A blue and black logo

Description automatically generated

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

|  |  |  |
| --- | --- | --- |
| **Title:** | Create one new genus (*Crabreovirus*) with three new species | |
| **Code assigned:** | 2024.016M.Sedoreoviridae\_1ng\_3nsp |

|  |  |  |  |
| --- | --- | --- | --- |
| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** |  |
| 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 |

**Part 1b: Taxonomy Proposal Submission**

|  |  |  |  |
| --- | --- | --- | --- |
| **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 - |  |

|  |
| --- |
| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| *Sedoreoviridae* study group |

|  |  |  |  |
| --- | --- | --- | --- |
| **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 |  |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** | 14/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

|  |  |
| --- | --- |
| **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| W - Withdrawn |  |

|  |
| --- |
| **Comments from the Executive Committee:** |
|  |

**Part 1d: Revised Taxonomy Proposal Submission**

|  |
| --- |
| **Response of proposer:** |
|  |

|  |  |
| --- | --- |
| **Revision date:** | DD/MM/YYYY |

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

|  |
| --- |
| **Name of accompanying Excel module:** |
| 2024.016M.Sedoreoviridae\_1ng\_3nsp.xlsx |

|  |  |  |  |
| --- | --- | --- | --- |
| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

|  |  |  |
| --- | --- | --- |
| **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** |

|  |
| --- |
| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  *Sedoreoviridae* family  *Description of current taxonomy*:  *Sedoreoviridae* currently has six genera, including: *Cardoreovirus*, *Mimoreovirus*, *Orbivirus*, *Phytoreovirus*, *Rotavirus*, and *Seadornavirus*.  *Proposed* *taxonomic change(s):*  A new genus, named *Crabreovirus*, should be established in the *Sedoreoviridae* family. This new genus should include three new species, including: *Crabreovirus callinectes*, *Crabreovirus scylla* and *Crabreovirus eriocheiris*.  *Justification*: Three representative viruses of the proposed new *Crabreovirus genus* exhibit less than 20% amino acid sequence identity in VP1 when compared to virus members of other established genera within the *Sedoreoviridae* family. The maximum likelihood phylogenetic tree shows that viruses in the three proposed new species form a distinct clade from members of other *Sedoreoviridae* genera, yet remain within the same clade with each other. The phylogenetic analysis supports the classification of these three species into a new genus, *Crabreovirus*. |

|  |
| --- |
| **Text of Taxonomy proposal** |
| *Taxonomic rank(s) affected*:  *Sedoreoviridae* family  *Description of current taxonomy*:  *Sedoreoviridae* currently has six genera, including: *Cardoreovirus*, *Mimoreovirus*, *Orbivirus*, *Phytoreovirus*, *Rotavirus*, and *Seadornavirus*.  *Proposed* *taxonomic change(s)*:  A new genus, named *Crabreovirus*, should be established in the *Sedoreoviridae* family. This new genus should include three new species, including: *Crabreovirus callinectes*, *Crabreovirus scylla* and *Crabreovirus eriocheiris*.  *Demarcation criteria:*  Genus demarcation criteria:  The number of genome segments (10, 11, or 12) is in most cases characteristic of viruses within a single genus of the family *Sedoreoviridae*. Host (and vector) range and disease signs also are important indicators that help to identify viruses from different genera. Available data suggest that isolates from different genera usually have <26% amino acid identity in comparisons between their VP1, while within a single genus, identities are usually >30% (1).  Species demarcation criteria:  Since this is a newly proposed genus, there is no established criteria for species demarcation ~~exist~~ in this genus. In this proposal, we introduce the following demarcation criteria: Sequence analysis reveals that viruses from distinct species exhibit less than 86% amino acid identity in the VP1. Additionally, there are amino acid identities of <70%, <72%, <77%, <75% and <76% respectively in the more variable VP8, VP9, VP10, VP11 and VP12 proteins, respectively. These criteria are subject to changes in the future when new species are being discovered.  *Justification*:    The three species should form a new genus based on the following evidence according to the genus demarcation criteria (1): 1. All exemplar virus strains of the three species proposed here show < 20% VP1 amino acid identity to the homologs of members of the other genera in *Sedoreoviridae*. They share >84% amino acid identity in VP1 with each other, much higher than 30% as stated in the genus demarcation criteria (1). 2. The proposed new genus includes three species, all of which possess 12 genomic segments. In addition, these segments display a genomic pattern of 1/5/6 on agarose gel electrophoresis for all three viruses (2). 3. All three virus species in this new genus infect crab hosts (3, 4, 5). 4. On the maximum likelihood phylogenic tree, the clade including the proposed species is distinct from branches of other genera in *Sedoreoviridae* family.  Three new viruses were recently reported from three different crab species: Callinectes sapidus reovirus 1 (CsRV1), Scylla serrata reovirus (SsRV), and Eriocheir sinensis reovirus (ESRV). These three viruses should be classified as three different species (*Crabreovirus callinectes*, *Crabreovirus scylla*, and *Crabreovirus eriocheiris*) based on the following species demarcation criteria: 1. Although they are identified from crab host, they are identified from different crab species, CsRV1 was identified from *Callinectes sapidus* in the United States (3), while SsRVwas identified from *Scylla serrata* in China (4), and ESRVwas detected in *Eriocheir sinensis* in China(5). 2. A trans-hemisphere study of CsRV1 shows that comparisons of concatenated genomes translated into coding regions (6614 AA) had amino acid similarity from 96.8% to 99.7% (6). However, when compared among the three viruses within the *Crabreovirus* genus - they exhibit much lower amino acid sequence similarity with each other,e.g., less than 86% identity for VP1 and less than 77% for other more variable proteins such as VP8 through VP12 (3,4,5). These suggest that CsRV1, SsRV, and EsRV should be classified as different viral species. 3. The phylogenetic tree shows that the three viruses fall into different branches but remain within the same clade on the tree, which is supported by high bootstrap values (Figure 1).  This evidence supports the classification of these three viruses into a new genus, *Crabreovirus*, and recognizes them as distinct species within this genus. |

|  |
| --- |
| **References:** |
| 1. 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. 2. 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. 3. Flowers, Emily M., et al. Genome sequence analysis of CsRV1: a pathogenic reovirus that infects the blue crab Callinectes sapidus across its trans-hemispheric range. Frontiers in microbiology 7 (2016): 126. 4. Shen, Huaishun, Yuanchao Ma, and Yacheng Hu. Near-full-length genome sequence of a novel reovirus from the Chinese mitten crab, Eriocheir sinensis. Genome announcements 3.3 (2015): 10-1128. 5. Zhang, S., et al. Purification and characterization of a new reovirus from the Chinese mitten crab, Eriocheir sinensis. Journal of Fish Diseases 27.12 (2004): 687-692. 6. Zhao, M., Plough, L. V., Behringer, D. C., Bojko, J., Kough, A. S., Alper, N. W., ... & Schott, E. J. Cross-Hemispheric Genetic Diversity and Spatial Genetic Structure of Callinectes sapidus Reovirus 1 (CsRV1). Viruses, 15.2 (2023)., 563. |

<Start here>

**Table 1: Amino acid sequence identity between viruses assigned to the three proposed species – *Crabreovirus callinectes*, *Crabreovirus scylla*, *Crabreovirus eriocheiris* in VP1, VP8, VP9 and VP10.** They share less than 86% amino acid sequence similarity in VP1, less than 70% in VP8, less than 72% in VP9 and less than 77% in VP10.



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

