

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

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| **Code assigned:** | **2021.016M** |  |
| **Short title:** Create 16 new genera, create 13 new species and rename all six established species (*Mononegavirales: Lispiviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Paraskevopoulou S |

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

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| There is currently no Study Group for this family. |

**ICTV study group comments and response of proposer**

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| N/A |

**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 |

**Submission dates**

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| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 13, 2021 |

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

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| * *arachnae* in *Arlivirus* *arachnae* is not the genitive singular of the Greek word but of the Latinized form of the Greek word.   Response: fixed.   * Excel: change Refseq record to GB record (NC\_031259 to KM817632)   Response: done.   * Excel: Insert virus name abbreviations   Response: done.   * Excel: Insert exemplar isolate designations   Response: done.   * Excel: Insert Genome coverage (Complete coding genome)   Response: done.   * Excel: Insert Genome composition (ssRNA(-))   Response: done.   * Excel: Insert host (invertebrates?)   Response: done.   * Correct errors from the automatic error check.   Response: done.   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

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

**Name of accompanying Excel module**

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| 2021.016M.R.Lispiviridae\_16ngen\_13nsp |

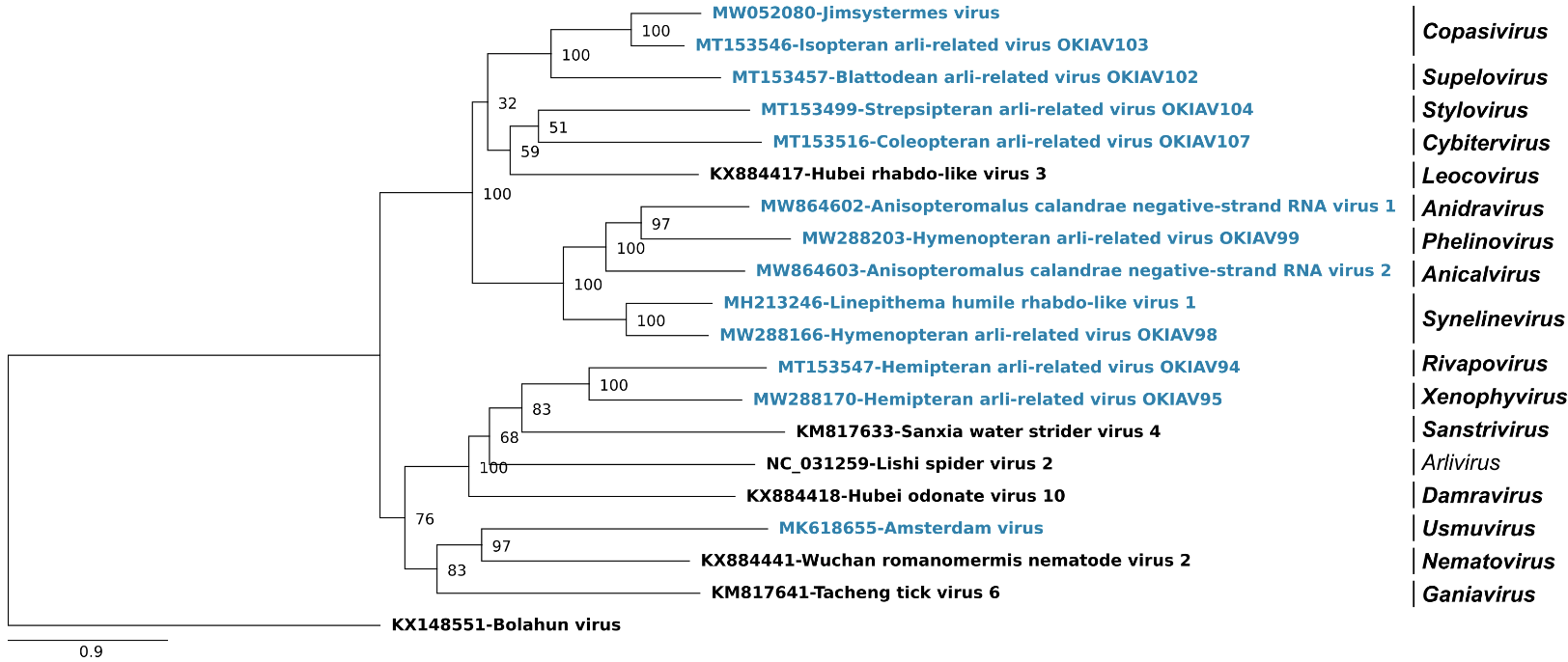
**Abstract**

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| We propose the creation of fourteen 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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| |  | | --- | | *Lispiviridae* is a monogeneric family of the haploviricotine order *Mononegavirales*. The family is currently monogeneric, including only genus *Arlivirus* with six species. Here, we propose that virus classification criteria for this family should include:   * a coding-complete RNA-directed RNA polymerase (RdRp) * at least 20% amino acid identity of the RdRp sequence   The above criteria were chosen to be similar to those used for other mononegaviral families.  Additionally, we propose that the lispivirid genus demarcation criterion should be RdRp amino acid identity of 50% or lower, and that the species demarcation criterion should be 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 sixteen new genera and thirteen new species.  Also, in March 2021, the ICTV ratified TaxoProp 2018.001G.R.binomial\_species, which requires all species names to follow a new codified rule:  "A species name shall consist of only two distinct word components separated by a space. The first word component shall begin with a capital letter and be identical in spelling to the name of the genus to which the species belongs. The second word component shall not contain any suffixes specific for taxa of higher ranks. The entire species name (both word components) shall be italicized."  