

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2022.012M*** |  |
| **Short title:** Create 7 new genera, create 11 new species (*Mononegavirales: Lispiviridae*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Lispiviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| Approved. |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Lispiviridae* Study Group | 3 | 0 | 0 |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | May 27, 2022 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2022.012M.N.v1.Lispiviridae\_7ngen\_11nsp.xlsx |

**Abstract**

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| We propose the creation of seven new genera to be included in mononegaviral family *Lispiviridae.* 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. |

**Text of proposal**

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| |  | | --- | | Here, we propose the establishment of new genera and species in the *Lispiviridae* family of the haploviricotine order *Mononegavirales*. As established in 2021, species and genera are proposed 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 an RdRp amino acid identity of 50% or lower, and the species demarcation criterion requires an RdRp amino acid identity of 50% or higher. Thus, based on the present phylogenetic analysis shown in **Figure 1**, we propose the demarcation of seven new genera and eleven new species.  We propose naming the new species as written below.  Etymologies:   * *Acridvirus hangzhouense* for Hángzhōu acrida cinerea lispivirus 1. The virus was discovered by HTS in *Acrida cinerea* (common name: chinese grasshopper; family: Acrididae) in Hángzhōu (杭州市), China. The genus is named after the family name Acrididae, and the species is named using its discovered geography location in an epithet form “*hangzhouense*”. * *Aranavirus guiyangense* for Guìyáng lispivirus 1. The virus was discovered by HTS in *Argiope bruennichi* (common name: rice spider; family: Araneidae) in Guìyáng (贵阳市), China. The genus is named after the family name Araneidae, and the species is named using its discovered geography location in an epithet form “*guiyangense*”. Considering that there are two lispviruses discovered in the same host species from same location, so we added an “a” in the genus name (*Aranavirus*) to distinguish from the other one (below). * *Aranbvirus guiyangense* for Guìyáng lispivirus 2. The virus was discovered by HTS in *Argiope bruennichi* (common name: rice spider; family: Araneidae) in Guìyáng (贵阳市), China. The genus is named after the family name Araneidae and the species is named using its discovered geography location in an epithet form “*guiyangense*”. This virus shares the same host species from the same location with *Aranavirus* *guiyangense*, so we named it as *Aranbvirus guiyangense.* * *Avesvirus sinense* for Arlivirus sp. virus isolate YSN1024. The virus was discovered by HTS in bird feces in China. The genus is named after the family name the class Aves, and the species is named using China as the location of virus discovery (“*sinense*”). * *Aleyavirus fuyangense* for Bemisia tabasi alrivirus 1. The virus was discovered by HTS in *Bemisia tabasi* (common name: whitefly; family: Aleyrodidae) Fùyáng (阜阳市), China. The genus is named after the family name Aleyrodidae, and the species is named using its discovered geography location Fùyáng in an epithet form “*fuyangense*”. Considering that there are two lispviruses discovered in the same host species from same location, so we added an “a” in the genus name (*Aleyavirus*) to distinguish from the other one (below). * *Aleybvirus fuyangense* for Bemisia tabasi alrivirus 2. The virus was discovered by HTS in *Bemisia tabasi* (common name: whitefly; family: Aleyrodidae) in Fùyáng (阜阳市), China. The genus is named after the family name Aleyrodidae, and the species is named using its discovered geography location Fùyáng in an epithet form “*fuyangense*”. Considering that there are two lispviruses discovered in the same host species from same location, so we added an “b” in the genus name (*Aleybvirus*) to distinguish from the other one. * *Hemipvirus scuti* for Hángzhōu eysarcoris guttigerus lispivirus 1. The virus was discovered by HTS in *Eysarcoris guttigerus* (common name: two spotted sesame bug; order: Hemiptera) in Hángzhōu (杭州市), China. The genus is named after the order name Hemiptera, and the species is named using the epithet “*scuti*”, Latin for “shield”, as *Eysarcoris* is a genus of shield bugs. * *Hemipvirus veri* for Hángzhōu cletus punctiger lispivirus 1. The virus was discovered by HTS in *Cletus punctiger* (common name: rice stink bug; order: Hemiptera) in Hángzhōu (杭州市), China. The genus is named after the order name Hemiptera, and the species is named using the word “*veri*” (true), as *Cletus* is a genus of true bugs. * *Damravirus fushunense* for Fǔshùn ischnura senegalensis lispivirus 1. The virus was discovered by HTS in *Ischnura senegalensis* (common name: damselfly) in Fǔshùn (抚顺市), China. The species is named using its discovered geography location Fǔshùn in an epithet form “*fushunense*”. * *Arlivirus ningboense* for Nbu stink bug virus 1. The virus was discovered by HTS in *Erthesina fullo* (common name: the brown marmorated stink bug) in Níngbō (宁波市), China. The species is named using its discovered geography location Níngbō in an epithet form “*ningboense*”. * *Arlivirus hangzhouense* for Hángzhōu scotinophara lurida lispivirus 1. The virus was discovered by HTS in *Scotinophara lurida* (common name: black rice bug) in Hángzhōu (杭州市), China. The species is named using its discovered geography location Hángzhōu in an epithet form “*hangzhouense*”. | |

**Supporting evidence**

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**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 substitution 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 Bolahun virus of the *Anphevirus* genus of the *Xinmoviridae* family.

**References**

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