

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:**  | Create five new genera and five new species in the family *Xinmoviridae*, order: *Mononegavirales* |
| **Code assigned:**  | 2025.011M.Ac.v3.Xinmoviridae\_5ng\_5nsp |

|  |
| --- |
| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email**  | **Corr. author(s)**  |
| Stephen R | Sharpe | Health and Biosecurity, CSIRO, East Geelong, Australia | stephen.sharpe@csiro.au | X |
| Binit | Lamichhane | Department of Microbiology, PathWest Laboratory Medicine WA, Nedlands, Australia | binit.lamichhane@health.wa.gov.au |  |
| Luis | Hernández-Pelegrín | Department of Genetics, University of Valencia, Valencia, Spain | luis.hernandez.pelegrin@gmail.com |  |

**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 *Xinmoviridae* 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** |
| ICTV *Xinmoviridae* Study Group | 3 |  |  |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** | 09/06/2025 |

**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| W - Withdrawn |  |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 minor typographical edits and consistent Abstract format across all Subcommittees |

**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** |
| ***Actovirus hainanense*** | From *Bactrocera dorsalis* in which Bactrocera dorsalis borna-like virus was discovered by HTS. The species epithet hainanense refers to Hainan Province, China, where the laboratory colony was originally collected. |
| ***Yahinvirus chinaense*** | From *Oxya chinensis* in which Guiyang xinmovirus 1 was discovered by HTS. The species epithet chinaense refers to China, the sampling location. |
| ***Hyatvirus russiaense*** | From *Haematopota* sampled in the Medvezhye region, in which Medvezhye haematopota xinmo-like virus was discovered by HTS. The species epithet russiaense refers to Russia, the sampling location. |
| ***Opavirus hayense*** | From *Inopus flavus* in which Soldier fly-associated anphevirus was discovered by HTS. The species epithet hayense refers to Hay Point, Australia, the sampling location. |
| ***Omyavirus bahiaense*** | From *Forcipomyia taiwana* in which unclassified forcipomyiae 1 virus was discovered by bioinformatic analysis of HTS data. The species epithet bahiaense refers to the Bahia region, Brazil, the sampling location. |

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

|  |
| --- |
| **Abstract of Taxonomy Proposal:**  |
| ***Taxonomic rank(s) affected***: This affects the genera and species ranks ofthe family *Xinmoviridae*.***Description of current taxonomy***: The family *Xinmoviridae* is currently made up of 22 genera and 25 species.***Proposed* *taxonomic change(s)****:* We propose the demarcation of 5 new genera and 5 new species within the family *Xinmoviridae*.***Justification***: We have based this proposal on the current demarcation criterion for species: Members of different species within a genus have RdRP amino acid identities of 66% or less, and genus: Members of different genera have RdRP amino acid identities of 60% or less.Thus, based on the phylogenetic analysis shown in **Figure 1** and BLAST match data in **Table 1**, we propose the demarcation of 5 new genera and 5 new species. |

