

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

<https://ictv.global/taxonomy/templates>**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new genus *Jinquanvirus* including two new species (Class *Caudoviricetes*). |
| **Code assigned:** | 2025.028B.Jinquanvirus\_1ng\_2ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Jinquan | Li | Huazhong Agricultural University, Wuhan, China | [lijinquan2017@163.com](mailto:lijinquan2017@163.com) | X |
| Yang | ZHOU | Huazhong Agricultural University, Wuhan, China |  |  |
| Zhiyong | SONG | Huazhong Agricultural University, Wuhan, China |  |  |
| Yongxin | LUO | Huazhong Agricultural University, Wuhan, China |  |  |
| Jiayi | OU | Huazhong Agricultural University, Wuhan, China |  |  |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | X |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** <https://ictv.global/sc> |
| Caudoviricetes Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** | 23/05/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:** |
| *Brief description of current situation:*  *Proposed changes:*  *Justification:* |

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| **Text of General Proposal:** |
| *Background:*  *Proposed* *changes:*  *Justification:* |

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| **References:** |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |

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

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | X | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| **Jinquanvirus** | The name of this genus comes from a river in China. |
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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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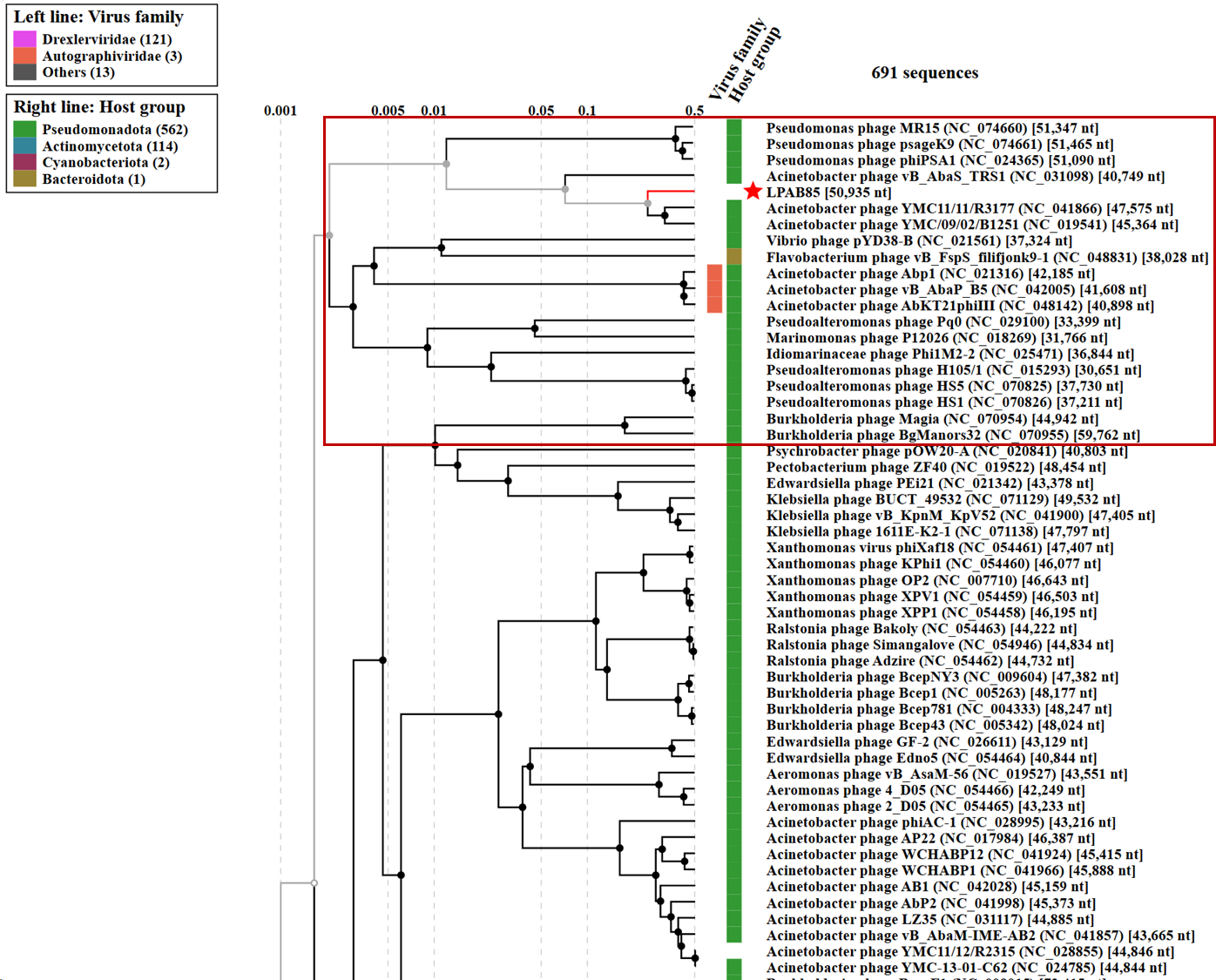
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  *Acinetobacter* phage LPAB85 is currently unclassified  *Proposed* *taxonomic change(s):*  A new genus “*Jinquanvirus*” containing a single species “*Jinquanvirus* LPAB85” is proposed.  *Justification*:  We isolated a new bacteriophageLPAB85infecting *Acinetobacter baumannii*. Based on analysis with VIRIDIC and ViPTree, LPAB85 was significantly different from other genera (less than 70% identity with phages of other genera)*.* Thus, we propose the creation of a new genus, *Jinquanvirus,* containing a single species, *Jinquanvirus LPAB85.* |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  *Acinetobacter* phage LPAB85 is currently unclassified  *Proposed* *taxonomic change(s)*:  A new genus “*Jinquanvirus*” containing a single species “*Jinquanvirus* LPAB85” is proposed.  *Demarcation criteria:*  **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:** 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]  *Justification*:  A tblastx distance tree of *Acinetobacter baumannii* phage LPAB85 was constructed using VIPTree [3-4].The results showed that LPAB85 belonged to one clade with 17 other phages, and we then added two additional phages from other branches, and a total of 20 phages were selected for VIRIDIC analysis *(*Fig. 1). VIRIDIC analysis computed the pairwise genomic distances and similarities between the phage genomes, revealing significant divergence between *LPAB85* from the phages of other genera, with nucleotide similarity levels below 70% (Fig. 2*)*. In conclusion, we propose a new genus, *Jinquanvirus*, containing a new species, *Jinquanvirus LPAB85*, which includes the isolates: *Acinetobacter baumannii* phage LPAB85. |

