

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
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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:**  |
| Bacterial Viruses |

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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:** |  06/06/2025 |

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| W - Withdrawn |  |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

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| * **Text of Taxonomy proposal:**
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| *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”.* |

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

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

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**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:**

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