

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Addition of novel genera and species, and reclassification of some species in the *Nudiviridae* |
| **Code assigned:**  | *2025.002D.v4.Nudivirdae\_2ng\_17ns\_1mvsp* |

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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 | **x** | Bacterial viruses |  |
| 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:** |
| Baculoviridae and Nudiviridae 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:** |  29/5/2025 |

**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| W - Withdrawn |  |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:** Not applicable

**Part 3:** **TAXONOMIC PROPOSAL**

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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 | **x** |

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| **Etymology (origin) of proposed taxonomic names:**  |
| **Taxon name**  | **Etymology of the term** |
| *Epsilonnudivirus* | Derived from appropriate Greek letter in order of discovery |
| *Zetanudivirus* | Derived from appropriate Greek letter in order of discovery |
| *Alphanudivirus apimelliferae* | Epithet derived from the genitive of the host species name as explained in van Oers et al. [2023); In this case from the host Epithet derived from ***Api****s mellifera* **(**genitive **melliferae**) (letters in bold used for epithet). |
| *Gammanudivirus arapsonii* | Epithet derived from ***Ara****tus* ***pisonii*** (already a gentive) |
| *Gammanudivirus casapidi* | Epithet derived from ***Ca****llinectes sapidus* (genitive **sapidi**) |
| *Gammanudivirus marosenbergii* | Epithet derived from ***Ma****crobrachium* ***rosenbergii*** (already a genitive) |
| *Gammanudivirus memercanariae* | Epithet derived from ***Me****nippe mercenaria* (genitive **mercenariae**) |
| *Gammanudivirus pevannamei* | Epithet derived from ***Pe****naeus* ***vannamei*** (already a genitive) |
| *Epsilonnudivirus cracrangonis* | Epithet derived from ***Cra****ngon crangon* (genttive **crangonis**) |
| *Epsilonnudivirus dikhaemobaphes* | Epithet derived from ***Dik****erogammarus* ***haemobaphes*** (same as genitive) |
| *Epsilonnudivirus faxopropinqui* | Epithet derived from ***Faxo****nius propinquus* (genitive **propingui**) |
| *Epsilonnudivirus faxorustici* | Epithet derived from the host species name ***Faxo****nius rusticus* (genitive **rustici**) |
| *Epsilonnudivirus faxovirilis* | Epithet derived from ***Faxo****nius* ***virilis*** (same as genitive) |
| *Zetanudivirus cucafricani* | Epithet derived from ***Cuc****uloecus* (genitive **africani**) |
| *Zetanudivirus echiclaytoni* | Epithet derived from ***Echi****nophilopterus* ***claytoni*** (already a genitive) |
| *Zetanudivirus hespinigeri* | Epithet derived from ***He****terodoxus spiniger* (genitive **spinigeri**) |
| *Zetanudivirus laperplexi* | Epithet derived from ***La****gopoecus perplexus* (genitive **perplexi)** |
| *Zetanudivirus fraroseicapillae* | Epithet derived from ***Fra****nciscoloa* ***roseicapillae*** (already a genitive) |
| *Zetanudivirus myptilorhynchi* | Epithet derived from ***My****rsidea* ***ptilorhynchi*** (already a genitive) |

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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**  |
| NA | NA | NA |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: Genus and species*Description of current taxonomy*: The current taxonomy in place includes the *Alphanudivirus* (n=7 species), *Betanudivirus* (n=1 species), *Gammanudivirus* (n=4 species), and *Deltanudivirus* (n=1 species), within the *Nudiviridae*.*Proposed* *taxonomic change(s):* We propose to create two new genera, move one species to a new genus, and create 17 new species.*Justification*:New discoveries of nudiviruses from crustaceans and insects (Petersen et al. 2024) have resulted in a more diverse understanding of the *Nudiviridae*. The crustacean nudiviruses split clearly into two groups, which should be considered at the genus level for this viral family. Two new genera found to infect lice are new to science and require incorporation into the nudivirus taxonomy. In addition to the genus level amendments, there are also several species that now need to be appropriately placed into the *Alphanudivirus*, *Gammanudivirus*, and the two new genera, *Epsilonnudivirus* and *Zetanudivirus*.  |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Genus and species*Description of current taxonomy*: The *Nudiviridae* currently includes the genera *Alphanudivirus*, *Betanudivirus*, *Gammanudivirus*, and *Deltanudivirus*.*Proposed* *taxonomic change(s)*: We propose to add three new genera, move one existing species, and create 18 new species. The reasoning behind this is as follows for each taxon affected: 1. The *Alphanudivirus* will have the following new species included, due to phylogenetic clustering within this genus, and significant genetic difference from existing species: *Alphanudivirus apimelliferae*.
2. The *Gammanudivirus* will have the following new species included, due to phylogenetic clustering within this genus, and significant genetic difference from existing species: *Gammanudivirus memercanariae*; *Gammanudivirus casapidi*; *Gammanudivirus marosenbergii*; *Gammanudivirus arapsonii*; *Gammanudivirus pevannamei*.
3. Several new species also have significant phylogenetic divergence from existing genera, denoting the need for two new genera: *Epsilonnudivirus* and *Zetanudivirus*.
4. The newly erected *Epsilonnudivirus* will have the following new species included, due to phylogenetic clustering outside of other genera, and significant genetic difference from existing genera groups: *Epsilonnudivirus cracrangonis* (this species is moved from *Gammanudivirus*); *Epsilonnudivirus dikhaemobaphes*; *Epsilonnudivirus faxopropinqui*; *Epsilonnudivirus faxovirilis*; and *Epsilonnudivirus faxorustici.*
5. The newly erected *Zetanudivirus* will have the following new species included, due to phylogenetic clustering outside of other genera, and significant genetic difference from existing genera, including: *Zetanudivirus hespinigeri*; *Zetanudivirus laperplexi*; *Zetanudivirus cucafricani*; *Zetanudivirus echiclaytoni; Zetanudivirus fraroseicapillae; Zetanudivirus myptilorhynchi*

