

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

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| **Code assigned:** | **2022.044B** |  |
| **Short title:** Create a new genus (*Ludhianavirus*) with three species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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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** |
|  |  |  |  |
|  |  |  |  |

**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 | April 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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| 2022.044B.N.v1.Ludhianavirus\_ng.xlsx |

**Abstract**

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| We have created a new genus, *Ludhianavirus*, for a group of phages, the exemplars of which infect *Aeromonas hydrophila* and possess jumbo genomes. |

**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] | |

**Supporting evidence**

**Origin of the name of this taxon:** This taxon is named the city Ludhiana, north Indian state of Punjab where several phages of this type were isolated.

**Historical aspects:** Three of these lytic myophages were isolated in India, and one in Australia. They are all active against Aeromonas hydrophila. Only phage LAh10 has been described in a publication [11]. It has a capsid diameter of ≈ 116 nm and tail length ≈ 183 nm

**Electron micrograph:** N/A

**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Aeromonas phage LAh10 | [MK838116.1](https://www.ncbi.nlm.nih.gov/nuccore/MK838116.1) | 260.31 | 47.5 | [228](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82454/604117|Aeromonas phage LAh10/viral segment/) | 4(\*\*\*) | 100 | 100 |
| Aeromonas phage D3 | [MN102098.2](https://www.ncbi.nlm.nih.gov/nuccore/MN102098.2) | 262.37 | 47.5 | [267](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82651/927105|Aeromonas phage D3/viral segment/) | 3 | 91.1 | 97.4 |
| Aeromonas phage D6 | [MN131137.2](https://www.ncbi.nlm.nih.gov/nuccore/MN131137.2) | 259.83 | 47.6 | [267](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82652/976527|Aeromonas phage D6/viral segment/) | 3 | 94.7 | 98.7 |

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

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

**(\*\*\*) None listed in NCBI Replicon Info. These were discovered using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[12]**

**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. The black box delineates strains.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars** and a **blue rectangle**.



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**Phylogeny:** The phylogenetic tree was constructed using the MCPs from D6 and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of the *Ludhianavirus* are indicated with a **blue rectangle**.



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