

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

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| **Code assigned:** | **2020.134B** |  |
| **Short title:** Create one new genus (*Riverridervirus*) including 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; *Caudovirales* Study Group |

**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 *Riverridervirus* 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, Xanthomonas phage Riverrider

**History:** Phage RiverRider is a member of the *Podoviridae* family and the superfamily of N4-like viruses that was isolated from a strawberry plant and that infects specifically the plant-pathogen *Xanthomonas fragariae*. Its genome consists of 76,335 bp with 90 protein coding genes and 7 tRNA genes [4].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| RiverRider |  | MG983743 | 76.34 | 49.4 | 90 | 7 |

**BLASTN homologs:** None, genomic orphan/singleton [1-3]. The next most closely related phage is *Stenotrophomonas* phage Pokken [MN062186] which shares 31.1% DNA sequence identity with RiverRider.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed with VICTOR [5], using whole genome sequences of N4-like phages at the nucleotide level.



**References**

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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.
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5. 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