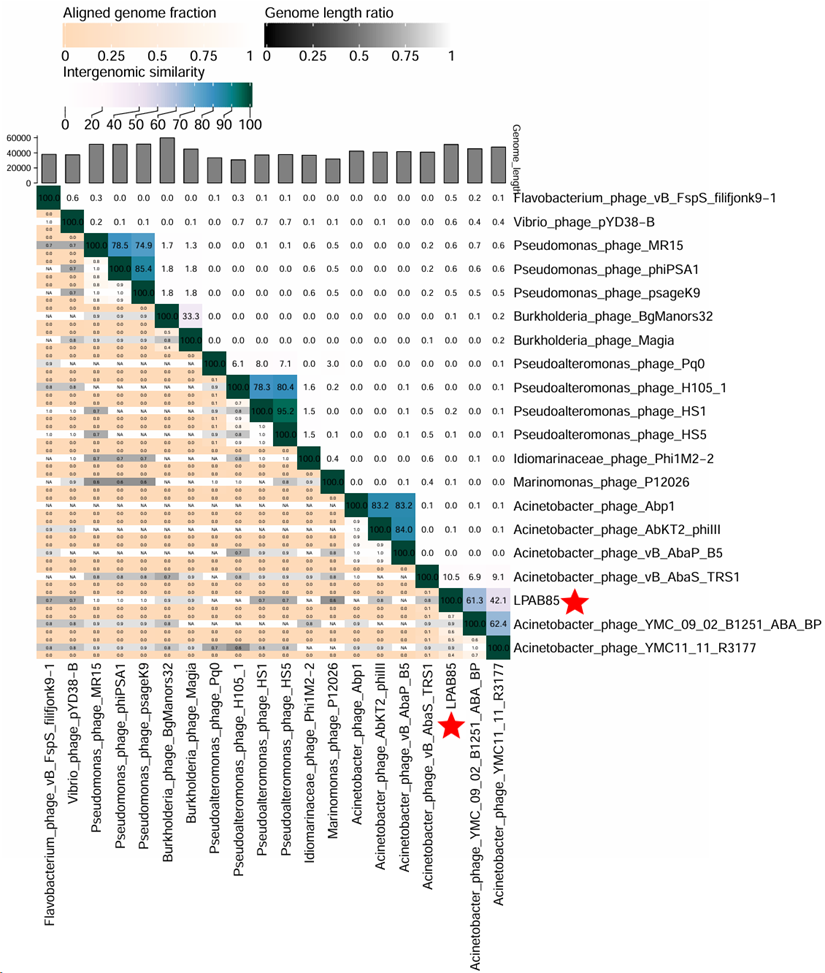
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| **References:** |
| 1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12(11):1268. PMID: 33172115 / PMCID: PMC7694805 doi: 10.3390/v12111268.  2. Turner D, Kropinski AM, Adriaenssens EM (2021) A Roadmap for Genome-Based Phage Taxonomy. Viruses 13(3):506. PMID: 33803862 / PMCID: PMC8003253 doi: 10.3390/v13030506.  3. Nishimura Y, Yoshida T, Kuronishi M et al (2017) ViPTree: the viral proteomic tree server. Bioinformatics 33(15):2379-2380. PMID: 28379287. doi: 10.1093/bioinformatics/btx157.  4. Rohwer F, Edwards R (2002) The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol 184(16):4529-35. PMID: 12142423 / PMCID: PMC135240. doi: 10.1128/jb.184.16.4529-4535.2002. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |



**Figure 1. ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree. The phages of interest are indicated with **red box**.

**Figure 2. VIRIDIC heatmap:** VIRIDIC (Virus Intergenomic Distance Calculator; <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>) computes pairwise intergenomic distances/similarities amongst phage genomes.

**Origin of the name of this taxon:** The name of this genus comes from a river in China.

**Historical aspects:** Phage samples are sourced from Waste Water in Hubei Province.

**Specific References:** None

**Genome summary:**

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| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| *Acinetobacter baumannii* phage LPAB85 | PV679990 | 50.935 | 39.18 | 74 | 0 |