

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

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| **Code assigned:** | ***2022.072B*** |  |
| **Short title:** Create a new genus (*Scappvirus*) with a single species (*Caudoviricetes*) |
|  |

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

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|  |  |
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**Author(s) institutional address(es) (optional)**

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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** |
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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 |

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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 | March 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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| 2022.072B.N.v1.Scappvirus\_ng.xlsx |

**Abstract**

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| The genus *Scappvirus* was created for the genotypically unique siphophage, Serratia phage Scapp. |

**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] |

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**Supporting evidence**

**Origin of the name of this taxon:** This taxon’s name derives directly from that of the first phage of its type Serratia phage Scapp.

**Historical aspects:** The siphophage Scapp was isolated using an S. marcescens strain from activated sludge collected from the water treatment plant in College Station, TX. [11]

**Electron micrograph:** N/A

**Genome summary:** genomic orphan

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| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Serratia phage Scapp | [MH553517.1](https://www.ncbi.nlm.nih.gov/nuccore/MH553517.1) | 42.97 | 55.9 | [59](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71941/399813|Serratia phage Scapp/viral segment/) | 100 | 100 |

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

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

**Phylogeny:** The phylogenetic tree was constructed using the MCPs from pAEv1818 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 *Scappvirus* are indicated with a **blue rectangle**.

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**References**

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