*Demarcation criteria:*Demarcation criteria are not fully defined for nudiviruses, at any level of organisation currently. We propose the following for our new genera and the species they contain. In terms of core gene alignments, each exemplar virus of a new species in this proposal is identical for 88% or less at the nucleotide level and equal to or less than 88% identical at the protein sequence level to earlier defined exemplar nudiviruses. For example, the average percent identity of the 17 core genes that show no duplication (38k, ac81, DNApol, helicase, lef-4, lef-8, lef-9, p33, p47, p74, pif-1, pif-2, pif-3, pif-4, pif-6, vp39, vp91), separating HzNV1 and HzNV2 is 99.0%, separating isolates CoNV1, CoNV2, and CoNV3 is 99.6-99.8%, and the percent identity separating FrrNV from FrpNV (Petersen et al. 2024) is 98.9%. The closest species to this boundary are FvNV and FrNV (86.97% nucleotide similarity; 87.84% core protein similarity). Based on this, we suggest that the protein and genomic similarity should sit at 90% as the barrier for defining isolates that present within the same species, relative to the first viral genome sequenced. At the genera level, intragenus and intergenus average pairwise core protein sequence identities for exemplar viruses in current and proposed genera are as follows:

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| --- | --- | --- | --- |
| Alpha | 35% - 100% |  | Core protein similarity range (%) |
| Beta | 26% - 29% | 99% - 100% |  |  |  |  |
| Gamma | 26% - 28% | 29% - 30% | 43% - 100% |  |  |  |
| Delta | 27% - 29% | 29% | 30% - 32% | 100% |  |  |
| Epsilon | 26% - 28% | 29% - 31% | 35% - 38% | 30% - 32% | 39% - 100% |  |
| Zeta | 25% - 28% | 27% - 29% | 27% - 29% | 29% - 31% | 27% - 30% | 38% - 100% |
|  | Alpha | Beta | Gamma | Delta | Epsilon | Zeta |

From this table, we propose a provisional cut-off value of 38% for determining if two viruses belong to the same or different genera. This should be fortified with phylogenetic topology and branch distance, to show their relatedness. If the viruses being compared exhibit an average core gene amino acid sequence identity equal to or less than 38%, then they are considered to belong to different genera. There is some inconsistency in the alphanudivirus group as it currently stands, which may need revisiting, where GbNV is distinct (35% core protein similarity), which, when removed, changes to 43% core protein similarity within the *Alphanudivirus* genus. However, GbNV is rather unique, and few available viruses can be used to develop a more robust placement for this species at this time.The following additional criteria for future species to be included in the new genera are as follows:*Epsilonnudivirus* – to be included in this genus, the host should be a crustacean, and the viral genome should phylogenetically group together with existing species in this genus, sharing above 38% protein similarity. *Zetanudivirus* – to be included in this genus, the host should be a louse, and the viral genome should phylogenetically group together with existing species in the genus, sharing above 38% protein similarity. *Justification*: Placement of new species in new and proposed genera is consistent with the species and genus demarcation criteria described above and their phylogenetic clustering in Figure 1. Please also see the level of identity of core genes in pairwise amino acid comparisons between nudiviruses in Figure 2.  |

