

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create two new species in genus *Peropuvirus* and two new species in genus *Hexartovirus* (*Mononegavirales*: *Artoviridae*) | |
| **Code assigned:** | 2024.003M.Artoviridae \_4nsp |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** |  | **Email address** | **Corresponding author(s)** |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses | **X** | 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:** |
| ICTV *Artoviridae* 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** |
| *Artoviridae* Study Group | 4 | 0 | 0 |
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| **Submission date:** | 21/06/2024 |

**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| W – Withdrawn |  |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:** | DD/MM/YYYY |

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

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| **Name of accompanying Excel module:** |
| 2024.003M.Artoviridae \_4nsp.xlsx |

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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 |  |

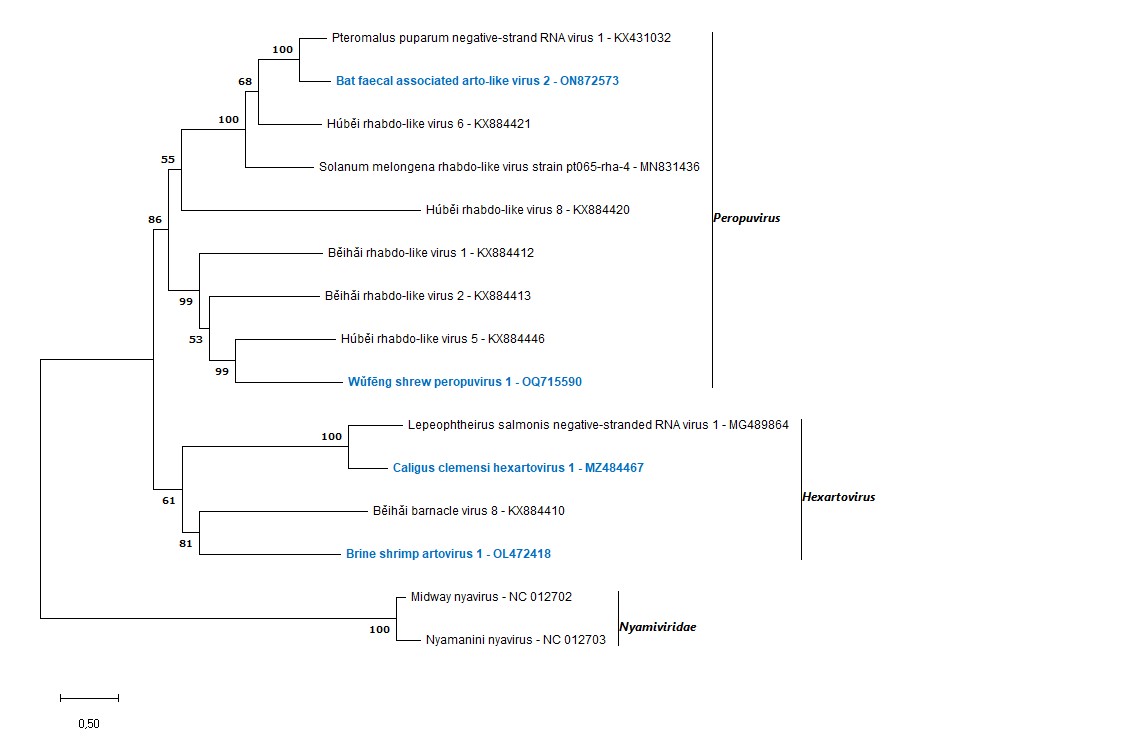
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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  The family *Artoviridae* currently includes two genera, *Hexartovirus* (2 species) and *Peropuvirus* (7 species).  *Proposed* *taxonomic change(s):*  Create two new species in genus *Hexartovirus* and two new species in genus *Peropuvirus*.  *Justification*:  The viruses proposed to be assigned to novel species have a minimum amino acid divergence of 44 % in their L proteins compared to classified family members and occupy different ecological niches. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genera *Hexartovirus* and *Peropuvirus,* species  *Description of current taxonomy*:  The family *Artoviridae* currently includes two genera, *Hexartovirus* (2 species) and *Peropuvirus* (7 species). The viruses of genus *Hexartovirus* infect crustaceans such as barnacles and copepods. The viruses of genus *Peropuvirus* infect parasitoid wasps, pillworms, woodlice, odonates or plants.  *Proposed* *taxonomic change(s)*:  We propose to classify Caligus clemensi hexartovirus 1 in the new species *Hexartovirus caligi*, brine shrimp artovirus 1 in the new species *Hexartovirus artemiae*, Wùfēng shrew peropuvirus 1 in the new species *Peropuvirus wufengense* and bat faecal associated arto-like virus 2 in the new species *Peropuvirus pteropi*.  *Demarcation criteria:*  The viruses proposed to be assigned to novel species have a minimum amino acid divergence of 44 % in their L proteins compared to classified family members and occupy different ecological niches.  *Justification*:  The viruses Caligus clemensi hexartovirus 1 (Chang et al., 2023), brine shrimp artovirus 1 (Dong et al., 2024), Wùfēng shrew peropuvirus 1 (Chen et al., 2023) and bat faecal associated arto-like virus 2 (Van Brussel et al., 2022) all show at least 28.1 % amino acid identity with other members of the family *Artoviridae* and phylogenetic analysis shows that the new viruses clearly cluster with the established species (Figure 1). The L proteins of all four viruses are at least 44% divergent. This significant difference supports the formation of new species. In addition, the new viruses infect or are associated with hosts (sea lice, brine shrimp, shrews, and bats, respectively) that have not been previously reported in the family *Artoviridae*. |

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| **References:** |
| CHANG, T., HUNT, B., HIRAI, J. & SUTTLE, C. 2023. Divergent RNA viruses infecting sea lice, major ectoparasites of fish. *PLoS Pathogens,* 19**,** e1011386.  CHEN, Y. M., HU, S. J., LIN, X. D., TIAN, J. H., LV, J. X., WANG, M. R., LUO, X. Q., PEI, Y. Y., HU, R. X., SONG, Z. G., HOLMES, E. C. & ZHANG, Y. Z. 2023. Host traits shape virome composition and virus transmission in wild small mammals. *Cell,* 186**,** 4662-4675.e12.  DONG, X., LI, C., WANG, Y., HU, T., ZHANG, F., MENG, F., GAO, M., HAN, X., WANG, G., QIN, J., NAUWYNCK, H., HOLMES, E. C., SORGELOOS, P., SUI, L., HUANG, J. & SHI, W. 2024. Diversity and connectedness of brine shrimp viruses in global hypersaline ecosystems. *Science China Life Sciences,* 67**,** 188-203.  VAN BRUSSEL, K., MAHAR, J. E., ORTIZ-BAEZ, A. S., CARRAI, M., SPIELMAN, D., BOARDMAN, W. S. J., BAKER, M. L., BEATTY, J. A., GEOGHEGAN, J. L., BARRS, V. R. & HOLMES, E. C. 2022. Faecal virome of the Australian grey-headed flying fox from urban/suburban environments contains novel coronaviruses, retroviruses and sapoviruses. *Virology,* 576**,** 42-51. |

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| **Tables, Figures:** |



**Figure 1**. Phylogenetic analysis of viruses in the family *Artoviridae*. Maximum likelihood tree of L protein amino acid sequences utilizing LG+G+I+F model and 1,000 bootstraps. *Nyamiviridae* is used as outgroup. Model test and phylogeny based on complete deletion of gaps.