

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

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| **Code assigned:** | ***2023.020B*** |  |
| **Short title:** To create forty-two (42) species in the genus *Dhillonvirus* [*Caudoviricetes*] | | |
|  | | |

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

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

|  |
| --- |
| 2023.020B.N.v1.Dhillonvirus\_42ns.xlsx |

**Abstract**

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| --- |
| This proposal adds 42 new species to the genus *Dhillonvirus*. |

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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**

**Proposals Data:**

1. **Create forty-two (42) new species in the genus, *Dhillonvirus***

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

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, while those in red boxes are existing species. Abbreviations: phg = phage; Shig = Shigella. Because of the number of Dhillon-like phages we have attached the file 2023.020B.N.v1.Dhillonvirus\_42ns\_Suppl.xlsx to aid the reader.

**Taxonomic Proposals:**

1. **Create 42 new species in the genus, *Dhillonvirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** This taxon was established through Taxonomy Proposal 2013.029a-dB.A.v3.Hk578likevirus with seven species: *Dhillonvirus EK99P1, Dhillonvirus EP23, Dhillonvirus HK578, Dhillonvirus JL1, Dhillonvirus SO1, Dhillonvirus SSL2009a*, and *Dhillonvirus YD2008s.* Many more exemplars of these viruses have been deposited in GenBank. All of the viruses listed below conform to the criteria with which we define species [10].

**Genome summary:**

|  |  |  |
| --- | --- | --- |
| Phage name | INSDC | Overall % DNA sequence identity (\*) |
| Enterobacteria phage HK578 | JQ086375.1 | 100.0 |
| Escherichia phage PEC14 | OP046317.1 | 74.5 |
| Escherichia phage Gluttony | KX534336.1 | 78.2 |
| Escherichia phage JLBYU60 | OK272474.1 | 78.9 |
| Escherichia phage vB\_EcoD\_Teewinot | OK499993.1 | 79.1 |
| Escherichia phage Envy | KX534335.1 | 77.4 |
| Escherichia phage JLBYU37 | OK272488.1 | 77.7 |
| Escherichia phage vB\_EcoD\_Opt212 | OL770278.1 | 77.4 |
| Escherichia phage rolling | MN850575.1 | 76.0 |
| Escherichia phage KarlBarth | MZ501088.1 | 76.6 |
| Escherichia phage vB\_EcoS\_WFI | MK373791.1 | 78.1 |
| Escherichia phage vB\_EcoS-CHD5UKE2 | MZ234029.1 | 79.1 |
| Escherichia phage vB\_EcoS\_WF5505 | MK373790.1 | 76.9 |
| Escherichia phage vB\_EcoS-101114BS4 | MZ234016.1 | 77.8 |
| Escherichia phage TheodorHerzl | MZ501107.1 | 83.3 |
| Escherichia phage vB\_EcoS\_PNS1 | MK138527.1 | 80.5 |
| Escherichia phage vB\_EcoS\_PTXU06 | MK373789.1 | 80.8 |
| Escherichia phage vB\_EcoS\_Zar3M | OM262541.1 | 79.3 |
| Escherichia phage GeorgBuechner | MZ501070.1 | 79.3 |
| Escherichia phage PaulFeyerabend | MZ501097.1 | 79.2 |
| Escherichia phage vB\_EcoD\_Pubbukkers | OK499988.1 | 78.9 |
| Escherichia phage B2 | MG581355.1 | 81.5 |
| Escherichia phage CEC\_Kaz\_2018 | MK728541.1 | 78.7 |
| Escherichia phage SECphi18 | LT960609.1 | 79.3 |
| Escherichia phage bob | MN850628.1 | 79.2 |
| Escherichia phage mckay | MN850629.1 | 78.9 |
| Escherichia phage UAE\_MI-01 | MW862804.1 | 80.1 |
| Escherichia phage ZCEC10 | OK310514.1 | 79.8 |
| Escherichia phage jat | MN850650.1 | 80.0 |
| Escherichia phage vB\_Eco\_Maverick | LR990702.1 | 81.4 |
| Escherichia phage welsh | MN850589.1 | 78.5 |
| Escherichia phage vB\_EcoD\_Over9000 | OK499985.1 | 80.7 |
| Escherichia phage EC115 | ON210136.1 | 81.0 |
| Escherichia phage vB\_EcoS\_Sponge | MW749005.1 | 80.6 |
| Shigella phage vB\_SboD\_StarDew | OL615010.1 | 81.4 |
| Escherichia phage BF9 | MW822006.1 | 78.3 |
| Escherichia phage vb\_EcoS\_bov22\_1 | MT884014.1 | 80.0 |
| Escherichia phage vB\_EcoS\_011D5 | MT478993.1 | 81.6 |
| Escherichia phage vB\_EcoS\_L-h | OM262540.1 | 79.0 |
| Escherichia phage Gluttony\_ev152 | LR597646.1 | 79.9 |
| Escherichia phage PC2 | ON184124.1 | 80.9 |
| Escherichia phage Oekolampad | MZ501095.1 | 79.1 |
| Escherichia phage slur05 | LN881730.1 | 79.9 |

**(\*) VIRIDIC analysis**

Paul Karl Feyerabend (1924-1994)

Johannes Oecolampadius (1482-1531)

Karl Georg Büchner (1813-1837)

Theodor Herzl (1860-1904)

Karl Barth (1886-1968)

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