

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

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| --- | --- | --- |
| **Code assigned:** | ***2022.037B*** |  |
| **Short title:** Create a new genus (*Hzauvirus*)in the family *Guelinviridae* including a new species (*Caudoviricetes*) | | |
|  | | |

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

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

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| Huazhong Agricultural University [LJQ] |

**Corresponding author**

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

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| Bacterial & Archaeal Virus Subcommittee |

**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 |

|  |  |  |
| --- | --- | --- |
| **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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| --- |
| 2022.037B.N.v1.Hzauvirus\_ng.xlsx |

**Abstract**

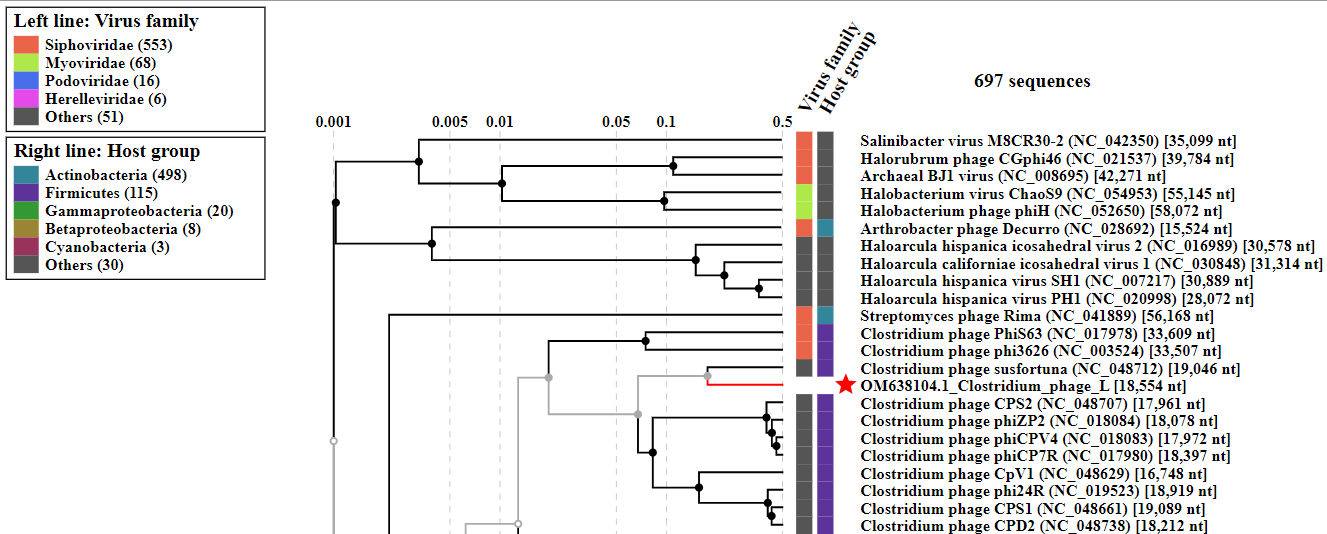
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| A new *Clostridium* phage LPCPA6 was isolated, and ViPTree analysis grouped this phage with members of the family *Guelinviridae*. According to the VIRIDIC and ViPTree analysis results, LPCPA6 differ significantly enough (less than 70% identity with phages of other *Clostridium* species) to classify it as a separate genus.  Therefore, we propose to classify LPCPA6 as a newgenus *Hzauvirus*, including one species Clostridiumphage LPCPA6. The genome of LPCPA6 is available from the NCBI GenBank database under the accession number: OM638104.1. |

