

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

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| **Code assigned:** | **2020.120B** |  |
| **Short title:** Create one new genus (*Pokkenvirus*) including one new species (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Johannes Wittmann |

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

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| N4-like phages 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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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of the genus “Pokkenvirus” including one species, Stenotrophomonas phage Pokken based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analyses of terminase and vRNA polymerase protein sequences. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm [1-3]. | |

**Supporting evidence**

**Source of the name of this taxon:** The name is derived from the name of the isolated phage of this type, Stenotrophomonas phage.

**History:** Stenotrophomonas phage is a member of the *Podoviridae* family and infects *S. maltophilia*. It was isolated from lake surface water in the US [4].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Pokken |  | MN062186 | 76.24 | 55.1 | 93 | 5 |

**BLASTN homologs:** None, genomic orphan/singleton

**Electron micrograph:** None available

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [5]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. Column 2 - (P) partial genome. The colour codes in columns 3 and 4 indicate the boundaries of the proposed subfamilies and genera.

**Phylogenetic analysis** using the (A) terminase and (B) vRNA polymerase protein sequences of N4-like phages. The amino acid sequences were compared using MUSCLE with MEGA7 [6]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (100).

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**References**

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