

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:** | Create a new species in the genus *Dinovernavirus* (*Reovirales: Spinareoviridae*) |
| **Code assigned:** | 2025.012M.Ac.v2.Spinareoviridae\_1nsp | |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Author(s), affiliation and email address(es)** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Qun | Wu | *Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China* | wuqunreceptor@163.com |  |
| Fei | Wang | Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China | wangfei@wh.iov.cn |  |
| Shunlong | Wang | Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China | wangsl2024@outlook.com |  |
| Zhiming | Yuan | Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China | yzm@wh.iov.cn |  |
| Han | Xia | Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China | hanxia@wh.iov.cn | 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:** |
| ICTV *Spinareoviridae* 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** |
| *Spinareoviridae* | 9 |  |  |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** | 23062025 |

**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 | **x** |
| 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:** |
| Ac for typographical corrections and standardized abstract formatting across all Subcommittees. Suggest using the epithet *albopictus.* |

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

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

|  |  |
| --- | --- |
| **Revision date:** | 19/08/2025 |

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

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

|  |  |
| --- | --- |
| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Dinovernavirus albopictus* | Named for the host mosquito *Aedes albopictus.* |

|  |  |  |
| --- | --- | --- |
| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
| NA |  |  |

|  |
| --- |
| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species in the family *Spinareoviridae.*  *Description of current taxonomy*:  The *Spinareoviridae* family includes nine genera: *Aquareovirus* (7 species), *Coltivirus* (5 specie), *Cypovirus* (16 species), *Dinovernavirus* (1 species), *Fijivirus* (9 species), *Idnoreovirus* (5 species), *Mycoreovirus* (3 species), *Orthoreovirus* (10 species), *Oryzavirus* (2 species).  *Proposed* *taxonomic change(s):*  We propose the creation of one new species in the genus *Dinovernavirus*.  *Justification*:  The proposed species is distinct based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparisons to established species in the family *Spinareoviridae*. |

|  |
| --- |
| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Species in the family *Spinareoviridae.*  *Description of current taxonomy*:  The *Spinareoviridae* family includes nine genera: *Aquareovirus* (7 species), *Coltivirus* (5 specie), *Cypovirus* (16 species), *Dinovernavirus* (1 species), *Fijivirus* (9 species), *Idnoreovirus* (5 species), *Mycoreovirus* (3 species), *Orthoreovirus* (10 species), *Oryzavirus* (2 species).  *Proposed* *taxonomic change(s)*:  We propose the creation of one new species in the genus *Dinovernavirus*.  *Demarcation criteria:*  Species are proposed for classification according to the established classification criteria:   * Nucleotide and amino acid sequence analysis (viruses within different species should have low levels of sequence similarity between cognate genome segments). * Serological comparisons of antigens or antibodies using either polyclonal antisera or monoclonal antibodies against conserved antigens. Methods used may include ELISA, complement fixation, and agar gel immunodiffusion. Closely related isolates and serotypes generally belong to the same species. * Analysis of electropherotype by agarose gel electrophoresis (AGE) but not by polyacrylamide gel electrophoresis (PAGE). Virus isolates within the same species will show a relatively uniform electropherotype. However, a major deletion/insertion event may sometimes result in two distinct electropherotypes within a single species, and apparent similarities can exist between more closely related species. * Identification of the conserved terminal regions of the genome segments. These are usually conserved across all segments within a species, although some closely related species also can have identical terminal sequences of at least some segments.   *Justification*:  The new species *Dinovernavirus albopictus,* is proposed to include Aedes albopictus reovirus (AARV) isolate HN-SY22-Ae03. The virus was originally isolated from field collected *Aedes albopictus* mosquitoes in 2022, Hainan, China, which shows non-enveloped spherical virions with turrets, approximately 49-50 nm in diameter (Figure 1).  The virus genome consists of nine linear segments of dsRNA, with segments coding sequences ranging from 3.6kb to 0.8 kb (Table1), analysis of genomic RNAs by 1.0% Agarose shows a 5-1-2-1 migration pattern (electropherotype) (Figure 2).  The phylogenetic tree based on RdRp amino acid sequences indicated AARV grouped into the genus *Dinovernavirus* (Figure 3). The RdRp (segment 2) of this virus has 66.1% amino acid identity with that of the RdRp of Aedes pseudoscutellaris reovirus (*Dinovernavirus aedis*) and 65.4% identity with Fako virus (*Dinovernavirus aedis*) (Table 1). |

