

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

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| **Code assigned:** | ***2022.078B*** |  |
| **Short title:** Create a new genus (*Siatvirus*) with a single species (*Caudoviricetes*) | | |
|  | | |

**Author(s) and email address(es)**

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|  |  |
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**Corresponding author**

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| Andrew M. Kropinski |

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

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| Bacterial Viruses Subcommittee, 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**

|  |  |
| --- | --- |
| **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 2022 |
| 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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| 2022.078B.N.v1.Siatvirus\_ng.xlsx |

**Abstract**

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| The genus Siatvirus was created for a series of jumbo phages isolated at the Shenzhen Institute of Advanced Technology in China. Only one genome has been annotated and therefore only one species is created. |

**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] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **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. [8] | |

**Supporting evidence**

**Origin of the name of this taxon:** This taxon is named in honour of the Shenzhen Institute of Advanced Technology where these phages were isolated.

**Historical aspects:** These lytic phage was isolated against Klebsiella pneumonia from sea water in China.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Klebsiella phage KpLz-2\_45 | [MN871446.1](https://www.ncbi.nlm.nih.gov/nuccore/MN871446.1) | 296.71 | 45.7 | [354](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87455/795061|Klebsiella phage KpLz-2_45/viral segment/) | 6 | 100 | 100 |
| Serratia phage KpZh\_1 | [MN871452.1](https://www.ncbi.nlm.nih.gov/nuccore/MN871452.1) | 298.9 | 45.7 | \*\*\* | \*\*\* | 90.7 | NA |
| Serratia phage KpYy\_2\_45 (#) | [MN871451.1](https://www.ncbi.nlm.nih.gov/nuccore/MN871451.1) | 302.44 | 45.7 | \*\*\* | \*\*\* | 93.0 | NA |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**(\*\*\*) not annotated**

**(#) actual host Klebsiella pneumoniae**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars** and a with a **blue rectangle**.



**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from KpLz-2\_45 and related phages with phylogeny.fr in “one click” mode [6]. It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. See Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [7] for details. The members of the *Siatvirus* are indicated with a **blue rectangle**.

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