

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

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| **Code assigned:** | **2020.099B** |  |
| **Short title:** Create one new species in the genus *Marthavirus* (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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

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

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

**Corresponding author**

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| Andrew 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 |  |
| 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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| 2020.099B.R.Marthavirus.xlsx |

**Abstract**

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| Minor changes to the genus *Marthavirus* |

**Text of proposal**

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| |  | | --- | | **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 | |

**Supporting evidence**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [1]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The colour codes in columns 1 indicate ICTV recognized species.

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1. **Proposal 1: To add *Arthrobacter virus Zartrosa* to this genus**
2. **Proposal 2: To abolish *Arthrobacter virus Sonny* due to similarity to *Arthrobacter virus Shade***

**Strain table**

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| --- | --- | --- |
| **Phage** | **Accession** | **Belongs to species** |
| Arthrobacter phage Franzy | MF377442.1 | *Arthrobacter virus Brent* |
| Arthrobacter phage Timinator | MF377441 | *Arthrobacter virus BarretLemon* |
| Arthrobacter phage LeeroyJ | MH825703 | *Arthrobacter virus BarretLemon* |
| Arthrobacter phage StevieBay | MT310895 | *Arthrobacter virus BarretLemon* |
| Arthrobacter phage TaeYoung | KU160668 | *Arthrobacter virus Martha* |
| Arthrobacter phage Grekaycon | MK919479 | *Arthrobacter virus Martha* |
| Arthrobacter phage BossLady | MN183283 | *Arthrobacter virus Martha* |
| Arthrobacter phage Jkerns | MT114161 | *Arthrobacter virus Zartrosa* |
| Arthrobacter phage Jordan | MF189176 | *Arthrobacter virus Shade* |
| Arthrobacter phage Sonny | KU160665.1 | *Arthrobacter virus Shade* |

**References**

1. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>