

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create one new species in the genus *Cardoreovirus* (*Reovirales*: *Sedoreoviridae*) | |
| **Code assigned:** | <to be assigned by ICTV officers> |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** |
| Mingli Zhao | Department of Pathobiology and Population Sciences, Royal Veterinary College, London, UK | mzhao@rvc.ac.uk | X |
| Eric Schott | Institute of Marine and Environmental Technology, University of Maryland Center for Environmental Science, Baltimore, Maryland, USA | schott@umces.edu | X |
| Camila Tavares | Integrated Group of Aquaculture and Environmental Studies, Federal University of Paraná, Curitiba, Paraná, Brazil | camilapstavares@gmail.com |  |

**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 -Submit to Proposals Secretary |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**. |
| *Sedoreoviridae* 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** |
| *Sedoreoviridae* study group | 9 | 0 |  |
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| **Submission date:** | 14/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting** <To be completed by the subcommittee chair after EC evaluation>

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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** <To be completed for the revised version>

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| **Response of proposer:** Please describe in detail how you have responded to the EC meeting feedback |
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| **Revision date:** | DD/MM/YYYY |

Enter date of the revised version.

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

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| **Name of accompanying Excel module:** |
| 2024.###.M.*Cardoreovirus*\_1nsp |

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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*:  *Cardoreovirus* genus  *Description of current taxonomy*:  The genus *Cardoreovirus* currently has only one species of *Cardoreovirus eriocheiris* (EsRV)  *Proposed* *taxonomic change(s):*  A new species belonging to the *Cardoreovirus* genus should be established.  *Justification*:  The proposed new *Cardoreovirus* species – *Cardoreovirus callinectes* exhibits amino acid sequence similarities ranging from 46% to 79% for segments 1-12 compared to the established *Cardoreovirus* species - *Cardoreovirus eriocheiris*. The maximum likelihood phylogenetic tree indicates that the proposed species falls on a different branch but within the same clade as EsRV, suggesting that the new species should be classified within the *Cardoreovirus* genus. |

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| **Text of Taxonomy proposal:** . |
| *Taxonomic rank(s) affected*:  *Cardoreovirus* genus  *Description of current taxonomy*:  The genus *Cardoreovirus* currently has only one species of *Cardoreovirus eriocheiris*  *Proposed* *taxonomic change(s)*:  A new species belonging to the *Cardoreovirus* genus should be established.  *Demarcation criteria:*  Since only one species has been identified within the genus *Cardoreovirus*, no established criteria for species demarcation exist for this genus. In this proposal, we introduce the following demarcation criteria in terms of sequence identity: Sequence analysis reveals that viruses from distinct species exhibit less than 80% amino acid identity in VP1. Additionally, there are amino acid identities of <55%, <65%, <55%, <65% respectively in the more variable VP7, VP8, VP9 and VP10 proteins, respectively. These species demarcation criteria may be revised upon detection of other members of this genus in the future.  *Justification*:  The proposed new *Cardoreovirus* species, *Cardoreovirus callinectes*, was initially identified from blue crab, *Callinectes sapidus,* captured near Tramandaí, Brazil (1). The representative virus of this novel species was designated as *Callinectes sapidus* reovirus 2 (CsRV2) (1). Subsequently, CsRV2 was also detected in *Callinectes danae* specimens in Paraná, Brazil (2). Its electrophoretic genome organization closely resembles that of *Cardoreovirus eriocheiris* (EsRV) from *Eriocheir sinensis* (3), exhibiting a pattern of 3/4/2/3 (4). The nearly complete genome sequence of *Cardoreovirus callinectes*, encompassing complete ORFs but missing most 5’ and 3’-terminal non-coding sequences, measures approximately 21 kbp (Table 1) (1). This virus demonstrates high amino acid sequence similarity (>99%) between viral strains identified from the two hosts, *C. sapidus* and *C. danae* for all 12 segments (1, 2). However, when compared to the only established species within the *Cardoreovirus* genus - EsRV (5), *Cardoreovirus callinectes* exhibits much lower amino acid sequence similarity, with less than 80% similarity in VP1 and less than 65% in other more variable proteins such as VP7 through VP11 (3, 6) (Table 1), suggesting they are different species. The maximum likelihood phylogenetic tree reveals that *Cardoreovirus callinectes* forms a distinct branch on the tree but remains within the same clade as EsRV, supported by high bootstrap values (Figure 1). This evidence suggests that *Cardoreovirus callinectes* should be classified as a novel species within the *Cardoreovirus* genus. |

