

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:**  | Create three new species in the genus *Kagunavirus* (Class *Caudoviricetes*, Family *Sarkviridae*)  |
| **Code assigned:**  | 2025.030B.Ac.v3.Kagunavirus\_3ns |

|  |
| --- |
| **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 | X |
| Michael Angelou L. | Nada | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | 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 |  |
| Ursela G. | Bigol | Industrial Technology Development Institute, Department of Science and Technology (DOST – ITDI), DOST Compound, Taguig, 1631, Philippines | 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**

|  |
| --- |
| **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:** <https://ictv.global/sc> |
| *Caudoviricetes* Study Group |

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

**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 | **X** |
| 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:** |
| Genus in-filling (3 species) |

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

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

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

<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** |
| *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* |
|  |  |

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

|  |
| --- |
| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: Species*Description of current taxonomy*: The genus *Kagunavirus* currently includes 12 species. The genus was originally established in 2015 and was included within the family *Sarkviridae* in 2024.*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 in the genus *Kagunavirus*. *Kagunavirus ligaya* is named after the Filipino term “Ligaya” which explicitly means joy or happiness. *Kagunavirus malou* is derived from a nickname of one of co-authors parents. *Kagunavirus* ohbeberoi is derived from the Filipino slang term “bebe”thatrefers to friends and family. |

|  |
| --- |
| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Species*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* 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*,* within the 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). |

|  |
| --- |
| **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.

  |

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

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

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