

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.075B** |  |
| **Short title:** Create one new genus (*Huelvavirus*) including one new species (*Caudovirales*: *Schitoviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Kropinski AM, Moraru C, Wittmann J | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@gmail.com; liliana.cristina.moraru@uol.de; jow12@dsmz.de |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  DSMZ, Germany [JW] |

**Corresponding author**

|  |
| --- |
| Johannes Wittmann |

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

|  |
| --- |
| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

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

|  |
| --- |
|  |

**Authority to use the name of a living person**

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | July 2020 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

|  |
| --- |
|  |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

|  |
| --- |
| Here, we propose the creation of the genus “Huelvavirus” including one species, Sinorhizobium phage ort11 based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analyses of terminase and vRNA polymerase protein sequences. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **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 geographic origin of the isolated phage of this type, Sinorhizobium phage ort11.

**History:** Phage ort11 is a member of the *Podoviridae* family and infects *S. meliloti*. Bacteriophage ort11 was isolated from soil samples associated with rhizosphere of *Medicago marina* in Spain [4].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| ort11 |  | MN228696.1 | 75.24 | 44.3 | 103 | 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.



**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).

****

B

A

**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. [Cubo MT](https://europepmc.org/search?query=AUTH:%22Mar%C3%ADa%20Teresa%20Cubo%22), [Alías-Villegas C](https://europepmc.org/search?query=AUTH:%22Cynthia%20Al%C3%ADas-Villegas%22), Balsanelli E, Mesa D, de Souza E, Espuny MR Diversity of Sinorhizobium (Ensifer) meliloti Bacteriophages in the Rhizosphere of Medicago marina: Myoviruses, Filamentous and N4-Like Podovirus.Frontiers in Microbiology. 2020: 11:22. DOI: 10.3389/fmicb.2020.00022 PMID: 32038600.
5. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. http://kronos.icbm.uni-oldenburg.de/viridic/
6. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol. Biol. Evol. 2016,33, 1870–4, doi:10.1093/molbev/msw054. PMID: 27004904.