

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

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| **Code assigned:** | **2021.002B** |  |
| **Short title:**  Create one new subfamily (*Andrewesvirinae*) including two new genera (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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

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

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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 |  |
| 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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| 2021.002B.R.Andrewesvirinae |

**Abstract**

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| Here, we propose the creation of a new subfamily “Andrewesvirinae” comprising two new genera, the new genus “Denvervirus” comprising one new species and the new genus “Vipetofemviru*s”* comprising three new species based on genome-based comparisons. |

**Text of proposal**

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**Supporting evidence**

Andrewesvirinae: The name is derived from the author of the first description of the genus *Enterococcus* [1].

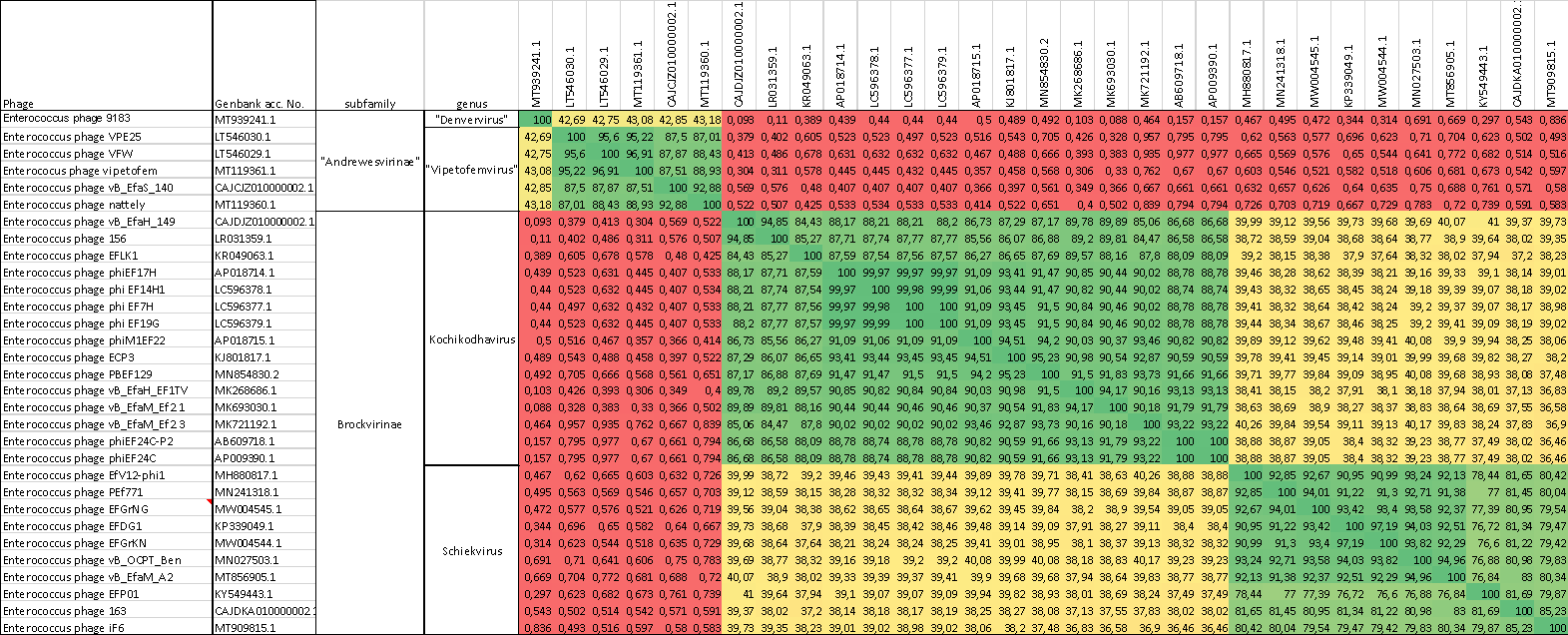
*Denvervirus*: The name is derived from the geographic origin of the first isolated phage of this type, Enterococcus phage 9183 which was isolated from wastewater from Denver in 2018. Its genome consists of 86,301 bp with 109 CDS and 2 tRNA genes.

*Vipetofemvirus*: The name is derived from phage vipetofem which was isolated together with phage nattely from waste water from Denmark in 2017 [2]. The third member of this genus, phage vB\_EfaS\_140, was isolated from Gamoneu cheese in Spain. Their genome sizes range from 85,371 to 85,669 bp, analysis revealed 1 tRNA gene in each genome.

