

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

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| **Code assigned:** | **2020.093B** |  |
| **Short title:** Create one new genus (*Leicestervirus*)including three new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| --- | --- |
| Adriaenssens EM, Tolstoy I, Turner D, Kropinski AM | [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk);  [tolstoy@ncbi.nlm.nih.gov](mailto:tolstoy@ncbi.nlm.nih.gov);  [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk);  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com) |

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

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| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of the West of England, UK [DT]  University of Guelph, Canada [AMK] |

**Corresponding author**

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| Andrew M. Kropinski |

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

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| *Caudovirales* 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**

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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 | May 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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| 2020.093B.R.Leicestervirus.xlsx |

**Abstract**

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| To create a new genus, *Leicestervirus,* representing three species of *Clostridioides* phages isolated in Canada and France. |

**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 the University of Leicester where much of the research on *Clostridioides* phages has taken place.

**History:**  Temperate phage φCD38-2 was isolated by mitomycin C induction of a bacterial lysogen. It is “a pac-type temperate *Siphoviridae* phage that stimulates toxin expression when introduced as a prophage into *C. difficile*. Host range analysis showed that φCD38-2 was able to infect 99/207 isolates of *C. difficile* representing 11 different PCR ribotypes. (Sekulovic et al. 2011)”

**Specific Reference:** Sekulovic O, Meessen-Pinard M, Fortier LC. Prophage-stimulated toxin

production in *Clostridium difficile* NAP1/027 lysogens. J Bacteriol. 2011 Jun;193(11):2726-34. doi: 10.1128/JB.00787-10. Epub 2011 Mar 25. PubMed PMID: 21441508

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| phiCD38-2 | [NC\_015568.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_015568.1) | [HM568888.1](https://www.ncbi.nlm.nih.gov/nuccore/HM568888.1) | 41.09 | 30.8 | 55 | 100 | 100 |
| phiCD111 | [NC\_028905.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028905.1) | [LN681535.1](https://www.ncbi.nlm.nih.gov/nuccore/LN681535.1) | 41.56 | 30.9 | 55 | 93.3 | 90.9 |
| phiCD146 | [NC\_028958.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028958.1) | [LN681536.1](https://www.ncbi.nlm.nih.gov/nuccore/LN681536.1) | 41.51 | 30.7 | 52 | 90.0 | 89.1 |

**\* 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/) **[6]**

**Clostridium phage CDSH1 [KU057941.1] should be considered a strain in this genus**

**BLASTN homologs:** The next closely related phage to phiCD38-2 is Clostridium phage phiCD506 [1-3]. They share 19.1% overall DNA sequence identity.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase protein of phiCD38-2 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."

**TerL protein  
  
A screenshot of a cell phone

Description automatically generated**

**Strain table**

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| --- | --- | --- |
| **Phage** | **Accession** | **Belongs to species** |
| Clostridium phage CDSH1 | KU057941.1 | *Clostridioides virus phiCD111* |
| Clostridium phage slur17 | LN881738 | *Clostridioides virus phiCD111* |

**References**

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