This rule requires most established species names to be changed. Here, we propose to change the names of the established lispivirid species names to follow this rule by adopting binomial species names, and such names are also adopted for newly proposed species.  Etymologies:   * *Sanstrivirus gerridis* for Sānxiá water strider virus 4 discovered by HTS in Gerridaesp. water striders sampled in Sānxiá, China. The genus is named after a syllable combination from the exemplar virus name Sānxiá water strider virus 4. The species is named using the likely singular genitive of the order name Gerridae in Latin. * *Leocovirus coleopteris* forHúběi rhabdo-like virus 3discovered by HTS in Coleopterasp. sampled in HúběI province, China. The genus name is a scrambled contraction of “Coleoptera”. The species is named using the likely singular genitive of the order name Coleoptera in Latin. * *Arlivirus arachnae* forLĭshì spider virus 2discovered by HTS in Arraneaesp. spiders sampled in HúběI Province, China. The species is named using the singular genitive of the Latinized form of the Greek word for spider, ἀράχνη. * *Damravirus dentatis* forHúběi odonate virus 10discovered by HTS in Odonatasp. sampled in Húběi, China. The genus name is derived from odonate damselflies and dragonflies. The species is named using the singular genitive of dentatum, the Latin word for toothed (odonate is derived from the Greek word for tooth (ὀδούς)). * *Ganiavirus tachengense* forTǎchéng tick virus 6discovered by HTS in *Argas miniatus* ticks sampled in Tǎchéng Prefecture, China. The genus is derived from the host species name, *Argas miniatus*. * *Nematovirus wuchangense* forWǔchāng romanomermis nematode virus 2discovered by HTS in *Romanomermis* sp. nematodes sampled in Wǔchāng District, China. The genus name is derived from “nematode”. * *Copasivirus manlyvaleense* forJimsystermes virusdiscovered by HTS in *Occasitermes* sp. termites sampled in Manly Vale, New South Wales, Australia. The genus named is derived from host genus names *Coptotermes* and *Occasitermes*. * *Copasivirus ivindoense* forisopteran arli-related virus OKIAV103 discovered by HTS in *Coptotermes* sp. termites sampled in Ivindo National Park, Gabon. The genus name is derived from host genera *Coptotermes* and *Occasitermes*. * *Supelovirus thailandense* for blattodean arli-related virus OKIAV102discovered by HTS in *Supella longipalpa* cockroaches of laboratory culture samples originating from Thailand. The genus name is derived from host species name *Supella longipalpa*. * *Stylovirus niederense* for strepsipteran arli-related virus OKIAV104discovered by HTS in *Stylops melittae* endoparasites sampled in Osnabrück, Lower Saxony, Germany. The genus name is derived from host genus *Stylops*. The species epithet is derived from the German word “nieder” that means “low” (as a reference to “Lower Saxony”). * *Cybitervirus niederense* for coleopteran arli-related virus OKIAV107discovered by HTS in *Cybister lateralimarginalis* diving beetles sampled in