

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create five new genera and eleven new species in the family *Lispiviridae* (*Mononegavirales*) | |
| **Code assigned:** | 2024.008M.Ac.v2.Lispiviridae\_5ngen\_11nsp |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** |
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**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 |  |
| 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:** |
| *Lispiviridae* 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** |
| *Lispiviridae* Study Group | 3 | 0 | 0 |
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| **Submission date:** | 05/06/2024 |

**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| W - Withdrawn |  |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:** |
| Please check for completeness of genome. |

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

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| **Response of proposer:** |
| Incomplete genomes have been removed. |

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| **Revision date:** | 04/07/2024 |

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

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| **Name of accompanying Excel module:** |
| 2024.008M.Ac.v2.Lispiviridae\_5ngen\_11nsp.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*:  Mononegaviral family *Lispiviridae*.  *Description of current taxonomy*:  Currently, the family *Lispiviridae* includes 25 genera and 34 species according to ICTV Master Species List (MSL39.v3).  *Proposed* *taxonomic change(s):*  We propose the creation of 5 new genera and 11 new species to be included in mononegaviral family *Lispiviridae*.  *Justification*:  Genus (and species) demarcation is proposed to be based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparisons similar to established genus/species demarcation criteria for other mononegaviral families. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Mononegaviral family *Lispiviridae*.  *Description of current taxonomy*:  Currently, the family *Lispiviridae* includes 25 genera and 34 species according to ICTV Master Species List (MSL39.v3).  *Proposed* *taxonomic change(s)*:  We propose the creation of 5 new genera and 11 new species to be included in mononegaviral family *Lispiviridae*.  *Demarcation criteria:*  Species and genera are proposed for classification according to the established classification criteria:  • a coding-complete RNA-directed RNA polymerase (RdRp)  • at least 20% amino acid identity of the RdRp sequence  The above criteria are similar to those used for other mononegaviral families.  Accordingly, the lispivirid genus demarcation criterion requires a coding-complete RdRp with amino acid identity between 20-49%, and the lispivirid species demarcation criterion a coding-complete RdRp with amino acid identity 50%-85%. Thus, based on amino acid identity and the present phylogenetic analysis shown in **Figure 1**, we propose the demarcation of 5 new genera and 11 new species.  *Justification*:  Etymologies:  • ***Artemvirus bsafialis*** for brine shrimp arlivirus 1. The virus was discovered by HTS in brine shrimps (*Artemia franciscana*, family: Artemiidae) in Kenya. The RdRp of this virus has 28% amino acid identity with that of the RdRp of Guìyáng lispivirus 2 (*Aranbvirus guiyangense*). The genus is named after **Artem**iidae, and the species is named using virus name brine shrimp arlivirus 1 (first) in an epithet form “bsafialis”.  • ***Artemvirus bsasecalis*** for brine shrimp arlivirus 2. The virus was discovered by HTS in brine shrimps. The RdRp of this virus has 55% amino acid identity with that of the RdRp of brine shrimp arlivirus 1 (*Artemvirus bsafialis*). The species is named using virus name brine shrimp arlivirus 2 (second) in an epithet form “bsasecalis”.  • ***Artemvirus bsathalis*** for brine shrimp arlivirus 3. The virus was discovered by HTS in brine shrimps. The RdRp of this virus has 63% amino acid identity with that of the RdRp of brine shrimp arlivirus 1 (*Artemvirus bsafialis*). The species is named using virus name brine shrimp arlivirus 3 (three) in an epithet form “bsathalis”.  • ***Artemvirus bsafalis*** for brine shrimp arlivirus 4. The virus was discovered by HTS in brine shrimps. The RdRp of this virus has 67% amino acid identity with that of the RdRp of brine shrimp arlivirus 3 (*Artemvirus bsathalis*). The species is named using virus name brine shrimp arlivirus 4 (four) in an epithet form “bsafalis”.  • ***Artemvirus bsafivalis*** for brine shrimp arlivirus 5. The virus was discovered by HTS in brine shrimps. The RdRp of this virus has 67% amino acid identity with that of the RdRp of brine shrimp arlivirus 2 (*Artemvirus bsasecalis*). The species is named using virus name brine shrimp arlivirus 5 (five) in an epithet form “bsafivalis”.  • ***Artemvirus bsasialis*** for brine shrimp arlivirus 6. The virus was discovered by HTS in brine shrimps. The RdRp of this virus has 67% amino acid identity with that of the RdRp of brine shrimp arlivirus 1 (*Artemvirus bsafialis*). The species is named using virus name brine shrimp arlivirus 6 (six) in an epithet form “bsasialis”.  • ***Artemvirus bsaeighalis*** for brine shrimp arlivirus 8. The virus was discovered by HTS in brine shrimps. The RdRp of this virus has 67% amino acid identity with that of the RdRp of brine shrimp arlivirus 2 (*Artemvirus bsasecalis*). The species is named using virus name brine shrimp arlivirus (eight) in an epithet form “bsaeighalis”.  • ***Canmovirus mahaense*** for Pedras lispivirus. The virus was discovered by HTS in canopy mosquitoes (*Sabethes quasicyaneus*, family: Culicidae) in Maranhao, Brazil. The RdRp of this virus has 30% amino acid identity with that of the RdRp of Cát Tiên Hospitalitermes lispi-like virus (*Copasivirus cattienense*). The genus is named after canopy mosquitoes, and the species is named using its discovered geography location Maranhao in an epithet form “mahaense”.  • ***Coroavirus germense*** for Blattodean arli-related virus OKIAV101. The virus was discovered by HTS in cockroach (*Polyphaga aegyptiaca*) in Germany. The RdRp of this virus has 48% amino acid identity with that of the RdRp of Hángzhōu acrida cinerea lispivirus 1 (*Acridvirus hangzhouense*). The genus is named after **co**ck**roa**ch, and the species is named using its discovered geography location Germany in an epithet form “germense”.  • ***Robevirus hanzense*** for Hangzhou lispivirus 1. The virus was discovered by HTS in rove beetles (*Paederus fuscipes*) in Hángzhōu, China. The RdRp of this virus has 48% amino acid identity with that of the RdRp of hemipteran arli-related virus OKIAV95 (*Xenophyvirus mathesonense*). The genus is named after **ro**ve **be**etles, and the species is named using its discovered geography location **Hán**g**z**hōu in an epithet form “hanzense”.  • ***Weflthvirus itaense*** for Frankliniella occidentalis associated mononegavirales virus 1. The virus was discovered by HTS in western flower thrips (*Frankliniella occidentalis*) in Italy. The RdRp of this virus has 32% amino acid identity with that of the RdRp of Guìyáng lispivirus 1 (*Aranavirus guiyangense*). The genus is named after **we**stern **f**lower **t**hrips, and the species is named using its discovered geography location **Ita**ly in an epithet form “itaense”. |

