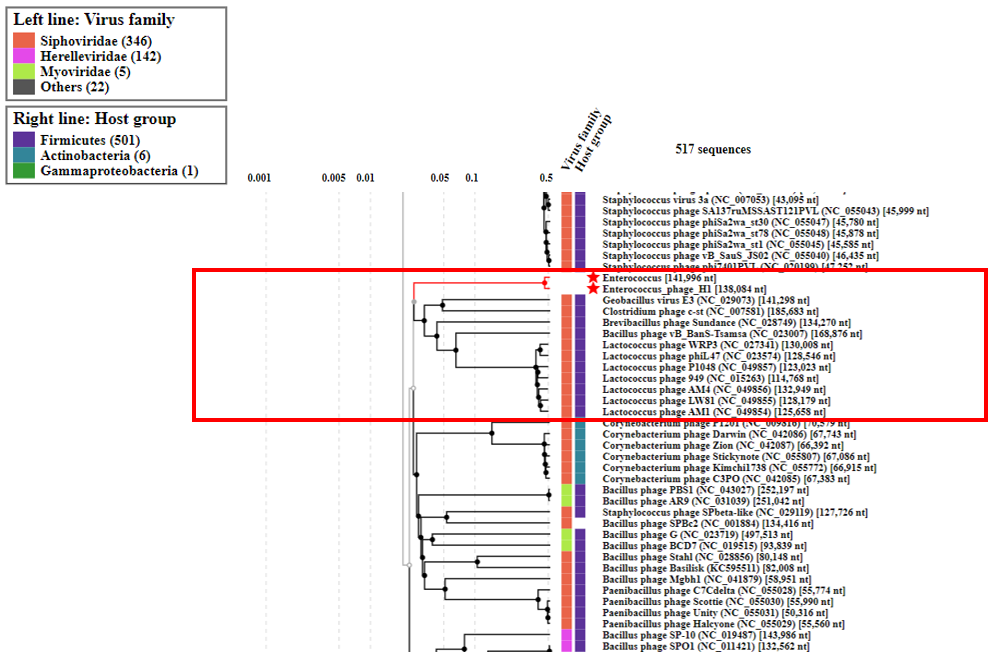


Figure 2. (A) A subsection of a ViPTree phylogram using phage genomes of 517 genome sequences of the tree showing the clade of phages phylogenetic related to phage H1 (highlighted in red) [5].

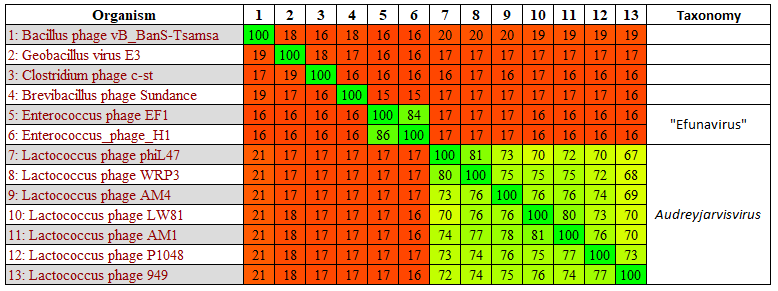


Figure 3. TBLASTX heat map generated using Gegenees with accurate parameters – fragment length: 200 bp; and step size: 100 kbp [6]. The map includes the genomes of Enterococcus phage H1 and siphovirus phages with genomes exceeding 100 kbp.

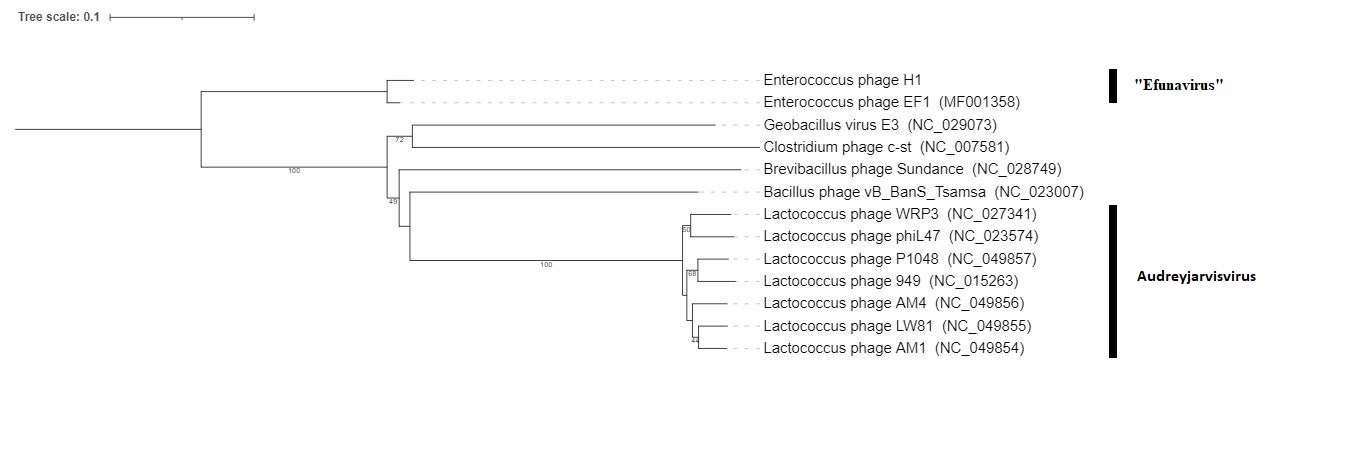


Figure 4. VICTOR-generated phylogenomic Genome-BLAST Distance Phylogeny (GBDP) trees of Enterococcus phage H1 and siphovirus phages with genomes exceeding 100 kbp using the formula D4 and yielding average support of 58% [7]. The numbers above branches are GBDP pseudo-bootstrap support values from 100 replications. Members of the genus *Audreyjarvisvirus* are illustrated.

