

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:**  | Create ten new species in genus *Shilevirus* (*Bunyaviricetes*: *Hareavirales*: *Leishbuviridae*) |
| **Code assigned:**  | 2024.017M.N.v1.Shilevirus\_10nsp |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)**  |
| Yurchenko, V | University of Ostrava, Ostrava, Czechia | Vyacheslav.Yurchenko@osu.cz  | X |
| Kuhn, JH | NIH/NIAID/DCR/Integrated Research Facility at Fort Detrick, Frederick, Maryland, USA | kuhnjens@mail.nih.gov  |  |
| Kostygov, AYu | University of Ostrava, Ostrava, Czechia | Alexej.Kostygov@osu.cz  |  |

**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:** |
| None. There is currently no Study Group for family *Leishbuviridae*. |

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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** |
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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 |  |
| 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| W - Withdrawn |  |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:**  |
| 2024.017M.N.v1.Shilevirus\_10nsp.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*: leishbuvirid genus *Shilevirus**Description of current taxonomy*: 1 species (*Shilevirus leptomonadis*)*Proposed* *taxonomic change(s):* add 10 new species*Justification*: Discovery of novel shileviruses in various hosts from various habitats with sufficient genetic divergence. |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: leishbuvirid genus Shilevirus*Description of current taxonomy*: 1 species (*Shilevirus leptomonadis*)*Proposed* *taxonomic change(s)*: add 10 new species*Demarcation criteria:* None established at the moment. Proposed to be “Less than 90% identity in the complete amino acid sequence of the L protein”. *Justification*: Family *Leishbuviridae* (*Bunyaviricetes*: *Hareavirales*) currently includes a single genus with a single species (*Shilevirus* *leptomonadis*) ([1](#_ENREF_1)) for Leptomonas moramango virus (LEPMV), a virus infecting a trypanosomatid protist (*Leptomonas moramango* Yurchenko et al., 2014) ([2](#_ENREF_2)). Numerous related viruses have been discovered in diverse protists ([2-14](#_ENREF_2)), of which at least 10 are associated with coding-complete genome sequences ([1-7](#_ENREF_1)), the minimum requirement for classification:* Blechmonas luni leishbunyavirus 1 (BlunLBV1);
* Blechomonas ayalai leishbunyavirus 1 (BayaLBV1);
* Blechomonas maslovi leishbunyavirus 1 (BmasLBV1);
* Crithidia abscondita leishbunyavirus (CabsLBV1);
* Crithidia bombi leishbuvirus 1 (CbomLBV1);
* Crithidia otongatchiensis leishbunyavirus (CotoLBV1);
* Leptomonas pyrrhocoris leishbunyavirus 3 (LeppyrLBV3);
* Leptomonas pyrrhocoris leishbunyavirus 4 (LeppyrLBV4);
* Leishmania martiniquensis leishbunyavirus 1 (LmarLBV1); and
* Leptomonas moramango leishbunyavirus isolate LepmorLBV1b (LmorLBV1b).

We propose to classify these 10 viruses into 10 novel shilevirus species based on their relationships in RNA-directed RNA polymerase (RdRp) phylogeny (Figure 1) and overall genomic sequence divergence. |

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| **References:**  |
|  1. Adkins S, Brown K, de la Torre JC, Digiaro M, Hughes HR, Junglen S, Lambert AJ, Maes P, Marklewitz M, Palacios G, Sasaya T, Turina M, Zhang Y-Z, Kuhn JH.2023. ICTV virus taxonomy profile: *Leishbuviridae* 2023. J Gen Virol 104:001934.2. Akopyants NS, Lye L-F, Dobson DE, Lukeš J, Beverley SM.2016. A novel bunyavirus-like virus of trypanosomatid protist parasites. Genome Announc 4:e00715-16.3. 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.e18.4. Grybchuk D, Kostygov AY, Macedo DH, Votýpka J, Lukeš J, Yurchenko V.2018. RNA viruses in *Blechomonas* (Trypanosomatidae) and evolution of *Leishmaniavirus*. mBio 9:e01932-18.5. Grybchuk D, Akopyants NS, Kostygov AY, Konovalovas A, Lye LF, Dobson DE, Zangger H, Fasel N, Butenko A, Frolov AO, Votýpka J, d'Avila-Levy CM, Kulich P, Moravcová J, Plevka P, Rogozin IB, Serva S, Lukeš J, Beverley SM, Yurchenko V.2018. Viral discovery and diversity in trypanosomatid protozoa with a focus on relatives of the human parasite Leishmania. Proc Natl Acad Sci U S A 115:E506-e515.6. Klocek D, Grybchuk D, Macedo DH, Galan A, Votýpka J, Schmid-Hempel R, Schmid-Hempel P, Yurchenko V, Kostygov AY.2023. RNA viruses of *Crithidia bombi*, a parasite of bumblebees. J Invertebr Pathol 201:107991.7. Macedo DH, Grybchuk D, Režnarová J, Votýpka J, Klocek D, Yurchenko T, Ševčík J, Magri A, Dolinská MU, Záhonová K, Lukeš J, Servienė E, Jászayová A, Serva S, Malysheva MN, Frolov AO, Yurchenko V, Kostygov AY.2023. Diversity of RNA viruses in the cosmopolitan monoxenous trypanosomatid *Leptomonas pyrrhocoris*. BMC Biol 21:191.8. Remnant EJ, Shi M, Buchmann G, Blacquière T, Holmes EC, Beekman M, Ashe A.2017. A diverse range of novel RNA viruses in geographically distinct honey bee populations. J Virol 91:e00158-17.9. Zhang W, Zhang Y-C, Wang Z-G, Gu Q-Y, Niu J-Z, Wang J-J.2022. The diversity of viral community in invasive fruit flies (*Bactrocera* and *Zeugodacus*) revealed by meta-transcriptomics. Microb Ecol 83:739-752.10. Mahar JE, Shi M, Hall RN, Strive T, Holmes EC.2020. Comparative analysis of RNA virome composition in rabbits and associated ectoparasites. J Virol 94:e02119-19.11. Ortiz-Baez AS, Holmes EC, Charon J, Pettersson JH-O, Hesson JC.2022. Meta-transcriptomics reveals potential virus transfer between *Aedes communis* mosquitoes and their parasitic water mites. Virus Evol 8:veac090.12. Li C-X, Shi M, Tian J-H, Lin X-D, Kang Y-J, Chen L-J, Qin X-C, Xu J, Holmes EC, Zhang Y-Z.2015. Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. Elife 4:e05378.13. Shi M, Lin X-D, Tian J-H, Chen L-J, Chen X, Li CX, Qin X-C, Li J, Cao J-P, Eden J-S, Buchmann J, Wang W, Xu J, Holmes EC, Zhang Y-Z.2016. Redefining the invertebrate RNA virosphere. Nature 540:539-543.14. Grybchuk D, Macedo DH, Kleschenko Y, Kraeva N, Lukashev AN, Bates PA, Kulich P, Leštinová T, Volf P, Kostygov AY, Yurchenko V.2020. The first non-LRV RNA virus in *Leishmania*. Viruses 12:168.  |

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| **Tables, Figures:**  |



Maximum likelihood phylogenetic tree of *Leishbuviridae* based on amino acid sequences of RDRP, rooted using *Phenuiviridae* as outgroup. Posterior probabilities and bootstrap supports are shown at branches, their respective values below 0.5 and 50 are omitted or replaced with dashes. Branches with absolute (1/100) supports are marked with black circles. Scale bar corresponds to the number of substitutions per site (6).