

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

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| **Code assigned:** | **2020.087B** |  |
| **Short title:** Create one new genus (*Lahexavirus*) including four new species (*Caudovirales*: *Podoviridae*) | | |
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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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| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**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)** |
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**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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| 2020.087B.R.Lahexavirus.xlsx |

**Abstract**

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**Text of proposal**

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| |  | | --- | | **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 name is derived from that of the first isolate Aeromonas phage LAh\_6.

**History:** Three of these lytic phages were isolated from fishpond and wastewater in Victoria, Australia, against biofilm-forming *Aeromonas hydrophila* cells. Phage 4\_4572 was isolated from Plateau Lake in Southwest China.

**Specific Reference: None**

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| LAh\_6(#) |  | [MK838112.1](about:blank) | 101.39 | 42.3 | [164](about:blank#!/proteins/82450/604113|Aeromonas phage LAh_6/viral segment/) | 21(\*) | 100 | 100 |
| 4\_4572 |  | [MK813943.1](about:blank) | 102.92 | 42.5 | [154](about:blank#!/proteins/83774/672165|Aeromonas phage 4_4572/viral segment/) | 20 | 92.5 | 87.2 |
| LAh\_8 |  | [MK838114.1](about:blank) | 97.41 | 42.2 | [143](about:blank#!/proteins/82452/604115|Aeromonas phage LAh_8/viral segment/) | 21(\*) | 92.5 | 81.7 |
| LAh\_9 |  | [MK838115.1](about:blank) | 97.99 | 42.4 | [147](about:blank#!/proteins/82453/604116|Aeromonas phage LAh9/viral segment/) | 19(\*) | 90.1 | 81.7 |

**\* None indicated in Replicon Info. These discovered using tRNAscan-Se at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](about:blank) **[5]**

**# This genome contains 6 ambiguous bases**

**BLASTN homologs:** Genomic orphans [1-3].

**Electron micrograph:**

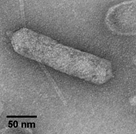


Figure 1: Electron Micrograph of LAh\_6

Capsid (L): 172±10nm

Capsid (W):35±2nm

Tail:18±1nm

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of LAh\_6 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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**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.
10. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. [http://kronos.icbm.uni-oldenburg.de/viridic/](about:blank)