

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

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| **Code assigned:** | **2020.013B** |  |
| **Short title:** Create ten new genera (*Caudovirales*: *Siphoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Lambda 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 | July 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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| 2020.013B.R.Assorted\_Siphoviridae |

**Abstract**

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| This proposal establishes assorted species and genera within the *Siphoviridae*. |

**Text of proposal**

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| |  | | --- | | **Background:** 5 phage genomes belonging to the genera *Lambdavirus* and *Ravinvirus* were downloaded along with 65 other reportedly complete phage genomes that a) are >30 kbp, b) have been associated with the lambda-like phages by historical report, the sequence submitter, or NCBI algorithms, c) have not yet been assigned to any ICTV-recognized taxonomic groups, and d) are not encompassed in the *Sepvirinae* or *Hendrixvirinae* proposals being submitted in parallel.  **Methods:** An all-against-all nucleotide sequence comparison was conducted in VIRIDIC (Moraru et al, 2020). Genus assignments were based on a 70% similarity threshold and species assignments were based on a 95% similarity threshold. In total, 10 new genera encompassing 20 new species are proposed based on Figure 1. All of the new genera were placed within the *Siphoviridae* family, though that placement is expected to change as the *Siphoviridae* continue to be re-organized.  One phage, ev017, sits on the boundary of *Bievrevirus* and *Jouyvirus*, having 70-71% nucleotide similarity to all of the phages in both genera (Figure 1). We placed the *Escherichia virus ev017* species within *Jouyvirus*, since both VIRIDIC (a nucleotide based method, 1) and ViPTree (a proteomic tree method, 2) show its exemplar phage, ev017, clustering within that genus (Figure 2).  **Genus name Origins:**  ***Sawaravirus:*** The studies describing stx-converting phage WGPS2, the exemplar for the type species, were conducted in Fukuoka, Japan. Sawara-ku is a ward in Fukuoka. Sawara is also a type of fish and a cypress tree.  ***Marienburgvirus***: Enterobacteria phage BP-4795, the exemplar for the type species, was isolated in Würzburg, Germany. Marienburg is one of the major hills in the city.  ***Pankowvirus***: Named after a district in Berlin. The exemplar of the type species was isolated from a German strain of *E. coli*.  ***Bievrevirus***: Named after the Bièvre River in France, near where the type species was isolated.  ***Jouyvirus***: The type species was isolated in Jouy-en-Josas, France. Jouy means “joy”.  ***Glaedevirus, Alegriavirus, Radostvirus, Nesevirus***: Many of the constituent species for these genera were also isolated in Jouy-en-Josas from Danish samples. “Joy” translates as glaede in Danish, alegria in Portuguese, radost in Czech and Croatian, neşe in Turkish.  ***Aguilavirus***: This genus is currently made up of Mexican *E. coli* phages. The Mexican flag bears an eagle (“aguila” in Spanish). | |

**Supporting evidence**

**Figure 1. VIRIDIC heatmap of assorted lambda-like phages.** Phage names are provided with GenBank accession numbers and indicate any previously recognized ICTV genus and species assignments. New and expanded genera are marked in gold boxes. Existing species are marked in pink boxes. New species established in this proposal are marked in red boxes. The semi-transparent green box highlights *Escherichia virus ev017*, which was ultimately placed in *Jouyvirus*.

**A screenshot of a cell phone

Description automatically generated**

**Figure 2. ViPTree constructed by adding new members of *Jouyvirus***, ***Glaedevirus, Alegriavirus, Radostvirus, Nesevirus, Bievrevirus,* and *Lambdavirus* to ViPTree’s existing viral database.** Red stars indicate manually uploaded sequences. Phage ev017 is marked with a blue star.

A screenshot of a social media post

Description automatically generated

**References**

1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv 2020.07.05.188268. <https://doi.org/10.1101/2020.07.05.188268>
2. Nishimura Y et al (2017) ViPTree: the viral proteomic tree server.Bioinformatics, 33: 2379–2380, <https://doi.org/10.1093/bioinformatics/btx157> PMID: 28379287 DOI: 10.1093/bioinformatics/btx157