

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

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| **Code assigned:** | **2021.072B** |  |
| **Short title:** Create four new species in the genus *Rosenblumvirus*, subfamily *Rakietenvirinae* (*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 |

|  |  |  |
| --- | --- | --- |
| **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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| 2021.072B.R.Rosenblumvirus |

**Abstract**

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| In a complete review of the *Staphylococcal* phages belonging to the family *Rountreeviridae* using VIRIDIC and ViPTree we have discovered 4 more species in the genus *Rosenblumvirus*.These phages share almost all properties with other phages of this genus, but differ significantly enough (less than 95% identity with phages of other *Rosenblumvirus* 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 family was established via Taxonomy Proposal 2020.140B.R.Rountreeviridae

**Specific References:**  Bonasera RM, Korn A, Newkirk H, et al. Coding-Complete Genome Sequence of *Staphylococcus aureus* Podophage Portland. Microbiol Resour Announc 8 (47), e01337-19 (2019) [Portland]

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein\* | tRNAs\*\* | Overall % DNA sequence identity (\*\*\*) | Overall % homologous proteins (\*\*\*\*) |
| SA46-CL1 |  | MK936476.1 | 17.51 | 28.8 | 21\* | 0 | 100 | 100 |
| Portland |  | MN098325.1 | 17.71 | 29.3 | 21\* | 0 | 82.2 | 100 |
| EBHT |  | MT926124.1 | 17.47 | 29.6 | 21\* | 0 | 79.8 | 100 |
| LSA2366 |  | MW363799.1 | 17.06 | 29.4 | 21 | 0 | 83.4 | 100 |

**(\*) determined using tBlastn [1,2]. The original sequence submissions does not include all genes**

**(\*\*) determined using RNAscan-SE [3]**

**(\*\*\*) determined using Viridic [4]**

**(\*\*\*\*) determined using CoreGenes 5.0 [5,6]**

**BLASTN homologs:**  **VIRIDIC analysis reveals that the closest relative besides other phages of *Rosenblumvirus* genus is Staphylococcus phageSt 134 [KY471386.1] of *Andhravirus* genus of *Rakietenvirinae* subfamily of *Rountreeviridae* family. It shares 43.7% DNA sequence identity with SA46-CL1.**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [4]) 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 staphylococcal *Andhravirus* and *Rosenblumvirus* 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 are those which will be added through this TaxoProp. New species are indicated by arrows.

Chart

Description automatically generated

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [7]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [8]. The **orange arrows** point to the new species of the *Rosenblumvirus* genus.





**References**

1: Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol 1990;215:403e10.

2: Sayers EW, Agarwala R, Bolton EE, et al. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res*. 2019;47(D1):D23-D28. doi:10.1093/nar/gky1069Sayers EW, Agarwala R, Bolton EE, et al. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res*. 2019;47(D1):D23-D28. doi:10.1093/nar/gky1069

3: 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.

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

5: 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.

6: 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

7: 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.

8: 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