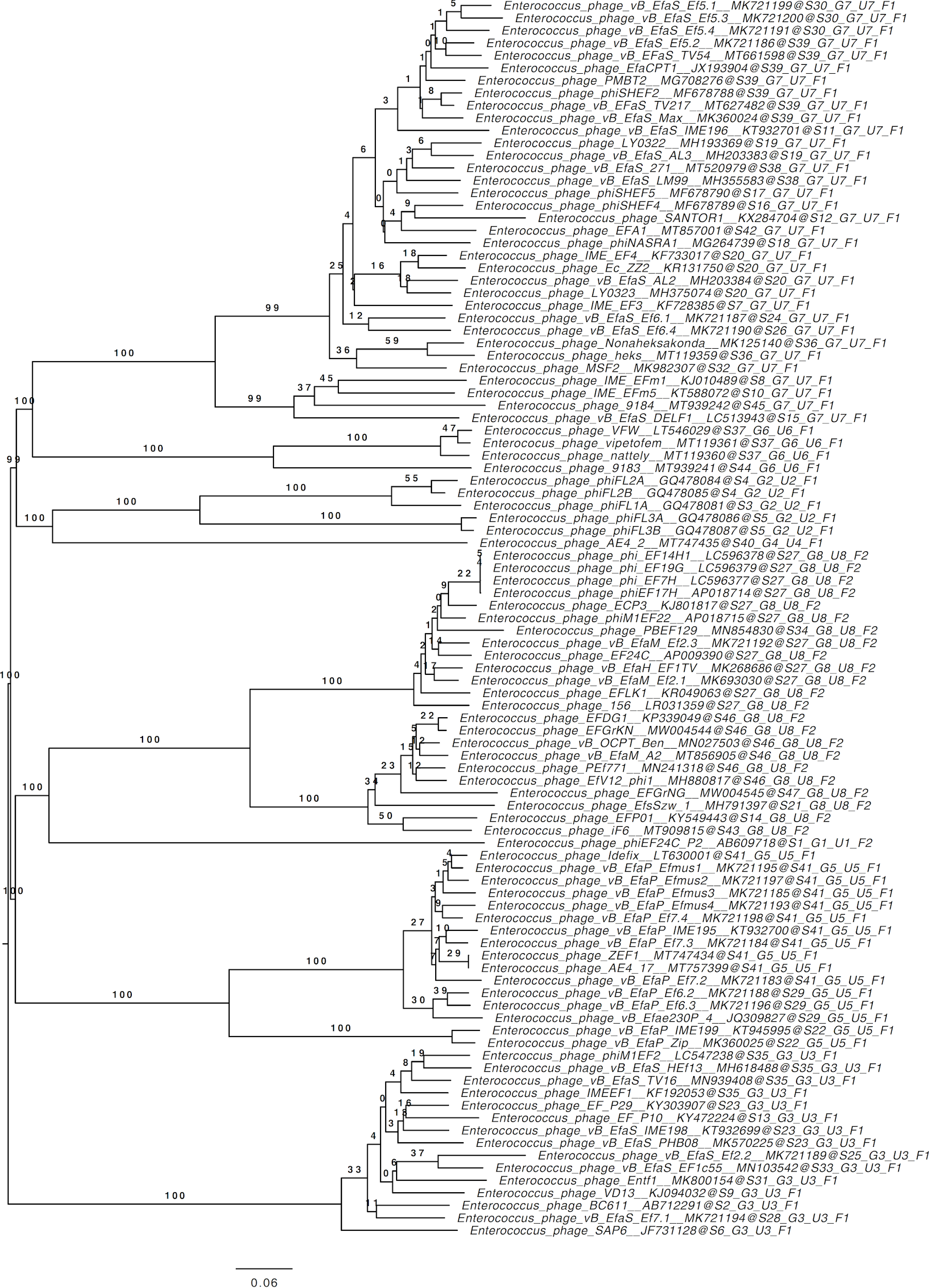
**Electron micrograph:** None available

**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 [3, 4].

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



**Phylogeny:** Phylogenetic analysis of several Enterococcus phage using VICTOR



All pairwise comparisons of the amino acid sequences were conducted using the Genome-BLAST Distance Phylogeny (GBDP) method [5] under settings recommended for prokaryotic viruses [6].

The resulting intergenomic distances were used to infer a balanced minimum evolution tree with branch support via FASTME including SPR postprocessing [7]. Branch support was inferred from 100 pseudo-bootstrap replicates each. Trees were rooted at the midpoint [8] and visualized with FigTree [9].

Fig shows the phylogenomic GBDP tree inferred using the formula D6 and yielding average support of 31 %. The numbers above branches are GBDP pseudo-bootstrap support values from 100 replications. The branch lengths of the resulting VICTOR trees are scaled in terms of the respective distance formula used.

**References**

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