

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.080B** |  |
| **Short title:** Create one new genus (*Kanagawavirus*) including two new species (*Caudovirales*: *Myoviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Kropinski AM, Adriaenssens EM, Turner D | [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com);  [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk);  [Dann2.Turner@uwe.ac.uk](mailto:Dann2.Turner@uwe.ac.uk) |

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

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

**Corresponding author**

|  |
| --- |
| Andrew M. Kropinski |

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

|  |
| --- |
| Bacterial and Archaeal Viruses Subcommittee; Caudovirales Study Group |

**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**

|  |
| --- |
| 2020.080B.R.Kanagawavirus.xlsx |

**Abstract**

|  |
| --- |
| Edwardsiella phages PEi20 and PEi26 are members of the *Myoviridae* isolated in Japan. Because of the high degree of DNA sequence identity they are grouped as a single species in the genus *Kanagawavirus*. Recently another species infectious for *Enterobacter* was isolated. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | |  | |

**Supporting evidence**

**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.

**Source of the name of this taxon:** This genus is named after Kanagawa which is a coastal prefecture just south of Tokyo. It was here at the National Research Institute of Fisheries Science, Fisheries Research Agency, Research Center for Aquatic Genomics that phage PEi20 was isolated.

**History:** Phage PEi20 was isolated using *Edwardsiella ictalurid* as the host bacterium.

**Reference:** Wang K, Tamayo MG, Penner TV, Cook BWM, Court DA, Theriault SS. Characterization of the Enterobacter phage vB\_EclM\_CIP9. Microbiol Resour Announc. 2020;9(13):e01600-19. Published 2020 Mar 26. doi:10.1128/MRA.01600-19

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | DNA sequence identity(\*\*) | Common proteins (\*\*\*) |
| Edwardsiella phage PEi20 | [NC\_028683.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028683.1) | [AP014714.1](https://www.ncbi.nlm.nih.gov/nuccore/AP014714.1) | 177.64 | 40.6 | 301 | 6 | 100 | 100 |
| Enterobacter phage vB\_EclM\_CIP9 |  | [MN882610.1](https://www.ncbi.nlm.nih.gov/nuccore/MN882610.1) | 174.92 | 39.9 | [296](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87264/770781|Enterobacter phage vB_EclM_CIP9/viral segment/) | 9(\*) | 68.5 | 87.4 |

**N.B. Edwardsiella phage PEi6 (AP014715) should be considered a strain of *Edwardsiella virus PEi20***

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

**(\*\*) Determined using BLASTN at NCBI [1-3]**

**(\*\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**BLASTN homologs:** The next most closely related sequence is that of Serratia phage CBH8 which shares 45.8% DNA sequence identity with Pei20 [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Pei20 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."

A screenshot of a cell phone

Description automatically generated

**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.