



ICTV Virus Taxonomy Profile: *Lispiviridae* 2023

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Abstract

Members of the family *Lispiviridae* are viruses with negative-sense RNA genomes of 6.5–15.5 kb that have mainly been found in arthropods and nematodes. The genomes of lispivirids contain several open reading frames, typically encoding a nucleoprotein (N), a glycoprotein (G), and a large protein (L) including an RNA-directed RNA polymerase (RdRP) domain. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Lispiviridae*, which is available at ictv.global/report/lispiviridae.

Table 1. Characteristics of members of the family *Lispiviridae*

Example	Anisopteromalus calandrae negative-strand RNA virus 2 (MW864603), species <i>Anicalvirus hangzhouense</i> , genus <i>Anicalvirus</i>
Virion	Unknown
Genome	6.5–15.5 kb of negative-sense RNA
Replication	Unknown
Translation	Unknown
Host range	Arthropods and nematodes of the superphylum Ecdysozoa
Taxonomy	Realm Riboviria, kingdom Orthornavirae, phylum Negarnaviricota, class Monjiviricetes, order Mononegavirales: >20 genera and >25 species

VIRION

Unknown.

GENOME

The genomes of lispivirids are single molecules of linear, negative-sense RNA of 6.5–15.5 kb (Table 1). Lispivirid genomes typically contain five to six open reading frames (ORFs). For example, the genome of *Anisopteromalus calandrae* negative-strand RNA virus 2 (species *Anicalvirus hangzhouense*, genus *Anicalvirus*) has six ORFs encoding a putative nucleoprotein (N), predicted phosphoprotein (P), predicted matrix protein (M), glycoprotein (G), unknown protein (X) and L protein (L) including an RNA-directed

RNA polymerase (RdRP) domain; these ORFs are organized in the order 3'-N-P-M-G-X-L-5' (Fig. 1) [1]. It should be noted that the genomes of some lispivirids lack one or more of these genes, which might be due to coding incompleteness.

REPLICATION

Unknown.

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The family *Lispiviridae* includes >20 genera and >25 species (Fig. 2) for viruses hosted by arthropods and nematodes of the superphylum *Ecdysozoa* [1–6]. Lispivirids have been detected in mammals

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Abbreviations: G, glycoprotein; L, large protein; M, matrix protein; N, nucleoprotein; P, phosphoprotein; RdRP, RNA-directed RNA polymerase; X, protein of unknown function.

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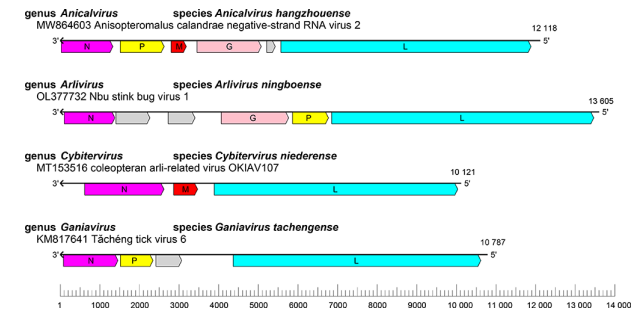


Fig. 1. Genome organization of representative viruses of the family Lispiviridae. The diagram shows the genome length, position of open reading frames and putative protein products: N, nucleoprotein (magenta); P, predicted phosphoprotein (yellow); M, predicted matrix protein (red); G, glycoprotein (salmon); L, large protein (cyan) including an RNA-directed RNA polymerase domain; predicted protein of unknown function (grey).

and bird faeces [7, 8], but it is still unclear whether they are capable of replicating in these hosts.

RESOURCES

Full ICTV Report on the family Lispiviridae: [ictv.global/report/lispiviridae](https://www.ictv.global/report/lispiviridae).

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References

- Wang F, Yuan B, Xiao S, Zhang J, Jia W, et al. Diverse RNA viruses discovered in three parasitoid wasps of the rice weevil *Sitophilus oryzae*. *mSphere* 2021;6:e00331-21.
- Huang H-J, Ye Z-X, Wang X, Yan X-T, Zhang Y, et al. Diversity and infectivity of the RNA virome among different cryptic species of an agriculturally important insect vector: whitefly *Bemisia tabaci*. *NPJ Biofilms Microbiomes* 2021;7:43.
- Käfer S, Paraskevopoulou S, Zirkel F, Wieseke N, Donath A, et al. Re-assessing the diversity of negative strand RNA viruses in insects. *PLoS Pathog* 2019;15:e1008224.
- Lay CL, Shi M, Buček A, Bourguignon T, Lo N, et al. Unmapped RNA virus diversity in termites and their symbionts. *Viruses* 2020;12:1145.

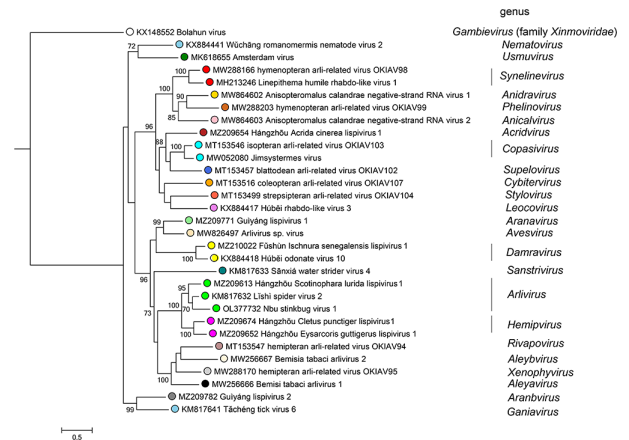


Fig. 2. Phylogenetic relationships of lispivirids. The phylogenetic tree is based on a MAFFT-alignment of the RdRP amino acid sequences using the L-INS-i algorithm and was inferred using ModelTest-NG and the LG substitution model. Numbers on branch nodes represent transfer bootstrap expectation values (1000 replicates). The tree is rooted to Bolahun virus of the Gambievirus genus of the Xinmoviridae family.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

- Viljakainen L, Holmberg I, Abril S, Jurvansuu J. Viruses of invasive Argentine ants from the European Main supercolony: characterization, interactions and evolution. *J Gen Virol* 2018;99:1129-1140.
- Ye Z-X, Wang S-M, Lu G, Chen J-P, Zhang C-X, et al. Complete genome sequence of a novel arlivirus from a yellow spotted stink bug (*Erthesina fullo* (Thunberg, 1783)). *Arch Virol* 2022;167:1205-1209.
- Williams SH, Che X, Oleynik A, Garcia JA, Muller D, et al. Discovery of two highly divergent negative-sense RNA viruses associated with the parasitic nematode, *Capillaria hepatica*, in wild *Mus musculus* from New York City. *J Gen Virol* 2019;100:1350-1362.
- Zhu W, Yang J, Lu S, Jin D, Pu J, et al. RNA virus diversity in birds and small mammals from Qinghai-Tibet Plateau of China. *Front Microbiol* 2022;13:780651.