

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)** |
| Aubrey Joy P. | Tejada | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | [ajptejada@gmail.com](mailto:ajptejada@gmail.com) | X |
| Michael Angelou L. | Nada | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | [mikeangelounada@gmail.com](mailto:mikeangelounada@gmail.com) |  |
| Ruth Antoinette D. | Chin | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | chinruthantoinette@gmail.com |  |
| Janna Ysabelle O. | Casidsid | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | jycasidsid@gmail.com |  |
| Joseph B. | Ancla | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | anclajoseph8492 |  |
| Marel Jan G. | Joloro | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | mgjoloro.dostvip@gmail.com |  |
| Mark Christian C. | Reterta | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | mcreterta@gmail.com |  |
| Anton Roi G. | Collado | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | colladoantonr@gmail.com |  |
| Sharmen C. | Berlin | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | scberlin@up.edu.ph |  |
| Arra B. | Asejo | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | nmry.dostvip@gmail.com |  |
| Nikka Marie R. | Yadao | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | abasejo.dost@gmail.com |  |
| Virgilio Jr. P. | De Paz | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | [virgdepazimperial@gmail.com](mailto:virgdepazimperial@gmail.com) |  |
| Ursela G. | Bigol | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | [ugbigol@itdi.dost.gov.ph](mailto:ugbigol@itdi.dost.gov.ph) |  |
| Rommel J. | Gestuveo | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | rjgestuveo@gmail.com |  |

**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* phage  vB\_VIPECOTH07 was isolated from a Tertiary Hospital in the Philippines, the *Escherichia* phage  vB\_VIPECOMC05A from Tarlac Provincial Hospital, and the *Escherichia* phage  vB\_VIPECOMC04 from Masalasa Creek, Tarlac, Philippines. Our taxonomic analyses revealed  that *Escherichia* phage vB\_VIPECOTH07, *Escherichia* phage vB\_VIPECOMC05A, and *Escherichia* phage  vB\_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>A screenshot of a graph

AI-generated content may be incorrect.Figure 1. Heatmap of inter-genomic similarities between members of the genus *Kagunavirus* and bacteriophages VIPECO04, VIPECOTPH05a and VIPECOTH07.