**Text of proposal**

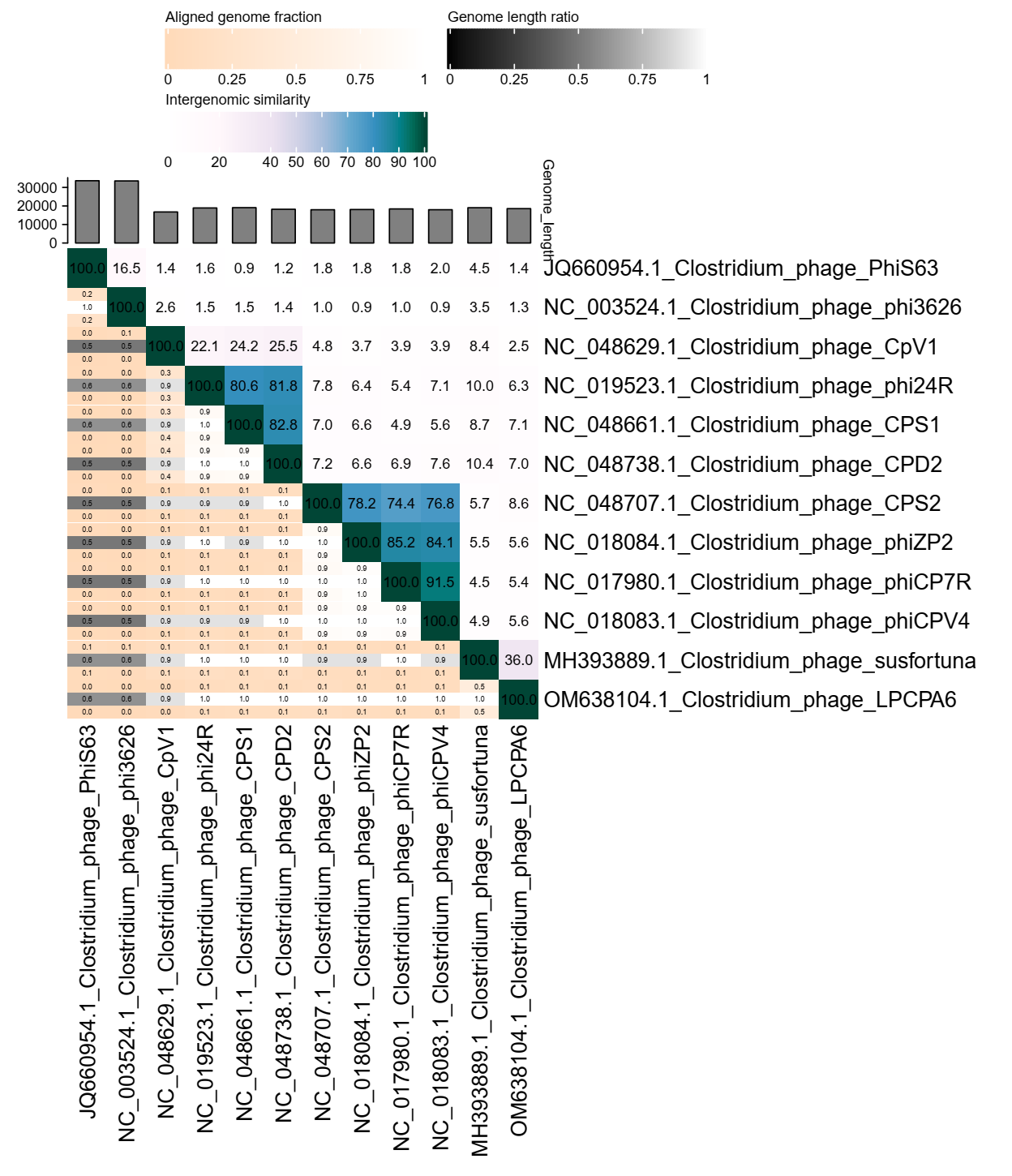
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| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic distance calculator VIRIDIC [1].  **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.[2] | |

**Supporting evidence**

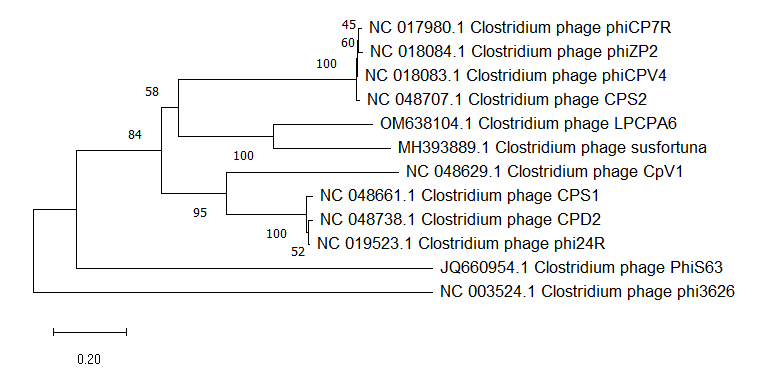
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red arrow and box.**



**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator [1]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.



**Phylogeny:**The phylogenetic tree was constructed using the major head proteins of phages [5]. MUSCLE was used for multiple alignment and MEGA(v11.0.10) was used for building phylogenetic tree using maximum-likelihood method with 500 bootstrap [6]. The new genus is indicated with red box and new species is indicated with red arrow.



**Origin of the name of this taxon:** This genus is named based on Huazhong Agricultural University, a university located in China*.*

**Historical aspects:** Clostridium phage LPCPA6 was isolated from the dog faeces by Huazhong Agricultural University in 2020, using Clostridiumas the host bacterium.

**Specific References:** None

**Genome summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| *Clostridium* phage LPCPA6 |  | OM638104.1 | 18.554 | 30.56% | [26](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84820/708377%7CMycobacterium%20phage%20Anthony/viral%20segment/) | 0 | 100 | 100 |

**(\*) Determined using VIRIDIC [2]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[8]**

**References**

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3. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017 Aug 1;33(15):2379-2380. doi: 10.1093/bioinformatics/btx157. PMID: 28379287.
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5. 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.
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