

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.107B** |  |
| **Short title:** Create one new genus (*Mydovirus*) including six new species in the subfamily *Vequintavirinae* (*Caudovirales*: *Myoviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Turner D, Kropinski AM | [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk);  [tolstoy@ncbi.nlm.nih.gov](mailto:tolstoy@ncbi.nlm.nih.gov);  [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk);  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com) |

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

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of the West of England, UK [DT]  University of Guelph, Canada [AMK] |

**Corresponding author**

|  |
| --- |
| Andrew Kropinski |

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

|  |
| --- |
| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**ICTV study group comments and response of proposer**

|  |
| --- |
|  |

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

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

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2020 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2020.107B.R.Mydovirus.xlsx |

**Abstract**

|  |
| --- |
| This proposal creates a genus for some currently unclassified myoviruses**.** |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **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:** This genus is derived from that of Proteus phage Mydo

**History:** These lytic phages were isolated against a variety of hosts including *Proteus mirabilis* (Mydo, USA), *Klebsiella pneumoniae* (vB\_KpnM\_BIS47, Poland), *K. pneumoniae* (vB\_KpnM\_KB57 and KpS8, Russian Federation) and *Raoultella ornithinolytica* (Ro1, Russian Federation). Phage KNP2 was isolated in India.

**Specific Reference:** Jones BT, Lessor L, O'Leary C, Gill J, Liu M. Complete Genome Sequence of

*Proteus mirabilis* Phage Mydo. Microbiol Resour Announc. 2019;8(47). pii: e01312-19. doi: 10.1128/MRA.01312-19. PubMed PMID: 31753956. [Mydo]

Parmar KM, Dafale NA, Tikariha H, Purohit HJ. Genomic characterization of key bacteriophages to formulate the potential biocontrol agent to combat enteric pathogenic bacteria. Arch Microbiol. 2018; 200(4):611-622. doi: 10.1007/s00203-017-1471-1. Epub 2018 Jan 12. PubMed PMID: 29330592. [KNP2]

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Mydo |  | [MK024806.1](https://www.ncbi.nlm.nih.gov/nuccore/MK024806.1) | 145.13 | 44.8 | [264](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/74253/429931|Proteus phage Mydo/viral segment/) | 23 | 100 | 100 |
| vB\_KpnM\_BIS47 |  | [KY652726.1](https://www.ncbi.nlm.nih.gov/nuccore/KY652726.1) | 147.44 | 44.6 | [262](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63104/465727|Klebsiella phage vB_KpnM_BIS47/viral segment/) | 23(\*) | 87.9 | 87.5 |
| vB\_KpnM\_KB57 | [NC\_028659.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028659.1) | [KT934943.1](https://www.ncbi.nlm.nih.gov/nuccore/KT934943.1) | 142.99 | 44.6 | [245](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42164/461875|Klebsiella phage vB_KpnM_KB57/viral segment Unknown/) | 16 | 84.3 | 84.5 |
| Ro1 |  | [MG250486.1](https://www.ncbi.nlm.nih.gov/nuccore/MG250486.1) | 145.76 | 44.5 | [245](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68296/369443|Raoultella phage Ro1/viral segment/) | 21 | 77.8 | 78.8 |
| KpS8 |  | [MT178275.1](https://www.ncbi.nlm.nih.gov/nuccore/MT178275.1) | 143.8 | 44.6 | [261](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89095/889210|Klebsiella virus KpS8/viral segment/) | 17 | 88.5 | 92.0 |
| KNP2 |  | [KX452695.1](https://www.ncbi.nlm.nih.gov/nuccore/KX452695.1) | 146.2 | 45.2 | (#) | 19(\*) | 75.2 | ND |

**\* None listed in Replicon Info; these found using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[5]**

**# - Genome not annotated**

****

**BLASTN homologs:** The next most closely related phage is *Escherichia* phage 4MG [KF550303] which shares 49.7% DNA sequence identity with Mydo [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the major capsid protein homologs of Mydo and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

****

**References**

1. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
2. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.
3. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.
4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6): doi: 10.1371/journal.pone.0039107. PMID: 22723939.
5. Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.
6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
7. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.
8. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.
9. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.