

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create three new species in the genus *Kagunavirus* (Class *Caudoviricetes*, Family *Sarkviridae*)  |
| **Code assigned:**  | 2025.030B.Kagunavirus\_3ns |

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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:**  |
| *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:** |  12/04/2025 |

**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| W - Withdrawn |  |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** |
| *Kagunavirus ligaya* | ligaya – means joy or happy in Filipino language |
| *Kagunavirus malou* | malou – in honor of Marel Jan Joloro’s mom, Marilou |
| *Kagunavirus ohbeberoi* | ohbeberoi – from the Filipino slang term *bebe* |
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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**  |
| *Kagunavirus malou* | Marilou Joloro | deceased |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: Realms *Duplodnaviria*, Kingdom *Heunggongvirae*, Phylum *Uroviricota*, Class *Caudoviricetes*, Family *Sarkviridae*, Subfamily *Guernseyvirinae*, Genus *Kagunavirus**Description of current taxonomy*: The genus *Kagunavirus* currently includes 12 species.*Proposed* *taxonomic change(s):* Create three new species in the genus *Kagunavirus*; “*Kagunavirus ligaya”*, *“Kagunavirus malou”* and *“Kagunavirus ohbeberoi”**Justification*:Based on VIRIDIC analysis, we propose the creation of three new phage species, *Kagunavirus ligaya,* named after a Filipino term “Ligaya” which explicitly means “joy” or “happiness. “*Kagunavirus malou”* is derived from a nickname of one of co-authors mom, Marilou. *Kagunavirus ohbeberoi*, from the Filipino slang term “bebe”thatrefers to people we are close with (i.e., friends and special someone) |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Realms *Duplodnaviria*, Kingdom *Heunggongvirae*, Phylum *Uroviricota*, Class *Caudoviricetes*, Family *Sarkviridae*, Subfamily *Guernseyvirinae*, Genus *Kagunavirus**Description of current taxonomy*: The genus *Kagunavirus* currently includes 12 species.*Proposed* *taxonomic change(s):* Create three new species in the genus *Kagunavirus*; “*Kagunavirus ligaya”*, *“Kagunavirus malou”* and *“Kagunavirus ohbeberoi”**Demarcation criteria:*Species demarcation criteria: A demarcation value of 95% intergenomic similarity was used to define different species according to intergenomic similarity. Members of the same species have >95% intergenomic similarity. *Justification*: The three new species were isolated from three different sources. The *Escherichia* phagevB\_VIPECOTH07 was isolated from a Tertiary Hospital in the Philippines, the *Escherichia* phagevB\_VIPECOMC05A from Tarlac Provincial Hospital, and the *Escherichia* phagevB\_VIPECOMC04 from Masalasa Creek, Tarlac, Philippines. Our taxonomic analyses revealedthat *Escherichia* phage vB\_VIPECOTH07, *Escherichia* phage vB\_VIPECOMC05A, and *Escherichia* phagevB\_VIPECOMC04 remain unclassified at the species level. Here, we proposed the creation of 3 new species,*Kagunavirus ligaya, Kagunavirus malou, and Kagunavirus ohbeberoi respectively, under* Realms*Duplodnaviria*, Kingdom *Heunggongvirae*, Phylum *Uroviricota*, Class *Caudoviricetes*, Family*Sarkviridae*, Subfamily *Guernseyvirinae*, Genus *Kagunavirus*Analysis of species included in the genus *Kagunavirus* and bacteriophages VIPECO04, VIPECOTPH05a and VIPECOTH07 indicates that these should be classified as new species within the genus (Figure 1). |

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| **References:**  |
| 1. Nayfach, S., Camargo, A. P., Schulz, F., Eloe-Fadrosh, E., Roux, S., & Kyrpides, N. C. (2021). CheckV assesses the quality and completeness of metagenome-assembled viral genomes. *Nature biotechnology*, *39*(5), 578-585.
2. Turner, D., Kropinski, A. M., & Adriaenssens, E. M. (2021). A roadmap for genome-based phage taxonomy. *Viruses*, *13*(3), 506.
3. Millard, A. D., Denise, R., Lestido, M., Thomas, M., Webster, D., Turner, D., & Sicheritz-Ponten, T. (2024). taxmyPHAGE: Automated taxonomy of dsDNA phage genomes at the genus and species. *bioRxiv*, 2024-08.
4. Nishimura, Y., Yoshida, T., Kuronishi, M., Uehara, H., Ogata, H., & Goto, S. (2017). ViPTree: the viral proteomic tree server. *Bioinformatics*, *33*(15), 2379-2380.
5. Moraru, C. (2023). VirClust—A tool for hierarchical clustering, core protein detection and annotation of (prokaryotic) viruses. *Viruses*, *15*(4), 1007.
6. Ondov, B. D., Treangen, T. J., Melsted, P., Mallonee, A. B., Bergman, N. H., Koren, S., & Phillippy, A. M. (2016). Mash: fast genome and metagenome distance estimation using MinHash. *Genome biology*, *17*, 1-14.
7. Cook, R., Brown, N., Redgwell, T., Rihtman, B., Barnes, M., Clokie, M., ... & Millard, A. (2021). INfrastructure for a PHAge REference database: identification of large-scale biases in the current collection of cultured phage genomes. *Phage*, *2*(4), 214-223.
8. Moraru, C., Varsani, A., & Kropinski, A. M. (2020). VIRIDIC—A novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. *Viruses*, *12*(11), 1268.
9. Tamura, K., Stecher, G., & Kumar, S. (2021). MEGA11: molecular evolutionary genetics analysis version 11. *Molecular biology and evolution*, *38*(7), 3022-3027.
10. Edgar, R. C. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic acids research*, *32*(5), 1792-1797.

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| Kagunavirus\_3ns\_v3.xlsx | An excel file containing the taxonomic classification of proposed 3 new *Kagunavirus* species |
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| **Tables, Figures:**  |

<Start here>Figure 1. Heatmap of inter-genomic similarities between members of the genus *Kagunavirus* and bacteriophages VIPECO04, VIPECOTPH05a and VIPECOTH07.