

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

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| **Code assigned:** | **2021.020B** |  |
| **Short title:** Create one new species in the genus *Copernicusvirus*, subfamily *Sarlesvirinae* (*Rountreeviridae*) | | |
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**Author(s) and email address(es)**

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| Malgorzata Łobocka |

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

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| *Salasmaviridae, Rountreeviridae, Guelinviridae* Study Group, Bacterial 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 | May 2021 |
| 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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| 2021.020B.R.Copernicusvirus |

**Abstract**

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| In a complete review of the enterococcal phages belonging to the *Rountreeviridae* family using VIRIDIC and ViPTree we have discovered one more species in the genus *Copernicusvirus*.These phages share almost all properties with other phages of this genus, but differ significantly enough (less than 95% identity with phages of other *Copernicusvirus* species) to classify them as separate species of this genus. |

**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 and Viridic algorithm | |

**Supporting evidence**

**History:** This genus was established via Taxonomy Proposal 2020.140B.R.Rountreeviridae.zip

**Specific References:**  None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs\* | Overall % DNA sequence identity (\*\*) | Overall % homologous proteins (\*\*\*) |
| Enterococcus phage AE4\_17 |  | MT757399.1 | 18.48 | 32.9 | 28 | 0 | 71.0 | 88.0 |

N.B.Type species strain exemplar of *Copernicusvirus* genus is Enterococcus phage vB\_Efae230P-4 (JQ309827.1). Enterococcus phage ZEF1 (MT747434)should be considered strain of the same species as *Copernicusvirus AE417*.

(\*) determined using RNAscan-SE [1]

(\*\*) determined using Viridic [2] and Enterococcus phage vB\_Efae340P-4 as a type species strain exemplar

(\*\*\*) determined using CoreGenes 5.0 [3,4] and Enterococcus phage vB\_Efae340P-4 as a type species strain exemplar

**BLASTN homologs:**  VIRIDIC analysis reveals that the closest relative besides other phages of *Copernicusvirus* genus is Enterococcus virus v\_EfaP\_IME199 [KT945995.1] of *Minhovirus* genus of *Sarlesvirinae* subfamily, *Rountreeviridae* family. It shares 22% DNA sequence with Enterococcus phage AE4\_17.

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [2]) computes pairwise intergenomic distances/similarities amongst phage genomes. The comparison below provides the results of DNA sequence comparison of strains of known and proposed new species of enterococcal *Copernicusvirus* genus phages. The phage names on a white background and those highlighted in yellow correspond to existing species (new strains of these species are highlighted in yellow), while the ones in orange represent the new species and will be added through this TaxoProp.

Chart

Description automatically generated with medium confidence

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [5]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [6]. The **blue** arrowhead points to *Copernicusvirus* genus. The **orange arrows** point to the new species of the *Copernicusvirus* genus, while the yellow one points to the new strain of known species of this genus.



**Phylogeny:** The phylogenetic trees weres constructed using the major capsid protein, tail protein and DNA polymerase homologs of Enterococcus phage AE4\_17 and related phages with phylogeny.fr in “one click” mode (7). "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 divergentregions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See (8) for details."

A picture containing graphical user interface

Description automatically generated

A picture containing diagram

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Text

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**References**

1: 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.

2: Moraru C (2020) VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>

3: 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.

4: Contreras-Moreira, B., & Vinuesa, P. (2013). GET\_HOMOLOGUES, a versatile software package for scalable and robust microbial pangenome analysis. Appl. Environ. Microbiol., 79(24), 7696-7701

5: 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.

6: 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

7: 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.

8: 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.