

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

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| **Code assigned:** | **2020.053B** |  |
| **Short title:** Create one new subfamily (*Emmerichvirinae*) including two new genera (*Ishigurovirus* and *Ceceduovirus*) (*Caudovirales*: *Myoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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

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

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

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Ishigurovirus* | Edward E. Ishiguro | Y |
|  |  |  |
|  |  |  |

**Submission dates**

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

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

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

**Name of accompanying Excel module**

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| 2020.053B.R.Emmerichvirinae.xlsx |

**Abstract**

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| According to the 2018 Master Species List Aeromonas virus 65 is an orphan species in the genus *Myoviridae*/subfamily *Tevenvirinae*. This proposal corrects this problem by assigning it to a genus in a new subfamily. |

**Text of proposal**

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**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 these taxa:** The subfamily is named in honour of R. Emmerich, who with C. Weibel (Arch. Hyg., 21 (1894), pp. 1-21) first described the fish furunculosis organism from a disease outbreak at a Bavarian brown trout hatchery and named it *Bacterium salmonicida*. The genus *Ishigurovirus* is named in honour of Canadian scientist Dr. Edward E. Ishiguro (former professor of Biochemistry and Microbiology, University of Victoria, BC) who also earlier in his career worked on *Aeromonas* phages. The name *Ceceduovirus* is derived directly from the name of the type phage CC2.

**History:** *Aeromonas salmonicida* virus 65 is an ICTV-recognized taxon (Fauquet et al. 2005). It is currently listed as a species in the family *Myoviridae*, subfamily *Tevenvirinae.* While the T4-related phages (Petrov et al. 2010) have been recently subject to ICTV reclassification (see 2015.020a-aeB) far more needs to be done, so in this proposal we will suggest the creation of a Tevenvirinae parallel subfamily in the Myoviridae. Phage 65 was isolated from “La Petite Mouge” River, France (Popoff et al, 1971; Ackermann et al. 1985), while Aeromonas hydrophila phage CC2 was isolated from sewage in China (Shen et al. 2012). Phages 65 and CC2 show sufficient DNA sequence identify to be considered members of two genera, in a subfamily. Phage CC2 was isolated at the Nanjing Agricultural University (Nanjing, Jiangsu, China).

**Reference:** Fauquet, C., Mayo, M.A., Maniloff, J., Desselberger, U. and Ball, L.A., Eds. (2005). Virus

taxonomy: Eighth Report of the International Committee on Taxonomy of Viruses. Elsevier

Academic Press.

Petrov VM, Ratnayaka S, Nolan JM, Miller ES, Karam JD. Genomes of the T4-related bacteriophages as windows on microbial genome evolution. Virol J. 2010 Oct 28;7:292.

H.-W. Ackermann, C. Dauguet, W.D. Paterson, M. Popoff, M.A. Rouf, J.-F. Vieu (1985). *Aeromonas* bacteriophages: Reexamination and classification. Ann. Inst. Pasteur, 136(2): 175–199.

Popoff, M. (1971). Etude sur les *Aeromonas salmonicida*. II. Caracterisation des bacteriophages actifs sur les “Aeromonas salmonicida” et lysotypie. Ann. Rech. Vet. 2, 33–45.

Shen CJ, Liu YJ, Lu CP. Complete Genome Sequence of *Aeromonas hydrophila* Phage CC2. J Virol. 2012 Oct;86(19):10900.

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| 65 | [NC\_015251.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_015251.1) | [GU459069.1](https://www.ncbi.nlm.nih.gov/nuccore/GU459069.1) | 235.23 | 37.2 | 437 | 16 | 100 | 100 |
| CC2 | [NC\_019538.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019538.1) | [JX123262.1](https://www.ncbi.nlm.nih.gov/nuccore/JX123262.1) | 231.74 | 38.8 | 427 | 10(\*) | 46.7 | 74.4 |
|  |  |  |  |  |  |  |  |  |
| CC2 | [NC\_019538.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019538.1) | [JX123262.1](https://www.ncbi.nlm.nih.gov/nuccore/JX123262.1) | 231.74 | 38.8 | 427 | 10(\*) | 100 | 100 |
| AS-zj |  | [MF448340.1](https://www.ncbi.nlm.nih.gov/nuccore/MF448340.1) | 229.93 | 38.7 | 402 | 9(\*) | 90.0 | 91.3 |
| AS-sw **(p)** |  | [MF498775.1](https://www.ncbi.nlm.nih.gov/nuccore/MF498775.1) | 230.02 | 38.8 | 406 | 9(\*) | 88.6 | 87.8 |
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**(\*) None indicated in the NCBI Replicon Info data; found using tRNAscan-SE 2.0 at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[5]**

**(p) Denotes that the replicon is described as partial in the associated INSDC record.**

**\*\* 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]**

**N.B. Aeromonas phage 65.2 should be considered a strain of 65; Aeromonas phage AS-yj is a strain of Aeromonas phages AS-zj and AS-szw.**

**BLASTN homologs:** The next closely related phage to CC2 is *Aeromonas* phage phiAS5, while to phage 65 it is Aeromonas phage Ah1 [1-3]. They share <10% overall DNA sequence identity.

**SymBets analysis:** The following tree was constructed by SymBets analysis:

1) ORF finder (https://www.ncbi.nlm.nih.gov/orffinder)is run with each phage genome using the default settings, with short ORFs located inside long ORFs were discarded

2) If the genome had been annotated the coding regions which ORF finder missed were used to calculate the total length of ORFs for each phage – L1 , L2

3) For each pair of phages BLASTp searches were made, using the default parameters, to identify all the “symmetrical best hit” (SymBets) pairs of ORFs using score column in BLAST results (N.B. no hits merge) [10]

4) Calculate total length of SymBet ORFs on each assembly: SB1 , SB2

5) Symmetrical Distance between assemblies = 1.0 - (SB1 + SB2)/(L1 + L2)

6) Create tree using FastMe 2.0 [11]

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**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of 65, CC2 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."

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Description automatically generated]()**

**References**

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