

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

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| **Code assigned:** | **2020.185B** |  |
| **Short title:** Create one new genus (*Zicotriavirus*) including two 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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**ICTV study group comments and response of proposer**

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

|  |  |  |
| --- | --- | --- |
| **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 “*Zicotriavirus*” comprising two 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 ZC03

**History:** Phages ZC03 and ZC08 were isolated in Brazil and are members of the *Podoviridae* family that infect *Pseudomonas aeruginosa*. The electron micrographs show their icosahedral head of ~72 nm by ~59 nm and a short tail ~21 nm long with terminal fibers [4].

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| ZC03 |  | KU356690 | 69.84 | 42.6 | 85 | 10 | 100 | 100 |
| ZC08 |  | KU356691 | 70.77 | 43.1 | 83 | 9 | 92.98 | 91.76 |

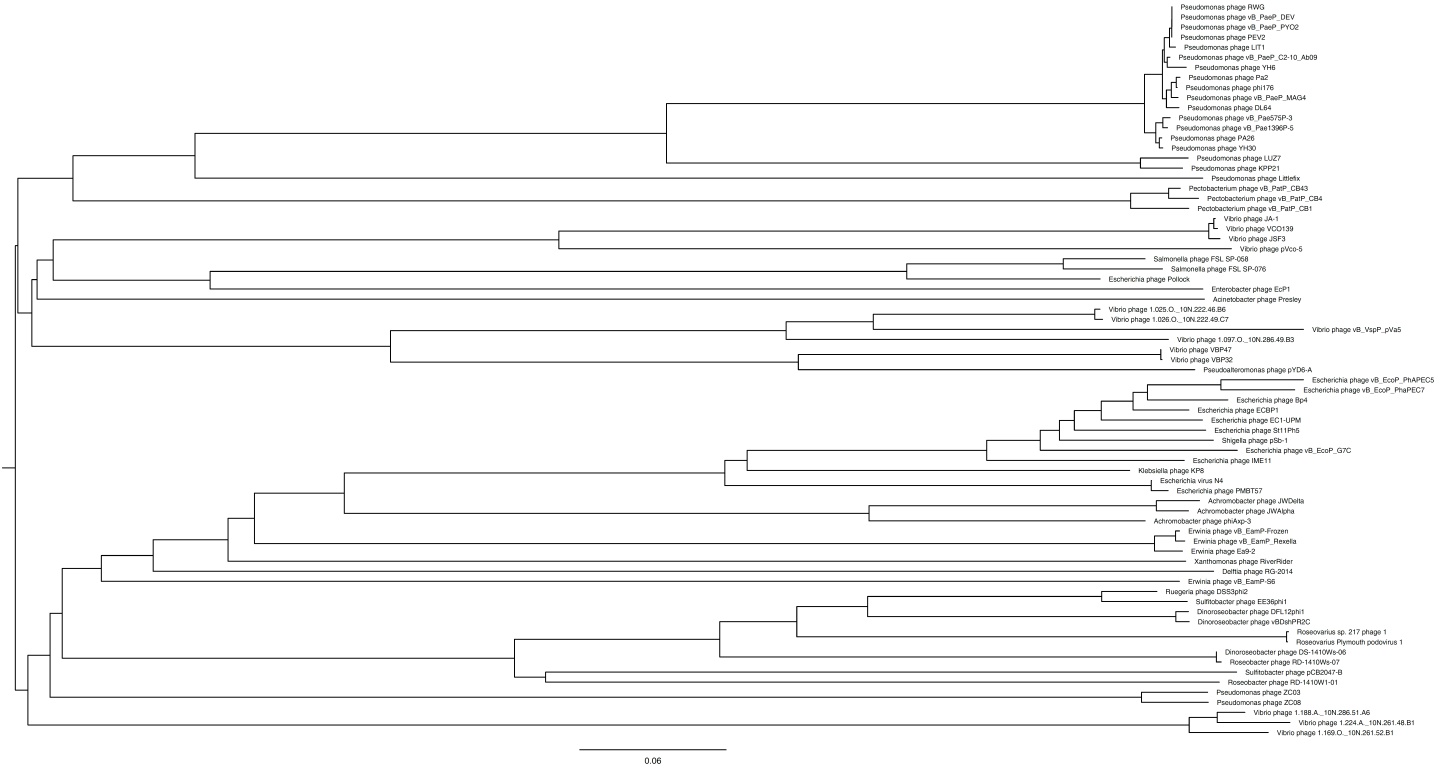
**\*\* Determined using BLASTn at NCBI [1-3]**

**\*\*\* Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

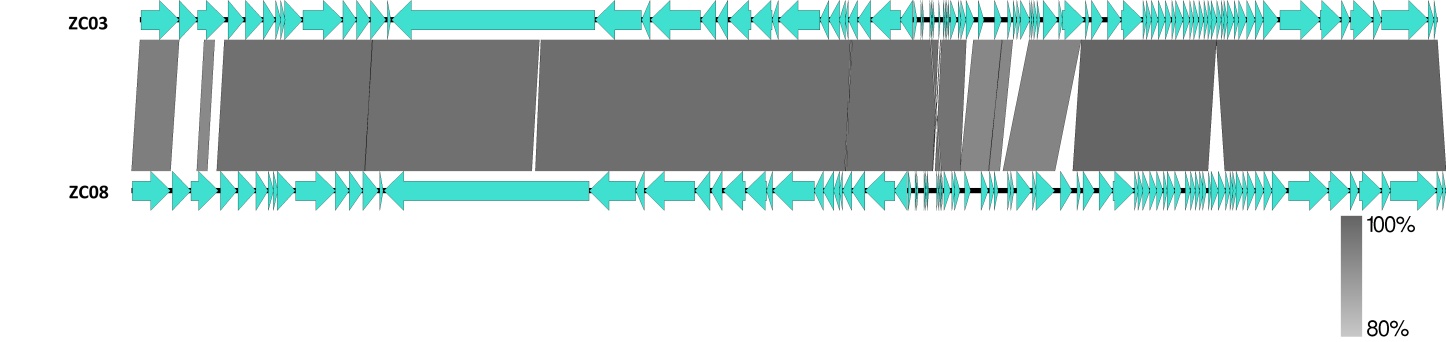
**Electron micrograph:** None available

**Phylogeny:**

The phylogenetic tree was constructed with VICTOR [5], using whole genome of phages ZC03, ZC08 and related N4-like phages.



Synteny plot of Pseudomonas phages ZC03 and ZC08 at the nucleotide level. Plot was visualized using EasyFig [6].



**References**

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2. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.