

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

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| **Code assigned:** | ***2023.073B*** |  |
| **Short title:** Create 28 new species in the genus *Vequintavirus* (*Caudoviricetes*) | | |
|  | | |

**Author(s) and email address(es)**

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| Andrew M. Kropinski |

**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**

|  |
| --- |
| 2023.073B.N.v1.Vequintavirus\_28ns.xlsx |

**Abstract**

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| We have added 28 new species of to the genus *Vequintavirus.* |

**Text of proposal**

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| |  | | --- | | **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, pattern

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. Yellow, existing species; green, new species. Abbreviations: phg = phage; vir = virus; Esch = Escherichia; Shig = Shigella; Ente = Enterobacteria. Due to the small size of this figure we have included the original Excel spreadsheet in this proposal: 2023.073B.N.v1.Vequintavirus\_28ns\_Suppl.xlsx

**Historical aspects:** The genus *Vequintavirus* was created through Taxonomy Proposal 2015.023a-oB.A.v2.Vequintavirinae. It currently consists of eight species we are now adding 28 new species.

**Genome summary: .**

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| --- | --- | --- |
| **Accession No.** | **Exemplar** | **Overall DNA sequence similarity (\*)** |
|  |  |  |
| DQ832317.1 | Escherichia coli bacteriophage rv5 | 100.0 |
| MT740314.1 | Escherichia phage JEP1 | 88.7 |
| OQ376695.1 | Escherichia phage YP-6 | 88.0 |
| MW883061.1 | Escherichia phage vB\_EcoM\_SYGMH1 | 88.9 |
| OX460980.1 | Vequintavirinae sp. EcoIv14a\_Aya | 89.2 |
| MK883718.1 | Escherichia phage vB\_EcoM-ECP32 | 89.4 |
| MK883717.1 | Escherichia phage vB\_EcoM-ECP26 | 89.1 |
| LC739541.1 | Escherichia phage phiWec193 | 92.1 |
| MH491969.1 | Escherichia phage LL12 | 91.9 |
| MN850649.1 | Escherichia phage nomine | 91.8 |
| LR699804.1 | Escherichia phage rV5\_ev146 | 89.6 |
| MT682716.1 | Escherichia phage vB\_EcoM\_Gotham | 92.1 |
| MZ501062.1 | Escherichia phage EmilHeitz | 91.8 |
| MN850627.1 | Escherichia phage pangalan | 92.1 |
| KP869112.1 | Escherichia phage TP-14\_[P] | 92.6 |
| MW748998.1 | Escherichia phage vB\_EcoM\_SophiaRose | 91.3 |
| LC739538.1 | Escherichia phage phiWec189 | 93.1 |
| MZ501048.1 | Escherichia phage AlexBoehm | 93.1 |
| MZ501060.1 | Escherichia phage DrSchubert | 93.2 |
| MN850646.1 | Escherichia phage nom | 91.7 |
| MK962749.1 | Shigella phage CM1 | 91.6 |
| ON286973.1 | Escherichia phage A51.2 | 92.0 |
| MZ501093.1 | Escherichia phage MaxBurger | 93.0 |
| LC739540.1 | Escherichia phage phiWec191 | 92.7 |
| MK373780.1 | Escherichia phage vB\_EcoM\_HdK5 | 93.6 |
| MZ501111.1 | Escherichia phage WalterGehring | 92.8 |
| MG963916.1 | Escherichia phage PDX | 93.6 |
| MN850642.1 | Escherichia phage navn | 91.8 |
| MZ501061.1 | Escherichia phage EduardKellenberger | 90.4 |

**(\*) determined using VIRIDIC [3]**

Emil Heitz (1892 – 1965)

Walter Jakob Gehring (1939 – 2014)

Eduard Kellenberger (1920 - 2004)

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