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| **References:** |
| 1. Käfer S, Paraskevopoulou S, Zirkel F, Wieseke N, Donath A, Petersen M, Jones TC, Liu S, Zhou X, Middendorf M, Junglen S, Misof B, Drosten C. Re-assessing the diversity of negative strand RNA viruses in insects. PLoS Pathog. 2019, 15(12):e1008224. doi: 10.1371/journal.ppat.1008224. 2. Chen YM, Hu SJ, Lin XD, Tian JH, Lv JX, Wang MR, Luo XQ, Pei YY, Hu RX, Song ZG, Holmes EC, Zhang YZ. Host traits shape virome composition and virus transmission in wild small mammals. Cell. 2023, 186(21):4662-4675.e12. doi: 10.1016/j.cell.2023.08.029. 3. Batson J, Dudas G, Haas-Stapleton E, Kistler AL, Li LM, Logan P, Ratnasiri K, Retallack H. Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. Elife. 2021, 10:e68353. doi: 10.7554/eLife.68353. 4. Chiapello M, Bosco L, Ciuffo M, Ottati S, Salem N, Rosa C, Tavella L, Turina M. Complexity and Local Specificity of the Virome Associated with Tospovirus-Transmitting Thrips Species. J Virol. 2021, 95(21):e0059721. doi: 10.1128/JVI.00597-21. 5. Aragão CF, da Silva SP, do Nascimento BLS, da Silva FS, Nunes Neto JP, Pinheiro VCS, Cruz ACR. Shotgun Metagenomic Sequencing Reveals Virome Composition of Mosquitoes from a Transition Ecosystem of North-Northeast Brazil. Genes (Basel). 2023, 14(7):1443. doi: 10.3390/genes14071443. 6. Dong X, Li C, Wang Y, Hu T, Zhang F, Meng F, Gao M, Han X, Wang G, Qin J, Nauwynck H, Holmes EC, Sorgeloos P, Sui L, Huang J, Shi W. Diversity and connectedness of brine shrimp viruses in global hypersaline ecosystems. Sci China Life Sci. 2024, 67(1):188-203. doi: 10.1007/s11427-022-2366-8. |

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| **Tables, Figures:** |

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**Supporting evidence: Figure 1**



**Figure 1**: Phylogenetic relationships of lispivirids. The phylogenetic tree is based on a MAFFT-alignment of the RdRp amino acid sequences using the L-INS-i algorithm and was inferred using ModelTest-NG and the LG+I+G4+F model. Numbers on branch nodes represent transfer bootstrap expectation values (1,000 replicates). Proposed new lispivirid genera or species are shown in red font. The tree is rooted to the viruses of the family *Chuviridae*.