

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

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| **Code assigned:** | ***2023.064B*** |  |
| **Short title:** To create 16 new species in the genus *Sugarlandvirus* [*Caudoviricetes*; Family *Demerecviridae*] | | |
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**Author(s) and email address(es)**

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| Andrew M. Kropinski |

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

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| *Caudoviricetes* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**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 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.064B.N.v1.Sugarlandvirus\_16ns.xlsx |

**Abstract**

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| We have added 16 new species of to the genus *Sugarlandvirus.* |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree [10]. | |

**Supporting evidence**

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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Yellow, existing species; green, new species. Abbreviations: phg = phage; vir = virus; Esch = Escherichia; Shig = Shigella; Ente = Enterobacteria; Salm = Salmonella.

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**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phages of interest are indicated with **red stars**.

**Origin of the name of this taxon:** N/A

**Historical aspects:** The genus *Sugarlandvirus* was created through Taxonomy Proposal 2018.129B.A.v1.Sugarlandvirus. It currently consists of two species we are now adding 16 new species.

**Genome summary: .**

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| **Accession No.** | **Exemplar** | **Overall DNA sequence similarity (\*)** |
| MG459987.1 | Klebsiella phage Sugarland | 100 |
| LR881116.1 | Klebsiella phage vB\_KaS-Veronica | 83.2 |
| MN434094.1 | Klebsiella phage AmPh\_EK80 | 89.6 |
| OP171943.1 | Klebsiella phage GZ8 | 92.1 |
| MN101228.1 | Klebsiella phage KPN4 | 81.4 |
| MN434096.1 | Klebsiella phage JIPh\_Kp127 | 82.2 |
| MZ571830.1 | Klebsiella phage vB\_KpnS-VAC51 | 77.8 |
| MN163280.1 | Klebsiella phage KpGranit | 85.7 |
| LR881113.1 | Klebsiella phage vB\_KppS-Totoro | 85.6 |
| LR881112.1 | Klebsiella phage vB\_KppS-Storm | 82.4 |
| LR881109.1 | Klebsiella phage vB\_KppS-Anoxic | 83.7 |
| MT380195.1 | Klebsiella phage vB\_Kpn\_B01 | 83.9 |
| MW713578.1 | Klebsiella phage Shaphc-TDM-1124-4 | 83.1 |
| MZ571828.1 | Klebsiella phage vB\_KpnS-VAC35 | 82.4 |
| ON637170.1 | Klebsiella phage vB\_KpnS\_Uniso31 | 83.3 |
| MK521907.1 | Klebsiella phage vB\_KpnS\_FZ41 | 84.8 |
| MZ634344.1 | Klebsiella phage PWKp9S | 83.5 |

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

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