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| **References:** |
| 1. Zhao, Mingli, Emily M. Flowers, and Eric J. Schott. Near-complete sequence of a highly divergent Reovirus genome recovered from *Callinectes sapidus*. Microbiology Resource Announcements 10.1 (2021): 10-1128. 2. dos Santos Tavares, Camila Prestes, et al. Virus discovery in cultured portunid crabs: Genomic, phylogenetic, histopathological and microscopic characterization of a reovirus and a new bunyavirus. *Journal of Invertebrate Pathology* (2024): 108118. 3. Zhang S, Shi Z, Zhang J, Bonami JR. Purification and characterization of a new reovirus from the Chinese mitten crab, *Eriocheir sinensis*. J Fish Dis, 27 (2004): 687-692. 4. Zhao, Mingli, Camila Prestes dos Santos Tavares, and Eric J. Schott. Diversity and classification of reoviruses in crustaceans: A proposal. Journal of Invertebrate Pathology 182 (2021): 107568. 5. Matthijnssens, J., Attoui, H., Bányai, K., Brussaard, C. P., Danthi, P., Del Vas, M., ... & Wei, T. ICTV virus taxonomy profile: *Sedoreoviridae* 2022. Journal of General Virology, 103.10(2022), 001782. 6. Guo, G., Wang, M., Zhou, D., He, X., Han, P., Chen, G., ... & He, J. Virome Analysis Provides an Insight into the Viral Community of Chinese Mitten Crab *Eriocheir sinensis*. Microbiology Spectrum, 11.4 (2023)., e01439-23. |

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| **Tables, Figures:** |

<Start here>

**TABLE 1. Annotation of the CsRV2 genome.** Amino acid sequence identity of CsRV2 to the established *Cardoreovirus* species - *Cardoreovirus eriocheiris*, including two strains of EsRV905 and EsRV1, was shown in the table.

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| **CsRV2 segment** | **Size (nt)** | **Protein names** | **GenBank #** | **Closest**  **sequence** | **Amino acid identity (%)** | **GenBank #** |
| 1  2  3  4  5  6  7  8  9  10  11  12 | 3742  3024  2807  1936  1679  1631  1531  1186  1062  923  798  790 | VP1  VP2  VP3  VP4  VP5A  VP5B  VP6  VP7  VP8  VP9  VP10  VP11  VP12 | MW208677  MW208678  MW208679  MW208680  MW208681  MW208682  MW208683  MW208684  MW208685  MW208686 MW208687  MW208688 | EsRV905  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1  EsRV1 | 79  79  73  78  67  46  49  67  53  63  53  61  63  65 | Q698V5  OP019112  OP019113  OP019114  OP019115  OP019116  OP019117  OP019118  OP019119  OP019120  OP019121  OP019122  OP019123  OP019124 |

**Figure 1.** **Phylogenetic tree of members of the family *Sedoreoviridae*, including the proposed novel virus species.** Maximum likelihood tree was contrasted with PhyML using amino acid sequences of VP1 (the putative RdRp) of representative viruses in the family *Sedoreoviridae*, alongside sequences from the newly suggested species, *Cardoreovirus callinectes*. Bootstrap support with 100 replicates is shown above the branches. The proposed new species is denoted with a red star, showing its position within the phylogeny.

