

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Creation of one new genus (*Bivalveiridovirus*) with one new species (*Bivalveiridovirus cerastoderma1*) in the subfamily *Betairidovirinae* |
| **Code assigned:** | *2025.003D.v3.* *Iridoviridae\_1ng\_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 | **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:** |
| *Iridoviridae* SG |

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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:** | 12/03/2025 |

**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| W - Withdrawn |  |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** |
| **Genus: *Bivalveiridovirus*** | **Derived from the designation of the class Bivalvia, in which *Cerastoderma edule* is a species.** |
| **Species: *Bivalveiridovirus cerastoderma1*** | **Following the naming convention in 2023.012D, the first word is the name of the proposed genus name (*Bivalveiridovirus*), and the second word is the genus that harbours the virus (*Cerastoderma*)** |

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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*:  Formation of a novel genus within *Betairidovirinae* containing a single confirmed species.  *Description of current taxonomy*:  The subfamily *Betairidovirinae* currently contains four genera, with its members primarily infecting invertebrate hosts.  *Proposed* *taxonomic change(s):*  Formation of the novel genus *Bivalveiridovirus* within *Betairidovirinae* and the recognition of novel iridovirus species *Bivalveiridovirus cerastoderma1.*  *Justification*:  Generation of the complete genome of a novel iridovirid from cockles (*Cerastoderma edule*) and determination of its tropism within the tissues of infected animals represents the most complete description of a bivalve-infecting iridovirid to date. The genome size and G+C% content of *Bivalveiridovirus cerastoderma1* was similar to other *Betairidovirinae.* Pathology of infection with *Bivalveiridovirus cerastoderma1* in cockles was similar to that described for *Decapodiridovirus litopenaeus1* infection in shrimp tissues, and icosahedral virions, typical of iridovirids, were observed in the cytoplasm of infected cockle haemocyte cells. Comparison of the amino acid sequence from conserved iridovirid genes in *Bivalveiridovirus cerastoderma1* to other iridovirids showed 76.36% amino acid similarity to the nearest iridovirus in the major capsid protein (MCP) and 65.46% in the AAA-ATPase protein. Phylogenetically, *Bivalveiridovirus cerastoderma1* branches within *Betairidovirinae*, but as a separate clade to other recognised genera.  Based on the host range, phylogenetic position, and sequence similarity of this novel virus to known iridovirids, we propose the construction of a new genus, designated *Bivalveiridovirus,* to indicate its infectivity toward a species within the Bivalvia class of animals, and that it be considered a fifth genus within the subfamily *Betairidovirinae*. |

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| * **Text of Taxonomy proposal:** |
| The family *Iridoviridae* currently contains seven genera placed within two subfamilies: *Alphairidovirinae* and *Betairidovirinae,* with members of species within a genus typically having >50% sequence identity within a 26 core iridovirus genes [1-2]*.* In addition to sequence identity, iridovirid genera are demarked by G+C% content, phylogenetics, host range, genome co-linearity, disease manifestation, and antigenicity [2]. The subfamily *Betairidovirinae* currently contains four genera: *Chloriridovirus, Daphniairidovirus, Decapodiridovirus,* and *Iridovirus.* We propose to establish a fifth genus (*Bivalveiridovirus*) within the subfamily, as the novel iridovirus branches phylogenetically within this *Betairidovirinae* clade and infects an invertebrate (*Cerastoderma edule*), like the majority of viruses within this subfamily. To date, we have characterized a single virus within the *Bivalveiridovirus* genus (*Bivalveirdiovirus cerastoderma1*) and tentatively identified a second member from publicly available whole genome sequencing (WGS) data from a species of deep-sea mussel, *Bathymodiolus septemdierum* (not included in this proposal) [3]. The exemplar for *Bivalveirdiovirus cerastoderma1,* given the common name “bivalve iridovirus 1” (BiIV1), was sequenced serendipitously while attempting to generate genomic data for a cockle parasite, *Marteilia cochillia,* from moribund cockles collected from the Wash Estuary, UK.  Assembly and annotation of BiIV1 revealed a 180 kbp genome with 193 predicted open reading frames. Genome size and %G+C of BiIV1 were consistent with other members of *Betairidovirinae* (Figure 1). Phylogenetic analysis on a concatenated set of six conserved genes [4] from a representative set of iridovirids showed that BiIV1 clustered with *Betairidovirinae*, but as a distinct, maximally supported, clade with the second tentatively identified bivalve iridovirus (Figure 2). Comparison of the amino acid sequence of conserved iridovirid genes in *Bivalveiridovirus cerastoderma1* to other iridovirids showed 76.36% amino acid similarity to the nearest iridovirid in the MCP and 65.46% in the AAA-ATPase protein. Homology analysis suggested that nine potential genes in the BiIV1 genome could have been gained by horizontal gene transfer (HGT) from its cockle host or its ancestors. These genes were intronless and appeared to have functions including DNA synthesis and replication, regulation of apoptosis and cell cycle, and viral budding. The annotated genome of BiIV1 has been deposited to GenBank with accession number PQ846775.    Transmission electron microscopy showed icosahedral particles (average equivalent diameter of 158 nm) within the haemocytes of cockles (Figure 3). This virion size is very similar to that of decapod iridovirus 1 (DIV1) [5], but much smaller than the iridovirus virions previously reported to infect other species of bivalve, which ranged from 288 – 380 nm [5-6]. Histopathology highlighted haemocytic infiltration within the connective tissues surrounding the digestive gland tubules. Some of these cells were observed to contain basophilic inclusion bodies within the cytoplasm, pathology similar to that described for DIV1 infections in shrimp tissues [7]. Nuclei of the affected cells were observed to possess condensed and marginalised chromatin (Figure 4).  In summary, features distinguishing the proposed genus from the four existing genera in *Betairidovirinae* are: (1) phylogenetic analysis based on six core iridovirid genes indicates that BiIV1 is distantly related to existing genera, (2) sequence comparison to other iridoviridsshows that the MCP and ATPase genes have less than 80% identity to other viruses within *Iridoviridae,* and (3) host range: BiIV1 infects the common cockle in contrast to decapodiridoviruses and daphniairidoviruses that infect crustaceans, and iridoviruses and chloriridoviruses that primarily infect insects. |

