

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

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| **Code assigned:** | **2020.155B** |  |
| **Short title:** Create one new genus (*Sozzivirus*) including three new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew M. Kropinski |

**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**

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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 | April 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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| 2020.155B.R.Sozzivirus.xlsx |

**Abstract**

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| To create a new genus, *Sozzivirus*, containing three species of temperate *Oenococcus oeni* siphoviruses. They are peripherally related to Lactobacillus siphoviruses such as Lactobacillus phage CL1. |

**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.

**Source of the name of this taxon:** This genus is named in honour of Tommaso Sozzi d. 2009, research scientist with Département Recherche et Développement de la Société d'Assistance Technique pour produits Nestlé S.A. Lausanne (Suisse) who was the first person to isolate an *Oenococcus* phage in 1976.

**History:** These temperate phages were isolated from wine or lysogenic cultures of the lactic acid

bacterium *Oenococcus oeni* and their integration sites thoroughly analyzed (Jaomanjaka et al., 2013).

**Reference:** Jaomanjaka F, Ballestra P, Dols-lafargue M, Le Marrec C. Expanding the diversity of oenococcal bacteriophages: insights into a novel group based on the integrase sequence. Int J Food Microbiol. 2013 Sep 2;166(2):331-40.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| phiS11 | [NC\_023571.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023571.1) | [KF183314.1](https://www.ncbi.nlm.nih.gov/nuccore/KF183314.1) | 46.24 | 38.6 | 59 | 1 | 100 | 100 |
| phiS13 | [NC\_023560.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023560.1) | [KF183315.1](https://www.ncbi.nlm.nih.gov/nuccore/KF183315.1) | 43.45 | 39.0 | 54 | 1 | 79.0 | 79.7 |
| phi9805 | [NC\_023559.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023559.1) | [KF147927.1](https://www.ncbi.nlm.nih.gov/nuccore/KF147927.1) | 46.15 | 38.9 | 55 | 1 | 77.7 | 79.7 |

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**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of phiS11 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**![A screenshot of a cell phone

Description automatically generated]()**

**References**

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