

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

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| **Code assigned:** | ***2023.077B*** |  |
| **Short title:** Create sixty-eight (68) species in the genus *Webervirus* (*Caudoviricetes*; *Drexlerviridae*) | | |
|  | | |

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

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| Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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| --- |
| No comments |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2023 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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|  |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2023.077B.N.v1.Webervirus\_68ns.xlsx |

**Abstract**

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| We have added 68 new species to the genus *Webervirus* based on nucleotide sequence similarity analyses. |

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| **Text of proposal**   |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [10] | |

**Supporting evidence**

**A picture containing screenshot, text, line, rectangle

Description automatically generated**

**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. The names in white boxes are strains. Names highlighted in yellow are existing species while those in blue are new species. Abbreviations: phg = phage; vir = virus; Kleb = Klebsiella; Sten = Stenotrophomonas; Ente = Enterobacteria. For a high resolution, see file 2023.077B.N.v1.Webervirus\_68ns\_Suppl.xls

**Historical aspects:** The genus *Webervirus* was established through Taxonomy Proposal 2019.100B with 32 species*.* Many more exemplars of these viruses have been deposited in GenBank. All of the viruses listed below conform to the genus and species demarcation criteria [10].

**Genome summary:**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Exemplar** | **DNA sequence similarity to phage KP36(\*)** |
| MZ571834.1 | Klebsiella phage vB\_KpnS-VAC113 | 82.5 |
| OM032871.1 | Klebsiella phage vB\_KpnS-VAC110 | 85.8 |
| OX335439.1 | Klebsiella phage mtp17 | 79.3 |
| OX335421.1 | Klebsiella phage mtp23 | 80.3 |
| OX335411.1 | Klebsiella phage mtp30 | 81.5 |
| MZ634346.1 | Klebsiella phage PWKp15 | 83.8 |
| MG552615.1 | Klebsiella virus GML-KpCol1 | 85.4 |
| OL702938.1 | Klebsiella phage pK8 | 84.7 |
| MK278861.1 | Klebsiella phage KpKT21phi1 | 85.4 |
| LR757892.1 | Klebsiella phage vB\_KpnS\_2811 | 83.8 |
| MF415412.1 | Klebsiella phage KPN | 85.9 |
| MZ428222.1 | Klebsiella phage vB\_KpnS-VAC4 | 83.4 |
| MZ428225.1 | Klebsiella phage vB\_KpnS-VAC7 | 86.3 |
| OQ267592.1 | Klebsiella phage phi\_KPN\_HS3 | 83.2 |
| ON602741.1 | Klebsiella phage VLCpiD7a | 81.1 |
| MT894005.1 | Klebsiella phage MMBB | 80.3 |
| OX335417.1 | Klebsiella phage cp1 | 84.1 |
| MW655991.1 | Klebsiella phage RAD2 | 86.4 |
| OX335381.1 | Klebsiella phage cp5 | 86.9 |
| OX335383.1 | Klebsiella phage cp3 | 86.9 |
| OP267563.1 | Klebsiella phage GZ9 | 84.1 |
| OW251746.1 | Klebsiella phage PSKP16 | 83.4 |
| MW672037.1 | Klebsiella phage B1 | 85.2 |
| OM938992.1 | Klebsiella phage BMac | 85.9 |
| MZ571833.1 | Klebsiella phage vB\_KpnS-VAC112 | 83.4 |
| ON881905.1 | Klebsiella phage vB\_KpnS-VAC111 | 81.6 |
| MZ172460.1 | Klebsiella phage BUCT556A | 81.6 |
| OK655936.1 | Klebsiella phage phiW14 | 80.3 |
| OX335386.1 | Klebsiella phage mtp12 | 83.1 |
| MZ428226.1 | Klebsiella phage vB\_KpnS-VAC8 | 84.4 |
| MZ428227.1 | Klebsiella phage vB\_KpnS-VAC10 | 84.9 |
| MZ428223.1 | Klebsiella phage vB\_KpnS-VAC5 | 82.0 |
| OX335422.1 | Klebsiella phage mtp19 | 83.5 |
| OX335430.1 | Klebsiella phage mtp13 | 84.7 |
| OL539460.1 | Klebsiella phage vB\_KpnD\_FairDinkum | 83.7 |
| OL539448.1 | Klebsiella phage vB\_KpnD\_PeteCarol | 82.8 |
| OX335387.1 | Klebsiella phage mtp31 | 83.0 |
| MZ428228.1 | Klebsiella phage vB\_KpnS-VAC11 | 81.6 |
| OX335370.1 | Klebsiella phage mtp2 | 83.1 |
| MZ221764.1 | Klebsiella phage ABTNL-2 | 85.0 |
| MH633485.1 | Klebsiella phage NJS2 | 85.6 |
| OL674249.1 | Klebsiella phage KpS4 | 81.7 |
| ON602750.1 | Klebsiella phage VLCpiD7b | 85.0 |
| OM938991.1 | Klebsiella phage NPat | 84.4 |
| OQ031071.1 | Klebsiella phage KPP2020 | 85.1 |
| MN395286.1 | Klebsiella phage PhiKpNIH-2 | 80.7 |
| ON602735.1 | Klebsiella phage VLCpiD7c | 81.7 |
| OK138555.1 | Klebsiella phage vB\_Kp\_IME328 | 86.4 |
| MZ398242.1 | Klebsiella phage IME268 | 83.0 |
| OP413832.1 | Klebsiella phage pKP-BS317-1.1 | 83.0 |
| OL744210.1 | Klebsiella phage vB\_KvaS\_F1M1D | 83.1 |
| OL744213.1 | Klebsiella phage vB\_KvaS\_F2M1D | 85.3 |
| MZ428221.1 | Klebsiella phage vB\_KpnS-VAC2 | 67.9 |
| MT701592.1 | Klebsiella phage Solomon | 69.1 |
| MN013078.1 | Klebsiella phage vB\_KpnS\_KingDDD | 72.4 |
| MZ428224.1 | Klebsiella phage vB\_KpnS-VAC6 | 72.4 |
| MN013087.1 | Klebsiella phage vB\_KpnS\_Penguinator | 71.2 |
| MW021764.1 | Klebsiella phage P528 | 73.7 |
| OP611406.1 | Klebsiella phage mfs | 67.7 |
| OL539450.1 | Klebsiella phage vB\_KpnD\_Opt-817 | 69.2 |
| MW042802.1 | Klebsiella phage 066039 | 71.7 |
| MZ634348.1 | Klebsiella phage PWKp17 | 71.1 |
| MW722081.1 | Klebsiella phage vB\_KpnS\_ZX2 | 72.5 |
| MZ634351.1 | Klebsiella phage PWKp20 | 71.6 |
| OX335361.1 | Klebsiella phage cp24 | 73.9 |
| OL865411.1 | Klebsiella phage vB\_1086 | 71.9 |
| OM735690.1 | Stenotrophomonas phage vB\_SmeS\_BUCT705 | 74.0 |
| MW417503.1 | Klebsiella phage LF20 | 75.3 |
| OX335395.1 | Klebsiella phage cp17 | 74.3 |
| MZ598515.1 | Klebsiella phage P1 | 72.7 |
| MZ571831.1 | Klebsiella phage vB\_KpnS-VAC70 | 84.9 |
| OP617742.1 | Klebsiella phage KP13-2 | 80.4 |

**(\*) VIRIDIC analysis**

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