

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

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| **Code assigned:** | **2020.044B** |  |
| **Short title:** Create one new genus (*Dendoorenvirus*) 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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| J 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 (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 *Dendoorenvirus* 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 scientist, who discovered the genus Delftia, the host organism of the isolated phage of this type, Delftia phage RG-2014.

**History:** Phage RG-2014 is a member of the *Podoviridae* family and the superfamily of N4-like viruses that was isolated from a wastewater treatment plant in the US and that infects specifically the multidrug resistant bacterium *Delftia tsuruhatensis* ARB-1 [4].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| RG-2014 | NC\_027348 | KM879221 | 73.88 | 59.9 | 88 | 0 |

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

**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**

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:Bhattacharjee AS, Motlagh AM, Gilcrease EB, Islam MI. Complete genome sequence of lytic bacteriophage RG-2014 that infects the multidrug resistant bacterium *Delftia tsuruhatensis* ARB-1. Standards in Genomic Sciences. 2017; 12:82 PMID: 29270250 PMCID: PMC5735904 DOI: 10.1186/s40793-017-0290-y

5:  [Meier-Kolthoff](https://www.ncbi.nlm.nih.gov/pubmed/?term=Meier-Kolthoff%20JP%5BAuthor%5D&cauthor=true&cauthor_uid=29036289) 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.