

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create three new species in family *Bornaviridae* (*Mononegavirales*) | |
| **Code assigned:** |  |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **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 *Bornaviridae* 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** |
| *Bornaviridae* Study Group | 10 | 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| W - Withdrawn |  |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.###M.S.v1.Bornaviridae\_3nsp |

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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*:  Genus (*Cultervirus*, *Orthobornavirus*)    *Description of current taxonomy*:  *Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Haploviricotina*: *Monjiviricetes*: *Mononegavirales*: *Bornaviridae*: *Cultervirus* (three species) and *Orthobornavirus* (nine species).  *Proposed* *taxonomic change(s):*  Add two (2) new species to genus *Cultervirus* (*Cultervirus harpadoni*, *Cultervirus poeciliae*) and add one (1) new species to genus *Orthobornavirus* (*Orthobornavirus iridiscincum*).  *Justification*:  The proposed new species are based on newly released genome sequences in GenBank that meet the current bornavirid species demarcation criteria. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected:*  Genus (*Cultervirus*, *Orthobornavirus*)  *Description of current taxonomy:*  As of April 2024, the family *Bornaviridae* includes four (4) genera (*Carbovirus*, *Cartilovirus*, *Cultervirus*, and *Orthobornavirus*). Currently three (3) species are assigned to the genus *Cultervirus*:   * *Cultervirus electrophori* * *Cultervirus hemicultri* * *Cultervirus inflate*   Currently nine (9) species are assigned to the genus *Orthobornavirus*:   * *Orthobornavirus alphapsittaciforme* * *Orthobornavirus avisaquaticae* * *Orthobornavirus betapsittaciforme* * *Orthobornavirus bornaense* * *Orthobornavirus caenophidiae* * *Orthobornavirus elapsoideae* * *Orthobornavirus estrildidae* * *Orthobornavirus sciuri* * *Orthobornavirus serini*   *Proposed taxonomic change(s):*  We propose to create two (2) new species within the genus *Cultervirus* that are based on viral genome sequences that have recently been identified during data-mining of fish datasets in the Sequence Read Archive (SRA) [1]. In detail, Pará molly bornavirus (PrMBV; BK063657) was identified in datasets from a melanzona guppy (*Poecilia parae* (C. H. Eigenmann, 1894)), while Bombay duck fish bornavirus (BDFBV; BK063658) was identified in datasets from a Bombay duck (*Harpadon nehereus* (F. Hamilton, 1822)).  We propose the following species names:  Pará molly bornavirus (PrMBV; BK063657) → *Cultervirus poeciliae*  Bombay duck fish bornavirus (BDFBV; BK063658) → *Cultervirus harpadoni*  Furthermore, we propose to create a single (1) new species within the genus *Orthobornavirus*, that is based on a single new viral genome that have been found during sequencing of liver viromes of Australian geckos and skinks [2]. In detail, Carlia munda bornavirus (CrMBV; PP711183) was identified in a pooled liver sample from shaded-litter rainbow skinks (*Carlia munda* (C. W. De Vis, 1885)).  We propose the following species name:  Carlia munda bornavirus (CrMBV; PP711183) → *Orthobornavirus iridiscincum*  *Etymology:*  *Cultervirus poeciliae: “*poeciliae” from the fish genus *Poecilia*, the genus of mollies  *Cultervirus harpadoni: “*harpadoni*”* from the fish genus *Harpadon*  *Orthobornavirus iridiscincum: “*iridiscincum*”* as combination of “rainbow” and “skink” inspired from shaded-litter rainbow-skink (*Carlia munda* (C. W. De Vis, 1885)).  *Demarcation criteria:*  Criteria for bornavirid genus affiliation and species demarcation are based on genomic characteristics, including genome organization, Pairwise Sequence Comparison (PASC) [3, 4], in combination with biological characteristics, such as antigenic relationships and natural host range [5]. In agreement with these criteria, the PASC species demarcation criterion was defined ≥72% for coding-complete genome sequences [6, 7]. The genus-demarcation cut-off was tentatively set at approximately ≥42% genome nucleotide identity [8] (**Figure 1**).  *Justification:*  **Genomic architecture**  The genomic architectures of PrMBV and BDFBV are similar in structure to those of culterviruses and carboviruses, following the pattern 3'-N-X/P-**G-M**-L-5'. In contrast, the genome of CrMBV follows the pattern 3'-N-X/P-**M-G**-L-5' and is thus like members of the genus *Orthobornavirus*.  **Phylogenetic analysis**  Phylogenetic analysis of the L protein amino acid sequence of PrMBV, BDFBV, and CrMBV along with representative sequences grouped PrMBV and BDFBV within the group of culterviruses and CrMBV together with orthobornaviruses (**Figure 2**).  **PASC analysis**  Sequence similarity based on pairwise whole genome nucleotide comparison using PASC showed that PrMBV and BDFBV are more related to each other than to other viruses (65.8%), but do not represent the same species, according to the established species demarcation criteria (≥72%) (**Figure 3**). Both sequences show a PASC identity of 42.1–44.6% to other members of the genus *Cultervirus*, which is above the current genus demarcation cut-off (≥42%). Their PASC identity to other bornavirids is <42%.  PASC analysis of CrMBV shows 47.8–53.5% identity to members of the genus *Orthobornavirus* and 27.0-34.4% to bornavirids other than that.  Recently published genomes of barn owl bornavirus 1 (“BOBV-1” [corrected from BoBV-1]; OQ686614; [9]) and munia bornavirus 1 (“MuBV-1”; OQ550279; [10]) belong to the species *Orthobornavirus serini*, according to PASC analysis. |

