

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

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| **Code assigned:** | ***2022.086B*** |  |
| **Short title:** Create a new genus (*Stonewallvirus)* with a single species (*Caudoviricetes*) | | |
|  | | |

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

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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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| 2022.086B.N.v1.Stonewallvirus\_ng.xlsx |

**Abstract**

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| The *Stonewallvirus* genus encompasses three closely related siphoviruses isolated in the USA and Poland. |

**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 after the address “Stonewall Avenue” of Pharmaceutical Sciences, Univ. Oklahoma Health Sciences Center where the first virus of its type, Streptococcus phage A25, was isolated in 2015.

**Historical aspects:** This “lytic” phage was isolated against Streptococcus pyogenes ATCC 12204. A strain, Streptococcus phage Str01, possesses an integrase [11]. Phage Str01 has a tail that is 186 nm long and a head which is 62 nm wide and 66 nm long [11].

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptococcus phage A25 | [NC\_028697.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028697.1) | [KT388093.1](https://www.ncbi.nlm.nih.gov/nuccore/KT388093.1) | 33.9 | 38.4 | [46](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42140/461851|Streptococcus phage A25/viral segment Unknown/) | 100 | 100 |

**(\*) determined using BLASTn [1]**

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

**N.B. Streptococcus phages A1 (MW495853.1) and Str01 (KY349816) are strains of A25**

**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. N/A

**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from A25 and related phages with phylogeny.fr in “one click” mode [6]. The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [7] for details. The members of the *Stonewallvirus* are indicated with a **blue rectangle**.

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