|  |
| --- |
| **Text of Taxonomy proposal:**  |
| ***Taxonomic rank(s) affected***: The proposed addition of five new genera and five new species in the *Xinmoviridae* family of the haploviricotine, order *Mononegavirales*. Species and genera are proposed for classification according to the established classification criteria:-A coding/near complete genome.-At least 20% amino acid identity of the RNA-directed RNA polymerase (RdRP).The above criteria are similar to those used for other mononegaviral families. ***Description of current taxonomy***: Within the family *Xinmoviridae*, there are currently 22 genera and 25 species. ***Proposed* *taxonomic change(s)***: We propose the demarcation of 5 new genera and 5 new species within the family *Xinmoviridae*. The new genera are proposed to be named ***Actovirus, Yahinvirus, Hyatvirus, Opavirus,* and *Omyavirus.* The new species are proposed to be named *Actovirus hainanense, Yahinvirus chinaense, Hyatvirus russiaense, Opavirus hayense,* and *Omyavirus bahiaense.***Etymologies:***Actovirus hainanense***: From *Bactrocera dorsalis* in which Bactrocera dorsalis borna-like virus was discovered by HTS. The species epithet hainanense refers to Hainan Province, China, where the laboratory colony was originally collected.***Yahinvirus chinaense***: From *Oxya chinensis* in which Guiyang xinmovirus 1 was discovered by HTS. The species epithet chinaense refers to China, the sampling location.***Hyatvirus russiaense***: From *Haematopota* sampled in the Medvezhye region, in which Medvezhye haematopota xinmo-like virus was discovered by HTS. The species epithet russiaense refers to Russia, the sampling location***Opavirus hayense***: From *Inopus flavus* in which Soldier fly-associated anphevirus was discovered by HTS. The species epithet hayense refers to Hay Point, Australia, the sampling location.***Omyavirus bahiaense***: From *Forcipomyia taiwana* in which unclassified forcipomyiae 1 virus was discovered by bioinformatic analysis of HTS data. The species epithet bahiaense refers to the Bahia region, Brazil, the sampling location.***Demarcation criteria****:* Species demarcation - Members of different species within a genus have RdRP amino acid identities of 66% or less.Genus demarcation – Members of different genera have RdRP amino acid identities of 60% or less.*Sharpe, S. and Paraskevopoulou, S., 2023. ICTV Virus Taxonomy Profile: Xinmoviridae 2023. Journal of General Virology, 104(10), p.001906.****Justification***:  We have based this proposal on the current demarcation criterion for species: Members of different species within a genus have RdRP amino acid identities of 66% or less, and genus: Members of different genera have RdRP amino acid identities of 60% or less.Thus, based on the phylogenetic analysis shown in **Figure 1** and BLASTP match data in **Table 1**, we propose the demarcation of 5 new genera and 5 new species. |

|  |
| --- |
| **References:**  |
| **de Santana, S.F., Santos, V.C., Lopes, Í.S., Porto, J.A.M., Mora-Ocampo, I.Y., Sodré, G.A., Pirovani, C.P., Góes-Neto, A., Pacheco, L.G.C., Fonseca, P.L.C. and Costa, M.A., 2023.** Mining public data to investigate the virome of neglected pollinators and other floral visitors. *Viruses*, *15*(9), p.1850.**Divekar, G., Colmant, A.M., Furlong, M.J. and Etebari, K., 2024.** Transcriptome analysis reveals a diverse range of novel viruses in Australian sugarcane soldier fly (Inopus flavus) larvae. *Viruses*, *16*(4), p.516.**Edgar, R. C. (2022).** Muscle5: High-accuracy alignment ensembles enable unbiased assessments of sequence homology and phylogeny. *Nat Commun* **13**, 6968.**Litov, A. G., Belova, O. A., Kholodilov, I. S., Kalyanova, A. S., Gadzhikurbanov, M. N., Rogova, A. A., Gmyl, L. V., & Karganova, G. G. (2023).** Viromes of Tabanids from Russia. *Viruses*, *15*(12), 2368. **Sharpe, S. and Paraskevopoulou, S., 2023.** ICTV Virus Taxonomy Profile: *Xinmoviridae* 2023. *Journal of General Virology*, *104*(10), p.001906.**Tamura, K., Stecher, G. & Kumar, S. (2021).** MEGA11: Molecular Evolutionary Genetics Analysis Version 11. *Mol Biol Evol* **38**, 3022-3027. **Zhang, W., Gu, Q., Niu, J. and Wang, J.J., 2020.** The RNA virome and its dynamics in an invasive fruit fly, Bactrocera dorsalis, imply interactions between host and viruses. *Microbial ecology*, *80*(2), pp.423-434. |

|  |
| --- |
| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| **2025.011M.N.v2.Xinmoviridae\_5ng\_5nsp\_Table 1** | Details of the proposed new virus species and BLASTP search results for the amino acid sequences of the RdRP region. |
| **2025.011M.N.v2.Xinmoviridae\_5ng\_5nsp\_Figure 1** | Phylogenetic tree of the RdRP amino acid sequences of current exemplar members of *Xinmoviridae* (black)with the proposed new species’ virus names (blue), the virus used as the outgroup (red) was Wǔchāng romanomermis nematode virus 2 (family *Lispiviridae*), three viruses with partially complete genomes (grey), and three related viruses shown not to be part of the family *Xinmoviridae* (orange). Sequences were aligned using MUSCLE v5.2 (Edgar 2022) and a neighbour-joining tree of amino acid distances was created using the poisson correction and 1000 bootstraps within MEGA11 (Tamura et al., 2021).  |

|  |
| --- |
| **Tables, Figures:**  |

<Start here>