

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:**  | Move free-floating negarnaviricot family *Tosoviridae* into bunyaviricete order *Hareavirales* |
| **Code assigned:**  | 2024.018M.Ac.v2.Tosoviridae\_move |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)**  |
| Kuhn JH | Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, Maryland, USA | kuhnjens@mail.nih.gov |  |
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| Krupovic M | Institut Pasteur, Université Paris Cité, Archaeal Virology Unit, Paris, France | mart.krupovic@pasteur.fr |  |
| Wolf Y | National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Maryland, USA | wolf@ncbi.nlm.nih.gov | X |

**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 | **X** |
| 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:**  |
| ICTV *Negarnaviricota* 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** |
| ICTV *Negarnaviricota* Study Group | 4 | 0 | 0 |

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| **Submission date:** |  21/06/2024 |

**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 | **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 |  |

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| **Comments from the Executive Committee:** |
| Better explain how the new tree differs from the previous tree and, if possible, add support values. |

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

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| **Response of proposer:**  |
| Explanation and support values added, supplemental tree file included. |

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| **Revision date:** |  16/08/2024 |

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

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| **Name of accompanying Excel module:**  |
| 2024.018M.Ac.v2.Tosoviridae\_move.xlsx |

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| **Taxonomic changes proposed:**  |
| Establish new taxon |  | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon | **X** | 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*: Family (*Tosoviridae*)*Description of current taxonomy*: *Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Tosoviridae**Proposed* *taxonomic change(s):* Move family (*Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Polyploviricotina*: *Bunyaviricetes*: *Hareavirales*: *Tosoviridae*)*Justification*: Updated RdRp phylogeny unambiguously groups tosovirids with hareavirals (sister to hareaviral families *Nairoviridae* and *Wupedeviridae*) |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Family (*Tosoviridae*)*Description of current taxonomy*: *Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Tosoviridae**Proposed* *taxonomic change(s)*: Move family (*Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Polyploviricotina*: *Bunyaviricetes*: *Hareavirales*: *Tosoviridae*)*Demarcation criteria:* Negarnaviricota megataxonomy is determined by RNA-directed RNA polymerase (RdRp) phylogeny/clustering.*Justification*: Tosovirids (free-floating negarnaviricot family *Tosovirdae*) are bisgegmented negative-sense RNA viruses with a genomic organization identical to those of arenavirids (*Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Polyploviricotina*: *Bunyaviricetes*: *Hareavirales*) ([1](#_ENREF_1)). However, after their discovery, global RdRp trees failed to unambiguously assign tosovirids to either of the subphyla of *Negarnaviricota* (*Haploviricotina* and *Polyploviricotina*) ([1](#_ENREF_1)), and hence the family was assigned “free-floating” (unassigned) status ([2](#_ENREF_2), [3](#_ENREF_3)). For ([1](#_ENREF_1)), all 1,147 negarnaviricot RdRp sequences from the metagenomic set that was published a few months later in ([4](#_ENREF_4)) was supplemented with the only tosovirid (turle fraservirus 1) sequence and a few other metagenome-derived sequences from ([1](#_ENREF_1)). A diverse subset of 259 RdRps was then selected for tree construction using IQ-tree (Figure 10 in ([1](#_ENREF_1))). An updated, arguably superior, RdRp phylogeny, constructed using IQ-tree using 1,144 negarnaviricot full-length RdRP core sequences from the ICTV\_Master\_Species\_List\_2023\_MSL39.v1 combined with their associated species exemplars (VMR\_MSL38\_v3) , unambiguously groups tosovirids with hareavirals (sister to hareaviral families *Nairoviridae* and *Wupedeviridae*, the families most closely related to arenavirids; Figure 1). |

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| **References:**  |
|  1. Waltzek TB, Stacy BA, Ossiboff RJ, Stacy NI, Fraser WA, Yan A, Mohan S, Koonin EV, Wolf YI, Rodrigues TCS, Viadanna PHO, Subramaniam K, Popov VL, Guzman-Vargas V, Shender LA.2022. A novel group of negative-sense RNA viruses associated with epizootics in managed and free-ranging freshwater turtles in Florida, USA. PLoS Pathog 18:e1010258.2. Kuhn JH, Abe J, Adkins S, Alkhovsky SV, Avšič-Županc T, Ayllón MA, Bahl J, Balkema-Buschmann A, Ballinger MJ, Baranwal VK, Beer M, Bejerman N, Bergeron, Biedenkopf N, Blair CD, Blasdell KR, Blouin AG, Bradfute SB, Briese T, Brown PA, Buchholz UJ, Buchmeier MJ, Bukreyev A, Burt F, Büttner C, Calisher CH, Cao M, Casas I, Chandran K, CharrelI RN, Kumar K, Chaturvedi, Chooi KM, Crane A, Bó ED, Torre JCdl, Souza WMd, Swart RLd, Debat H, Dheilly NM, Paola ND, Serio FD, Dietzgen RG, Digiaro M, Drexler JF, Duprex WP, Dürrwald R, Easton AJ, Elbeaino T, Ergünay K, et al.2023. Annual (2023) taxonomic update of RNA-directed RNA polymerase-encoding negative-sense RNA viruses (realm *Riboviria*: kingdom *Orthornavirae*: phylum *Negarnaviricota*). J Gen Virol 104:001864.3. Zerbini FM, Siddell SG, Lefkowitz EJ, Mushegian AR, Adriaenssens EM, Alfenas-Zerbini P, Dempsey DM, Dutilh BE, García ML, Hendrickson RC, Junglen S, Krupovic M, Kuhn JH, Lambert AJ, Łobocka M, Oksanen HM, Robertson DL, Rubino L, Sabanadzovic S, Simmonds P, Smith DB, Suzuki N, Van Dooerslaer K, Vandamme A-M, Varsani A.2023. Changes to virus taxonomy and the ICTV Statutes ratified by the International Committee on Taxonomy of Viruses (2023). Arch Virol 168:175.4. Neri U, Wolf YI, Roux S, Camargo AP, Lee B, Kazlauskas D, Chen IM, Ivanova N, Zeigler Allen L, Paez-Espino D, Bryant DA, Bhaya D, RNA Virus Discovery Consortium, Krupovic M, Dolja VV, Kyrpides NC, Koonin EV, Gophna U.2022. Expansion of the global RNA virome reveals diverse clades of bacteriophages. Cell 185:4023-4037.e18.  |

Figure 1. Global phylogeny of negarnaviricot RdRps.

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1,144 full-length RNA-directed RNA polymerase (RdRp) cores of *Negarnaviricota* exemplar genomes per the ICTV\_Master\_Species\_List\_2023\_MSL39.v1 combined with their associated species exemplars (VMR\_MSL38\_v3) were extracted and assigned to their current 36 family ranks. Then, the consensus sequences were aligned, expanded, and filtered (removing columns with too many gaps or low homogeneity) to build the tree. Both FastTree and IQ-Tree agree in that *Bunyaviricetes* (according to MSL39.v1) are currently paraphyletic with respect to *Tosoviridae* (orange), and that *Tosoviridae* should be included in bunyaviricete order *Hareavirales*. Branch support values can be retrieved via the attached Supplementary .tre file.