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| **References:** |
| [1] Chinchar VG, Waltzek T, Subramaniam K, Faria VG, Ebert D, Jancovich J, Hick P, Zhang QY, Marschang R, Whittington R, Williams T, Ince IA, Jie H (2020). ICTV proposal [2020.018D.R.Betairidovirinae\_1ngen\_1nsp](https://ictv.global/ictv/proposals/2020.018D.R.Betairidovirinae_1ngen_1nsp.zip) “Create one new genus (*Daphniairidovirus*) including one new species in subfamily Betairidovirinae (*Pimascovirales*: *Iridoviridae*)”  [2] Chinchar VG​, Hick P, Huang J, Ince IA​, Jancovich JK, Marschang R​, Qin O, Subramaniam K​, Waltzek TB, Whittington R, Williams T and Zhang QY (2017). ICTV Virus Taxonomy Profile: *Iridoviridae*, Journal of General Virology, 98, 890–891.  [3] Hooper C, Tidy AM, Jessop R, Bateman KS, Green MJ, Ross SH, Ward GM, Hazelgrove R, Hunt JE, Parker M, Bass D. (2025) Genomic and morphological characterisation of a novel iridovirus, bivalve iridovirus 1 (BiIV1), infecting the common cockle (*Cerastoderma edule*). bioRxiv 2025.03.05.641634; doi: https://doi.org/10.1101/2025.03.05.641634  [4] Toenshoff ER, Fields PD, Bourgeois YX, Ebert D (2018) The end of a 60-year riddle: Identification and genomic characterization of an iridovirus, the causative agent of white fat cell disease in zooplankton. G3 (Bethesda) 8:1259-1272. PMID 29487186; doi:10.1534/g3.117.300429  [5] Arulmoorthy MP, Vijayan R, Sinduja K, Suresh E, Vasudevan S. 2022. Infection with Decapod iridescent virus 1: an emerging disease in shrimp culture. Archives of Microbiology. 204(11):685 doi:10.1007/s00203-022-03289-8  [6] Comps M, Duthoit J-L. 1976. Infection virale associée à la "maladie des branchies" de l'huître portugaise *Crassostrea angulata* LmK. Comptes Rendus Académie des Sciences de Paris. 283:1595-1597  [7] Comps M, Duthoit J-L. 1979. Infections virales chez les huîtres *Crassostrea angulata* Lmk. et Crassostrea gigas Th. Haliotis. 8:301-307  [6] Elston R. 1979. Viruslike particles associated with lesions in larval Pacific oysters (*Crassostrea gigas*). Journal of Invertebrate Pathology. 33(1):71-74 doi:10.1016/0022-2011(79)90132-0  [8] Xu L, Wang T, Li F, Yang F. 2016. Isolation and preliminary characterization of a new pathogenic iridovirus from redclaw crayfish *Cherax quadricarinatus*. Diseases of aquatic organisms. 120(1):17-26 doi:10.3354/dao03007 |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.003D.v3.Iridoviridae\_1ng\_1ns\_sup\_file\_1 | Contains figures 1-4 |
| 2025.003D.v3.Iridoviridae\_1ng\_1ns.xlsx | Accompanying Excel sheet |

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| **Tables, Figures:** |

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