

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

|  |  |
| --- | --- |
| **Title:** | Create a new genus, *Ranyuvirus*,and one new species (Class *Caudoviricetes*)*.* |
| **Code assigned:** | 2025.064B.Ranyuvirus\_1ng\_1ns | |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **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 | zhouyang@mail.hzau.edu.cn |  |
| Ranfeng | Ye | Huazhong Agricultural University, Wuhan, China | ranfeng.ye@mail.hzau.edu.cn |  |
| Miao | Lei | Huazhong Agricultural University, Wuhan, China | leimiao@webmail.hzau.edu.cn |  |

**Part 1b: Taxonomy Proposal Submission**

|  |  |  |  |
| --- | --- | --- | --- |
| **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 - |  |

|  |
| --- |
| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| Bacterial Viruses |

|  |  |  |  |
| --- | --- | --- | --- |
| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** | 06/06/2025 |

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

|  |  |
| --- | --- |
| **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| W - Withdrawn |  |

|  |
| --- |
| **Comments from the Executive Committee:** |
|  |

**Part 1d: Revised Taxonomy Proposal Submission**

|  |
| --- |
| **Response of proposer:** |
|  |

|  |  |
| --- | --- |
| **Revision date:** |  |

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

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

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

|  |
| --- |
| **References:** |
|  |

|  |  |
| --- | --- |
| **Accompanying files:** | |
| **Filename** | **Description of contents** |
|  |  |
|  |  |

|  |
| --- |
| **Tables, Figures:** |

<Start here>

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

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

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

|  |  |
| --- | --- |
| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
|  |  |
|  |  |
|  |  |
|  |  |

|  |  |  |
| --- | --- | --- |
| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

|  |
| --- |
| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  *Caudoviricetes* (Class)  *Proposed* *taxonomic change(s):*  Create one new genus “*Ranyuvirus”* including a new species (“*Ranyuvirus LPKP33”*)  *Justification*:  We isolated a new *Klebsiella* phage *LPKP33*. Based on the analysis of VIRIDIC and ViPTree, *LPKP33* was significantly different from other genera (less than 70% identity with phages of other genera)*.* Thus, this proposal will create a new genus *Ranyuvirus,* containing a new species *Ranyuvirus LPKP33.* |

|  |
| --- |
| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  To create a new genus containing a new species  *Description of current taxonomy*:  To create a new genus containing a new species in the *Caudoviricetes* class.  *Proposed* *taxonomic change(s)*:  We propose a new genus, *Ranyuvirus*, containing a new species, *Ranyuvirus LPKP33.*  *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:** 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]  *Justification*:  A tblastx distance tree of *Klebsiella* phage *LPKP33* was constructed using VIPTree [3-4].LPKP33, along with 9 other phages formed a single clade and were subsequently selected for VIRIDIC analysis. VIRIDIC analysis computed the pairwise genomic distances and similarities between the phage genomes, revealing that *LPKP33* exhibited <70% nucleotide similarity from the phages of other genera. In conclusion, we propose a new genus, “*Ranyuvirus”*, containing a new species, “*Ranyuvirus LPKP33”.* |

|  |
| --- |
| **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. |

|  |  |
| --- | --- |
| **Accompanying files:** | |
| **Filename** | **Description of contents** |
|  |  |
|  |  |

|  |
| --- |
| **Tables, Figures:** |
|  |

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

**A screenshot of a computer

AI-generated content may be incorrect.**

**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.

**A screenshot of a computer

AI-generated content may be incorrect.**

**Origin of the name of this taxon:** None

**Historical aspects:** *Klebsiella* phage LPKP33 was isolated in 2022 by Huazhong Agricultural University.

**Specific References:** None

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| *Klebsiella* phage LPKP33 | 2925135 | 47.6 | 48.8 | 80 | 0 |