

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

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| **Code assigned:** | **2020.047B** |  |
| **Short title:** Create one new genus (*Donellivirus*) to include the species *Bacillus virus G* (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Jakub Barylski |

**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)** |
| *Donellivirus* | Gianfranco Donelli | Y |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | July 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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| 2020.047B.R.Donellivirus.xlsx |

**Abstract**

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| According to the 2019 Master Species List the majority of myoviruses which infect members of the order *Bacillales belong to the* family *Herelleviridae.* There are nine phages, in five genera within the family *Myoviridae*. Here we propose a new genus *Donellivirus****.*** |

**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 *Donellivirus* in honour of Prof. Dr. Gianfranco Donelli, Professor of Microbiology and Former Research Director, Italian National Institute of Health (ISS), Rome who in 1968 isolated Bacillus phage G.

**History:** 2009.010a,bB

**Reference:** 2009.010a,bB

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| G | [NC\_023719.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023719.1) | [JN638751.1](https://www.ncbi.nlm.nih.gov/nuccore/JN638751.1) | 497.51 | 29.9 | 675 | 18 |

**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.