

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

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| **Code assigned:** | **2020.097B** |  |
| **Short title:** Create one new genus (*Littlefixvirus*) containing one new species (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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| J Wittmann |

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

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| Bacterial and Archaeal Viruses Subcommittee, N4-like viruses SG |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person (not applicable)**

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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 | 6 June 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 new genus “Littlefixvirus” comprising one new species, based on genome-based comparisons |

**Text of proposal**

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**Supporting evidence**

**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].

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

**History:** Phage Littlefix is a member of the *Podoviridae* family and a member of the N4-superfamily of viruses.It was originally isolated from plant compost and infects *Pseudomonas sp.* CT12. Its genome consists of 74,895 bp with 95 unique coding sequences (CDSs).

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Littlefix |  | MG775260 | 74.895 | 48.7 | 95 | 0 |

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

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed with VICTOR [4], using whole genome sequences of N4-like phages at the nucleotide level.



**References**

1. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
2. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.
3. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID:26553804.
4. Meier-Kolthoff JP, Goeker M. VICTOR: genome-based phylogeny and classification of prokaryotic viruses. [Bioinformatics](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5860169/). 2017; 33(21): 3396–3404. doi: 10.1093/bioinformatics/btx440 PMID: 29036289