

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

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| **Code assigned:** | ***2023.011M*** |  |
| **Short title:** Create one new genus (*Birfecvirus*) and four new species in the genera *Ganiavirus*, *Copasivirus*, *Anicalvirus*, and *Birfecvirus* (*Mononegavirales*: *Lispiviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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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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**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 | 4 | 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 |

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

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| 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**

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

**Name of accompanying Excel module**

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| 2023.011M.N.v1.Lispiviridae\_1ngen\_4nsp.xlsx |

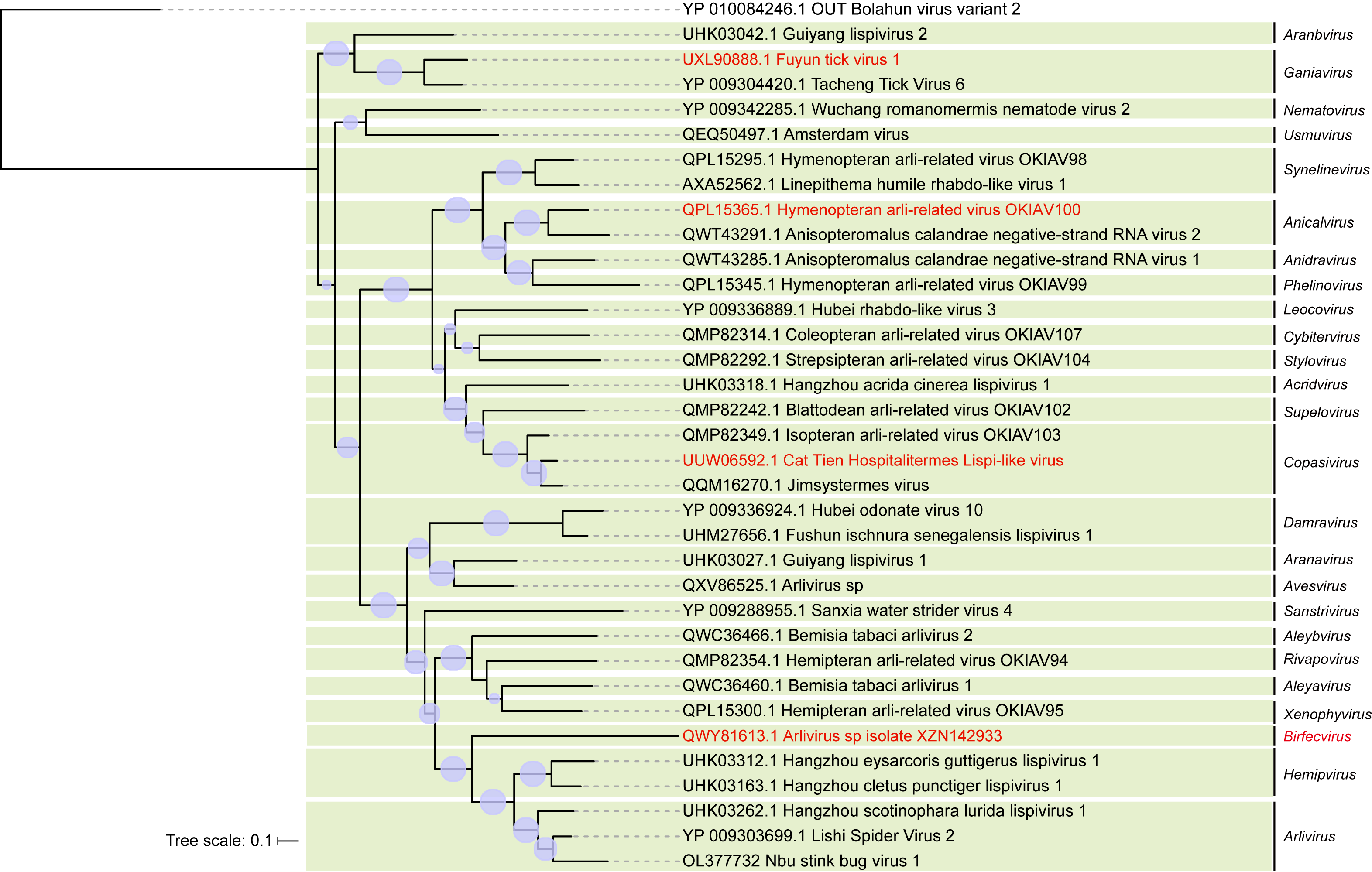
**Abstract**

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| We propose the creation of one new genus and four new species 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 classification of a new genera and four new species in the *Lispiviridae* family of the haploviricotine order *Mononegavirales*. 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% or higher. Thus, based on the present phylogenetic analysis shown in **Figure 1**, we propose the demarcation of 1 new genus and 4 new species.  Etymologies:   * ***Copasivirus cattienense*** for Cát Tiên Hospitalitermes lispi-like virus. The virus was discovered by HTS in termites (nasutitermitinine *Hospitalitermes bicolor* Holmgren, 1912) in Cát Tiên National Park, Vietnam. The RdRp of this virus has 66% amino acid identity with that of the RdRp of Jimsystermes virus (*Copasivirus manlyvaleense*). The species is named using its discovered geography location Cát Tiên in an epithet form “*cattienense*”. * ***Birfecvirus* *tibetense*** for Arlivirus sp. XZN142933. The virus was discovered by HTS in fecal samples of birds collected in Tibet, China. The RdRp of this virus has 35% amino acid identity with that of the RdRp of Hángzhōu scotinophara lurida lispivirus 1 (*Arlivirus hangzhouense*). The genus is named after bird and fecal, and the species is named using its discovered geography location Tibet in an epithet form “*tibetense*”. * ***Anicalvirus hesdarense*** for hymenopteran arli-related virus OKIAV100. The virus was discovered by HTS in parasitic wasps (orussid *Orussus unicolor* Latreille, 1812) in Darmstadt, Hesse, Germany. The RdRp of this virus has 51% amino acid identity with that of Anisopteromalus calandrae negative-strand RNA virus 2 (*Anicalvirus hangzhouense*). The species is named using its discovered geography location Hesse-Darmstadt in an epithet form “*hesdarense*”. * ***Ganiavirus fuyunense*** for Fùyùn tick virus 1. The virus was discovered by HTS in parasitic ticks collected from domestic animals (camels and sheep) in Fùyùn County (富蕴县) of Xīnjiāng Uygur Autonomous Region, China. The RdRp of this virus has 53% amino acid identity with that of Tǎchéng tick virus 6 (*Ganiavirus tachengense*). The species is named using its discovered geography location Fùyùn in an epithet form “*fuyunense*”. | |

**Supporting evidence**



**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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