

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

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| **Code assigned:** | ***2022.094B*** |  |
| **Short title:** Create a new genus (*Yanchengvirus)* with a single species (*Caudoviricetes*) |
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**Author(s) and email address(es)**

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

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**Corresponding author**

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| Andrew M. Kropinski |

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

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| Bacterial Viruses Subcommittee, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
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|  |  |  |  |

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

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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

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| Date first submitted to SC Chair | May 2022 |
| 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**

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| 2022.094B.N.v1.Yanchengvirus\_ng.xlsx |

**Abstract**

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| The genus Yanchengvirus was created for the genotypically unique phage Aeromonas phage pAEv1818 |

**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] – usually calculated using intergenomic distance calculator VIRIDIC [2].**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. [8] |

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**Supporting evidence**

**Origin of the name of this taxon:** This taxon is named after the address (Yancheng City Hope Avenue Road 1, Yancheng, Jiangsu 224051, China) where at the School of Marine and Biological Engineering, Yancheng Institute of Technology, the first phage of its type was isolated

**Historical aspects:** This temperate phage was isolated against an Aeromonas sp. from fresh water.

**Electron micrograph:** N/A

**Genome summary:** genomic orphan

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| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Aeromonas phage pAEv1818 | [OL964755.1](https://www.ncbi.nlm.nih.gov/nuccore/OL964755.1) | 40.81 | 55.2 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/109774/1766581|Aeromonas phage pAEv1818/viral segment/) | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. N/A

**Phylogeny:** The phylogenetic tree was constructed using the MCPs from pAEv1818 and related phages with phylogeny.fr in “one click” mode [6]. 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 [7] for details. The members of the *Yanchengvirus* are indicated with a **blue rectangle**.

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**References**

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