Lüchow-Dannenberg, Lower Saxony, Germany. The genus name is derived from host species name *Cybister lateralimarginalis*. The species epithet is derived from the German word “nieder” that means “low” (as a reference to “Lower Saxony”). * *Anidravirus hangzhouense* forAnisopteromalus calandrae negative-strand RNA virus 1discovered by HTS in *Anisopteromalus calandrae* parasitoid wasps sampled in Hángzhōu, China. The genus name is derived from species name *Anisopteromalus calandrae*. * *Phelinovirus aphidis* forhymenopteran arli-related virus OKIAV99discovered by HTS in *Aphelinus abdominalis* parasitoid wasps of laboratory culture samples of unknown geographical origin. The genus name is derived from host species name *Aphelinus abdominalis*. The species epithet is derived from the word “aphid” because these wasps are used as biocontrol agents for aphid species that are pests of agricultural crops. * *Anicalvirus hangzhouense* forAnisopteromalus calandrae negative-strand RNA virus 2discovered by HTS in *Anisopteromalus calandrae* parasitoid wasps sampled in Hángzhōu, China. The genus name is derived from the host species name *Anisopteromalus calandrae*. * *Synelinevirus paranaense* for Linepithema humile rhabdo-like virus 1discovered by HTS in *Linepithema humile* ants sampled in the European Main super-colony in Catalonia, Spain. The genus is derived from the host genus names *Synergus* and *Linepithema*. The species epithet comes from the native ant range which is detected around major waterways in the lowland areas of the Paraná River drainage in South America. * *Synelinevirus bonnense* forhymenopteran arli-related virus OKIAV98discovered by HTS in *Synergus umbraculus* gall wasps sampled in Bonn, North Rhine-Westphalia, Germany. The genus name is derived from the host genus names *Synergus* and *Linepithema*. * *Rivapovirus aleyrodidae* for hemipteran arli-related virus OKIAV94 discovered by HTS in *Trialeurodes vaporariorum* greenhouse whiteflies of commercial laboratory cultures from Biotech AG Baruth Brandenburg. The genus is derived from the host species name *Trialeurodes vaporariorum*. The species epithet is derived from the host family, Aleyrodidae. * *Xenophyvirus mathesonense* forhemipteran arli-related virus OKIAV95discovered by HTS in *Xenophyes metoponcus* moss bugs sampled in Lake Matheson, South Island Westland District, New Zealand. The genus name is derived from host genus name *Xenophyes*. * *Usmuvirus newyorkense* forAmsterdam virusdiscovered by HTS in *Mus musculus* mice sampled in New York, USA. The genus is derived from the host species name *Mus musculus*. | |

**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 E-INS-i algorithm and was inferred using IQtree and the LG substitution model. Numbers on branch nodes represent transfer bootstrap expectation values (1,000 replicates). Proposed new lispivirid genera are shown in bold at the right; viruses proposed to be classified into new species are shown in blue. The tree is rooted to Bolahun virus of the *Anphevirus* genus of the *Xinmoviridae* family.

**References**

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**References**

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