

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:**  | 2024.005.M.Cardoreovirus\_1nsp  |

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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 - |  |

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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**

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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:**  |
| 2024.005.M.Cardoreovirus\_1nsp.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*: *Cardoreovirus* genus*Description of current taxonomy*: The genus *Cardoreovirus* currently has only one species of *Cardoreovirus eriocheiris* whose exemplar member is Eirocheir sinensis reovirus (EsRV).*Proposed* *taxonomic change(s):* A new species (*Cardoreovirus callinectes*) belonging to the *Cardoreovirus* genus should be established.*Justification*: The exemplar virus (Callinectes sapidus reovirus 2, CsRV2) of the proposed new species – *Cardoreovirus callinectes* – exhibits amino acid sequence similarities ranging from 46% to 79% for segments 1-12 compared to EsRV in the established species - *Cardoreovirus eriocheiris*. The maximum likelihood phylogenetic tree indicates that CsRV2 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 (*Cardoreovirus callinectes*) 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*: Callinectes sapidus reovirus 2 (CsRV2 isolate BR8), the exemplar virus of 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, a virus very similar to CsRV2 (isolate BR37) was also detected in *Callinectes danae* specimens in Paraná, Brazil (2). Its electrophoretic genome organization closely resembles that of EsRV from *Eriocheir sinensis* (3), exhibiting a pattern of 3/4/2/3 (4). The nearly complete genome sequence of the two isolates of *Cardoreovirus callinectes*, encompassing complete ORFs but missing most 5’ and 3’-terminal non-coding sequences, measures approximately 21 kbp (Table 1) (1). Two CsRV2 isolates from the two hosts, *C. sapidus* and *C. danae* share high amino acid sequence similarity (>99%) between their 12 pairs of homologous proteins~~. viral strains identified from the two hosts,~~ *~~C. sapidus~~* ~~and~~ *~~C. danae~~* ~~for all 12 segments~~ (1, 2). However, when compared to the exemplar member (EsRV) of 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), strongly supporting our proposal ~~suggesting they are different species~~. The maximum likelihood phylogenetic tree reveals that *~~Cardoreovirus callinectes~~*CsRV2 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:**  |

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**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 #** |
| 123456789101112 | 374230242807193616791631153111861062923798790 | VP1VP2VP3VP4VP5AVP5BVP6VP7VP8VP9VP10VP11VP12 | MW208677MW208678MW208679MW208680MW208681MW208682MW208683MW208684MW208685MW208686 MW208687MW208688 | EsRV905EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1EsRV1 | 7979737867464967536353616365 | Q698V5OP019112OP019113OP019114OP019115OP019116OP019117OP019118OP019119OP019120OP019121OP019122OP019123OP019124 |

**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.

