

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

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| **Code assigned:** | **2020.004B** |  |
| **Short title:** Abolish the genus *Viunavirus* and move six existing species to the genus *Kuttervirus* and create 30 new species (*Caudovirales*: *Ackermannviridae*) | | |
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**Author(s) and email address(es)**

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**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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| 2020.004B.R.Ackermannviridae\_reassessment |

**Abstract**

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| When formulated the new family *Ackermannviridae* contained six species in the genus *Viunavirus* which were duplicated in the *Myoviridae*. We have abolished this genus and also added large number of new phages to the family *Ackermannviridae*. |

**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**

**Source of the name of this taxon:** NA

**History:** NA

**Specific Reference:** NA

**VIRIDIC heatmap 1:** VIRIDIC (Virus Intergenomic Distance Calculator; 10) computes pairwise intergenomic distances/similarities amongst phage genomes. The gold coloured genomes correspond to existing species in the genus *Kuttervirus*.

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1. ***Kuttervirus***

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| **Phage Name** | **Accession No.** |
| Salmonella phage allotria | MT074471.1 |
| Salmonella phage pertopsoe | MT074479.1 |
| Salmonella phage maane | MT074480.1 |
| Salmonella phage rabagast | MT074469.1 |
| Salmonella phage heyday | MT074470.1 |
| Salmonella phage SenASZ3 | MH709120.1 |
| Salmonella phage SE14 | MK972690.1 |
| Salmonella phage Se-G | MN871495.1 |
| Salmonella phage SenALZ1 | MH709121.1 |
| Salmonella phage dinky | MT074475.1 |
| Salmonella phage SP1 | MF001362.1 |
| Salmonella phage SeSz-1 | MH791405.1 |
| Salmonella phage aagejoakim | MT074474.1 |
| Salmonella phage Se-B | MN871491.1 |
| Salmonella phage moki | MT074478.1 |
| Salmonella phage BSP101 | KY787213.1 |
| Salmonella phage ST-W77 | KX765865.1 |
| Escherichia phage FEC14 | MG383452.2 |
| Salmonella phage S118 | MH370371.1 |
| Salmonella phage Se-J | MN871498.1 |
| Salmonella phage SS9 | MK972699.1 |
| Salmonella phage Mutine | MG428992.1 |
| Salmonella phage barely | MT074477.1 |
| Escherichia phage EP75 | MG748547.1 |
| Salmonella phage bering | MT074472.1 |

**VIRIDIC heatmap 2:** VIRIDIC (Virus Intergenomic Distance Calculator; 10) computes pairwise intergenomic distances/similarities amongst phage genomes. The yellow coloured genomes correspond to existing species in the genus *Taipeivirus*, while green accented names correspond to existing members of the *Agtrevirus*.

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1. ***Taipeivirus* and *Agtrevirus***

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| Klebsiella phage Magnus | MN045230.1 |
| Klebsiella phage UPM2146 | MN478483.1 |
| Enterobacter phage phiEM4 | LC373201.2 |
| Shigella phage MK13 | MK509462.1 |
| Salmonella phage P46FS4 | MT078988.1 |

**Electron micrograph:** NA

**Phylogeny:** NA

**References**

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