|  |
| --- |
| **References:** |
| 1. Attoui H, Fang Q, Jaafar FM, Cantaloube JF, Biagini P, de Micco P, et al. Common evolutionary origin of aquareoviruses and orthoreoviruses revealed by genome characterization of Golden shiner reovirus, Grass carp reovirus, Striped bass reovirus and golden ide reovirus (genus Aquareovirus, family Reoviridae). The Journal of general virology. 2002;83(Pt 8):1941-51. https://doi.org/10.1099/0022-1317-83-8-1941.  2. Attoui H, Mohd Jaafar F, Belhouchet M, Biagini P, Cantaloube JF, de Micco P, et al. Expansion of family Reoviridae to include nine-segmented dsRNA viruses: isolation and characterization of a new virus designated Aedes pseudoscutellaris reovirus assigned to a proposed genus (Dinovernavirus). Virology. 2005;343(2):212-23. https://doi.org/10.1016/j.virol.2005.08.028.  3. Auguste AJ, Kaelber JT, Fokam EB, Guzman H, Carrington CV, Erasmus JH, et al. A newly isolated reovirus has the simplest genomic and structural organization of any reovirus. Journal of virology. 2015;89(1):676-87. |

|  |  |
| --- | --- |
| **Accompanying files:** | |
| **Filename** | **Description of contents** |
|  |  |
|  |  |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Tables, Figures:**    Figure 1. The electron micrographs of purified Aedes albopictus reovirus particles.    Figure 2. Agarose and PAGE electrophoretic profiles of Aedes albopictus reovirus genome. (A) 1.0% agarose in TAE buffer running 2h with100V; (B) 1.0% agarose in TAE buffer running 3h with75V; (C) 4-20% polyacrylamide gel electrophoresis running 7h with 25mA.    Figure 3. Phylogenetic tree based on RdRP for family *Spinareoviridae*. Maximum likelihood tree constructed using the amino acid sequence of the putative RdRP of representative viruses. Tibet orbivirus was used as an outgroup.  Table 1. Nucleotide and Amino acid identities between AARV and Fako virus and Aedes pseudoscutellaris reovirus   |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | AARV | | Fako virus | | | | Aedes pseudoscutellaris reovirus | | | | | Nucleotide | | Nucleotide | | Amino acid | | Nucleotide | | Amino acid | | | Segment | length | Length  (bp) | Identity (%) | Length（aa） | Identity (%) | Length  (bp) | Identity (%) | Length  (aa) | Identity (%) | | 01 | 3826 | 3819 | 56.1 | 1189 | 44.6 | 3817 | 56.1 | 1189 | 44.2 | | 02 | 3716 | 3752 | 68.1 | 1233 | 65.4 | 3752 | 68.7 | 1233 | 66.1 | | 03 | 3790 | 3730 | 63.5 | 1202 | 57.2 | 3732 | 63.4 | 1202 | 56.9 | | 04 | 3381 | 3403 | 53.3 | 1011 | 35.4 | 3403 | 53.3 | 1003 | 34.0 | | 05 | 3237 | 3227 | 66.5 | 1056 | 61.5 | 3227 | 66.6 | 1056 | 61.6 | | 06 | 1782 | 1778 | 63.0 | 540 | 57.2 | 1775 | 63.2 | 540 | 57.2 | | 07 | 1130 | 1170 | 56.0 | 348 | 45.5 | 1171 | 55.6 | 348 | 46.1 | | 08 | 1174 | 1151 | 54.2 | 345 | 23.5 | 1151 | 57.0 | 345 | 20.1 | | 09 | 1141 | 1140 | 59.3 | 278 | 48.0 | 1147 | 57.9 | 278 | 47.7 | |

<Start here>