

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

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| **Code assigned:** | **2020.135B** |  |
| **Short title:** Create one new genus (*Rockefellervirus*) including six species (*Caudovirales*: *Siphoviridae*) | | |
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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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| *Caudovirales* 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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| --- | --- | --- |
| **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 | June 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.135B.R.Rockefellervirus.xlsx |

**Abstract**

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| Here, we propose the creation of new genus *Rockefellervirus* comprising six species of siphoviruses which infect *Staphylococcus epidermidis*. |

**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 algorithm. | |

**Supporting evidence**

**Source of the name of this taxon:** This genus is named after the name of the Rockefeller University, where the first phages of this genus were isolated and described.

**History:** All these phages were isolated with the use of *Staphylococcus epidermidis* as a host, and two of them PH15 and CNPH82 were the first *S. epidermidis* phages of sequenced genomes. They were clustered by Oliveira et al. (2019) [1] in the subcluster B(4) of staphylococcal *Siphoviridae* with three less related phages that infect *Staphylococcus aureus* or *Staphylococcus haemolyticus*. They are temperate and produce stable lysogens. Genomes of some but not all of them contain introns.

Four of the species were previously assigned to the genus *Phietavirus* which is broken up due to large genomic differences of the members phages.

**Specific References:** Daniel A, Bonnen PE, Fischetti VA. First complete genome sequence of two *Staphylococcus epidermidis* bacteriophages. J Bacteriol. 2007;189(5):2086‐2100. doi:10.1128/JB.01637-06 [PH15, CNPH82]

Gutiérrez D, Martínez B, Rodríguez A, García P. Isolation and characterization of bacteriophages infecting *Staphylococcus epidermidis*. Curr Microbiol. 2010;61(6):601‐608. doi:10.1007/s00284-010-9659-5 [vB\_SepiS-phiIPLA5, vB\_SepiS-phiIPLA7]

Gutiérrez D, Martínez B, Rodríguez A, García P. Genomic characterization of two *Staphylococcus epidermidis* bacteriophages with anti-biofilm potential. BMC Genomics. 2012;13:228. doi:10.1186/1471-2164-13-228 [vB\_SepiS-phiIPLA5, vB\_SepiS-phiIPLA7]

**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs\* | Overall % DNA sequence identity (\*\*) | Overall % homologous proteins (\*\*\*) |
| PH15 |  | [DQ834250.1](about:blank) | 44.04 | 34.9 | [6](about:blank)8 | 0 | 100 | 100 |
| vB-SepiS\_philPLA5 |  | [JN192400.1](about:blank) | 43.58 | 34.7 | 66 | 0 | 62.4 | 69.1 |
| vB-SepiS\_philPLA7 |  | [JN192401.1](about:blank) | 42.12 | 34.8 | 59 | 0 | 76.5 | 73.5 |
| IME1348\_01 |  | [KY653120.1](about:blank) | 42.37 | 34.7 | 63 | 0 | 65.8 | 63.2 |
| CNPH82 |  | [DQ831957.1](about:blank) | 43.42 | 34.7 | 65 | 0 | 69.1 | 75.0 |
| CNPx |  | [KU598975.1](about:blank) | 43.29 | 34.7 | [6](about:blank)9 | 0 | 83.0 | 86.8 |

**N.B. *Staphylococcus* phage PH15 should be considered strain of the type species in this genus.**

**(\*) determined using tRNAscan-SE [2]**

**(\*\*) determined using VIRIDIC [3]**

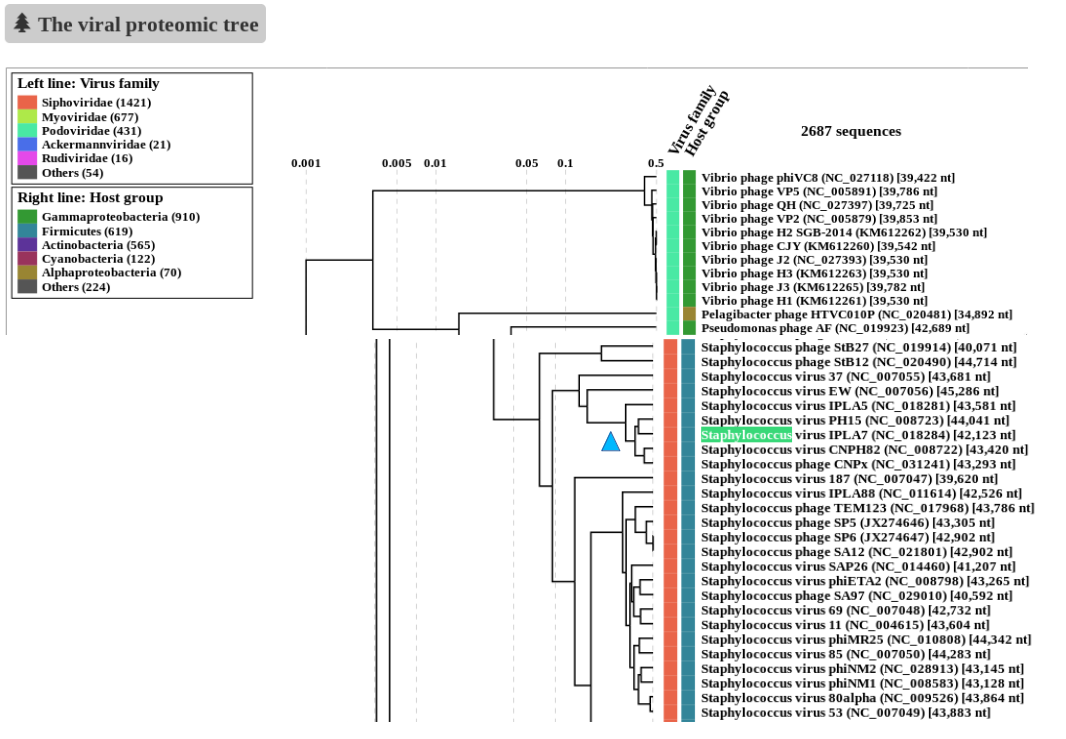
**(\*\*\*) determined using CoreGenes 3.5 [4]**

**BLASTN homologs:**  **BLASTN analysis reveals that the closest relative is *Staphylococcus* phage StB20 [JN700521.1] [5]. It shares 15% DNA sequence with PH15.**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [2]) computes pairwise intergenomic distances/similarities amongst phage genomes. The phage names highlighted in **yellow** are those which will be added through this TaxoProp.



**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [6]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [7]. The large **blue arrowhead** points to the *Rockefellervirus* genus.

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**References**

1. Oliveira H, Sampaio M, Melo LDR, et al. Staphylococci phages display vast genomic diversity and evolutionary relationships. *BMC Genomics*. 2019;20(1):357. doi:10.1186/s12864-019-5647-8 PMID: 31072320
2. 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.
3. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. http://kronos.icbm.uni-oldenburg.de/viridic/
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5. Zhang Z, Schwartz S, Wagner L, Miller W. A greedy algorithm for aligning DNA sequences. J Comput Biol, 2000; 7:203-14. doi: 10.1089/10665270050081478. PMID: 10890397.  
   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