

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create one new species *Kayfunavirus rjtwin* (Class *Caudoviricetes,* Order *Autographivirales*) |
| **Code assigned:**  | 2025.034B.Kayfunavirus\_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:**  |
| 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| W - Withdrawn |  |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 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** |
| *Kayfunavirus rjtwin* | rjtwin - derived from co-authors dogs’(Ruru and Jan) name initials |
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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*:** Realms *Duplodnaviria*, Kingdom *Heunggongvirae*, Phylum *Uroviricota*, Class *Caudoviricetes*, Order *Autographivirales*, Family *Autotranscriptaviridae*, Subfamily *Studiervirinae,* Genus *Kayfunavirus**Description of current taxonomy*: The genus *Kayfunavirus* currently has 19 ICTV listed species. *Proposed* *taxonomic change(s):* Create one new species, “*Kayfunavirus rjtwin”**Justification*:Based on VIRIDIC analysis, we propose the creation of a new phage species, *Kayfunavirus rjtwin* named after co-authors’ pets, Ruru and Jan.  |

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| **Text of Taxonomy proposal:**  |
| ***Taxonomic rank(s) affected*:** Realms *Duplodnaviria*, Kingdom *Heunggongvirae*, Phylum *Uroviricota*, Class *Caudoviricetes*, Order *Autographivirales*, Family *Autotranscriptaviridae*, Subfamily *Studiervirinae,* Genus *Kayfunavirus****Description of current taxonomy*:**The genus *Kayfunavirus* currently has 19 ICTV listed species. ***Proposed* *taxonomic change(s)*:** Create one new species, “*Kayfunavirus rjtwin*”***Demarcation criteria:****Species 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*: Enterobacter phage vB\_VIPECLMCO6 was isolated from Masalasa Creek, Tarlac, Philippines. The genome is complete with DTR based on checkV analysis and is publicly available in NCBI Genbank database. As a result of comparison of the genome of Enterobacter phage vB\_VIPECLMO6 to existing members of the genus *Kayfunavirus* using VIRIDIC (Figure 1), we propose the addition of new species, *Kayfunavirus rjtwin.*  |

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| **References:**  |
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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
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| **Tables, Figures:**  |

<Start here>Figure 1. Heatmap of intergenomic similarities between Enterobacter phage and members of the genus *Kayfunavirus* determined using VIRIDIC [8].