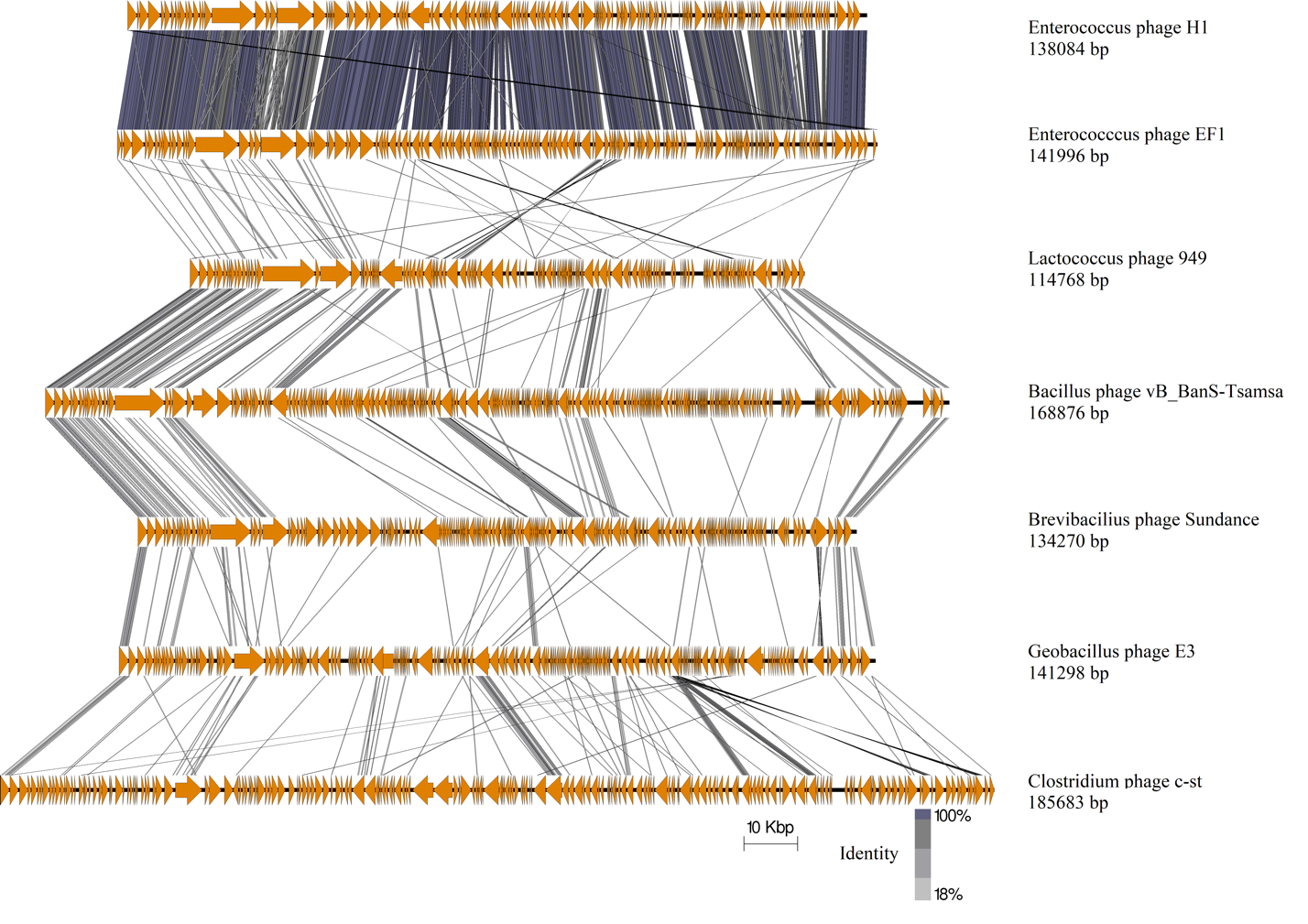


Figure 5. Pairwise comparison of the type phages representing six genera of Enterococcus phage H1 and EF1 with distantly related phages with virions with a siphovirus morphology and with genomes exceeding 100 kbp in size. Genomic maps were created using currently available annotation from Genbank with comparisons employing TBLASTX and visualization with Easyfig [8]. The genome maps display arrows indicating the locations and orientation of ORFs. Lines between genome maps indicate the level of identity. The large terminase was set as the first gene among all genomes. The genome size of all phages is illustrated.

**References**

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