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| **References:**  |
| Allain, T. W., Stentiford, G. D., Bass, D., Behringer, D. C., & Bojko, J. (2020). A novel nudivirus infecting the invasive demon shrimp *Dikerogammarus haemobaphes* (Amphipoda). *Scientific reports*, *10*(1), 14816.Bojko, J., Burgess, A. L., Allain, T. W., Ross, E. P., Pharo, D., Kreuze, J. F., & Behringer, D. C. (2022). Pathology and genetic connectedness of the mangrove crab (*Aratus pisonii*)–a foundation for understanding mangrove disease ecology. *Animal Diseases*, *2*(1), 8.Bojko, J., Walters, E., Burgess, A., & Behringer, D. C. (2022). Rediscovering “Baculovirus-A” (Johnson, 1976): The complete genome of ‘Callinectes sapidus nudivirus’. *Journal of Invertebrate Pathology*, *194*, 107822.Bojko, J., Duermit-Moreau, E., Gandy, R., & Behringer, D. C. (2023). A new member of the *Nudiviridae* from the Florida stone crab (Menippe mercenaria). *Virology*, *588*, 109910.Petersen, J. M., Burgess, A. L., van Oers, M. M., Herniou, E. A., & Bojko, J. (2024). Nudiviruses in free-living and parasitic arthropods: evolutionary taxonomy. *Trends in Parasitology 40, 744-762*.Stratton, C. E., Reisinger, L. S., Behringer, D. C., Gray, S. N., Larson, E. R., & Bojko, J. (2024). North American crayfish harbour diverse members of the *Nudiviridae*. *Virology*, *598*, 110183.van Oers, M.M., Herniou, E.A., Jehle, J.A., Krell, P.J., Abd-Alla, A.M.M., Ribeiro,. B.M., Theilmann, D.A., Hu, Z., Harrison, R.L. (2023). Developments in the classification and nomenclature of arthropod-infecting large DNA viruses that contain pif genes. *Archives of Virology* 168, 82. doi: 10.1007/s00705-023-05793-8.  |

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| **Accompanying files:** |
| **Filename** | **Description of contents** |
| 2025.002D.v4.Nudivirdae\_2ng\_17ns\_1mvsp.xlsx | Accompanying Excel sheet |
|  |  |

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| **Tables, Figures: Please see tables and figures below.** |

See following pages

Table 1. Novel virus genome sizes, open reading frame numbers, and accession numbers.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Novel species | Exemplar virus name | Abbr. | Genome size (bp) | ORF count | Accession |
| *Alphanudivirus apimelliferae* | Apis mellifera nudivirus | AmNV | 129467 | 106 | OR596894 |
| *Gammanudivirus arapsonii* | Aratus pisonii nudivirus | ApNV | 108983 | 90 | ON061174 |
| *Gammanudivirus casapidi* | Callinectes sapidus nudivirus | CsNV | 122436 | 98 | ON638996 |
| *Gammanudivirus marosenbergii* | Macrobrachium rosenbergi nudivirus | MrNV | 108126 | 115 | MW484891 |
| *Gammanudivirus memercanariae* | Menippe mercenaria nudivirus | MmNV | 99336 | 83 | OQ725696 |
| *Gammanudivirus pevannamei* | Penaeus vannamei nudivirus | PvNV | 119883 | 100 | OM066077 |
| *Epsilonnudivirus cracrangonis* | Crangon crangon nudivirus | CcNV | 132068 | 106 | NC\_076945 |
| *Epsilonnudivirus dikhaemobaphes* | Dikerogammarus haemobaphes nudivirus | DhNV | 119695 | 106 | MT488302 |
| *Epsilonnudivirus faxopropinqui* | Faxonius propinquus nudivirus | FpNV | 130164 | 120 | PP539709 |
| *Epsilonnudivirus faxorustici* | Faxonius rusticus nudivirus | FrNV | 147048 | 126 | PP539711 |
| *Epsilonnudivirus faxovirilis* | Faxonius virilis nudivirus | FvNV | 144948 | 127 | PP539710 |
| *Zetanudivirus cucafricani* | Cuculoecus africanus nudivirus | CafNV | 84329 | 89 | BK068074 |
| *Zetanudivirus echiclaytoni* | Echinophilopterus claytoni | EcNV | 85720 | 89 | BK068075 |
| *Zetanudivirus hespinigeri* | Heterodoxus spiniger nudivirus | HxsNV | 97269 | 104 | BK068078 |
| *Zetanudivirus laperplexi* | Lagopoecus perplexus nudivirus | LpNV | 90164 | 95 | BK068079 |
| *Zetanudivirus fraroseicapillae* | Franciscoloa roseicapillae nudivirus | FrrNV | 83884 | 100 | BK068077 |
| *Zetanudivirus myptilorhynchi* | Myrsidea ptilorhynchi nudivirus | MpNV | 87845 | 99 | BK068080 |

Table 2. Currently less-well characterized viruses with complete genomes that appear to belong to the family *Nudiviridae*

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| --- | --- | --- | --- | --- | --- |
| Novel species | Exemplar virus name | Abbr. | Genome size (bp) | ORF count | Accession |
| *NA* | Ctenocephalides orientis nudivirus | CoNV -1 | 90736 | 86 | BK068081 |
| *NA* | Phenacoccus solenopsis nudivirus | PsNV | 189841 | 139 | MT833891 |



**Figure 1.** A Phylogenetic tree incorporating all of the known nudivirus isolates, incorporating new discoveries from Petersen et al. (2024). Virus acronyms on the tree with a black star are already incorporated into the ICTV. Those with an orange star are new and being incorporated in this proposal. The proposed or existing genus is noted at each section of the tree that it represents. Viruses without a star remain to be defined. All nodes on the tree are above a minimum threshold of 70, but the majority factor above 95.The selected baculoviruses are added as an outgroup.



**Figure 2.** A sequence demarcation plot for the core protein concatenated file used to provide the phylogenetic tree in Figure 1. The same annotation is outlined on the figure, highlighting where different genera and families are represented.