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| **References:** |
| 1. Eshak MIY, Rubbenstroth D, Beer M *et al.* (2023) Diving deep into fish bornaviruses: Uncovering hidden diversity and transcriptional strategies through comprehensive data mining. *Virus Evol* 9:vead062. <https://doi.org/10.1093/ve/vead062> 2. Mahar JE, Wille M, Harvey E *et al.* (2024) The diverse liver viromes of Australian geckos and skinks are dominated by hepaciviruses and picornaviruses and reflect host taxonomy and habitat. *Virus Evol* 10:veae044. <https://doi.org/10.1093/ve/veae044> 3. Bao Y, Kapustin Y, Tatusova T (2008) Virus Classification by Pairwise Sequence Comparison (PASC). In: *Encyclopedia of Virology*. Elsevier, pp 342–348 4. Bao Y, Chetvernin V, Tatusova T (2014) Improvements to pairwise sequence comparison (PASC): a genome-based web tool for virus classification. *Arch Virol* 159:3293–3304. <https://doi.org/10.1007/s00705-014-2197-x> 5. Zimmermann V, Rinder M, Kaspers B *et al.* (2014) Impact of antigenic diversity on laboratory diagnosis of Avian bornavirus infections in birds. *J Vet Diagn Invest* 26:769–777. <https://doi.org/10.1177/1040638714547258> 6. Kuhn JH, Dürrwald R, Bào Y *et al.* (2015) Taxonomic reorganization of the family *Bornaviridae*. *Arch Virol* 160:621–632. <https://doi.org/10.1007/s00705-014-2276-z> 7. Rubbenstroth D, Briese T, Dürrwald R *et al.* (2015) Two (2) new species in the genus *Bornavirus*. TaxoProp2015.002aM.A.v2.Bornavirus\_2sp 8. Pfaff F, Eshak M, Rubbenstroth D (2023) Create one new genus and three new species in family *Bornaviridae* (*Mononegavirales*). TaxoProp 2023.005M.Bornaviridae\_1ngen\_3nsp 9. Aguilera-Sepúlveda P, Llorente F, Rosenstierne MW *et al.* (2024) Detection of a new avian bornavirus in barn owl (*Tyto alba*) by pan-viral microarray. *Vet Microbiol* 289:109959. <https://doi.org/10.1016/j.vetmic.2023.109959> 10. Komorizono R, Sassa Y, Horie M *et al.* (2020) Evolutionary selection of the nuclear localization signal in the viral nucleoprotein leads to host adaptation of the genus *Orthobornavirus*. *Viruses* 12:E1291. <https://doi.org/10.3390/v12111291> |



**Figure 1: Distribution of PASC distances within the family *Bornaviridae*.** Demarcation cut-offs: ≥72% for the same species (green), <72% and ≥42% for the same genus (yellow), <42% different genera (salmon red).



**Figure 2: Phylogenetic relationship within the family *Bornaviridae*.** The maximum-likelihood tree was based on an amino acid sequence alignment of the viral protein L of the new bornavirids (highlighted in red) together with representative members of the genera *Carbovirus* (blue), *Cartilovirus* (green), *Cultervirus* (yellow) and *Orthobornavirus* (pink). The tree was constructed using IQ-TREE (version 2.3.4), an optimal partition model and statistical support with each 100.000 replicates for ultrafast bootstrap and SH-aLRT. The statistical support is shown for major branches using the format [ultrafast bootstrap/SH-aLRT]. Asterisks indicate statistical support ≥ 95% and ≥ 80% for ultrafast bootstrap and SH-aLRT, respectively.



**Figure 3: Nucleotide distances within the family *Bornaviridae* as calculated by PASC.** Colors correspond to demarcation cut-offs: ≥72% for the same species (green), <72% and ≥42% for the same genus (yellow), <42% different genera (salmon red). Viruses analysed in this proposal are highlighted in red.