



ICTV Virus Taxonomy Profile: *Xinmoviridae* 2023

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Abstract

Xinmoviridae is a family of viruses with negative-sense RNA genomes of 9–14 kilobases. Xinmovirids typically infect beneficial and pest insects but their host range has not yet been investigated systematically and hence may be broader. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family of *Xinmoviridae*, which is available at [ictv.global/report/xinmoviridae](https://www.ictv.global/report/xinmoviridae).

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

Example	<i>Drosophila unispina</i> virus 1 (KR822819), species <i>Drunivirus chabonense</i> , genus <i>Drunivirus</i>
Virion	Unknown
Genome	9–14 kb of negative-sense RNA
Replication	Unknown
Translation	Unknown
Host range	Arthropoda
Taxonomy	Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Negarnaviricota</i> , class <i>Monjiviricetes</i> , order <i>Mononegavirales</i> ; >11 genera and >13 species

VIRION

Xinmovirids (viruses in the family *Xinmoviridae*) are only known from metagenomics studies. Virions have not yet been visualized and structural proteins have not been studied.

GENOME

Xinmovirids have negative-sense genomes of 9–14 kilobases with three to six ORFs (Table 1, Fig. 1) [1] that encode at least three structural proteins that have been identified via comparison with proteins encoded by other mononegavirals: a glycoprotein (G), a nucleoprotein (N), and an RNA-directed RNA polymerase (RdRP) [2].

REPLICATION

Xinmovirids are only known from metagenomics studies. Their replication cycles have not yet been studied.

PATHOGENICITY

Pathogenicity is unknown, but based on their host spectrum, xinmovirids likely have an effect on arthropod fitness.

TAXONOMY

Current taxonomy: [ictv.global/taxonomy](https://www.ictv.global/taxonomy). The family *Xinmoviridae* includes >11 genera and >13 species (Fig. 2). Hosts include arthropods, specifically insects from the orders Diptera, Hymenoptera, and Orthoptera. Related, unclassified viruses have been discovered in mosquitoes [3–6] and tephritid fruit flies [7, 8].

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Abbreviations: G, glycoprotein; N, nucleoprotein; RdRP, RNA-directed RNA polymerase.

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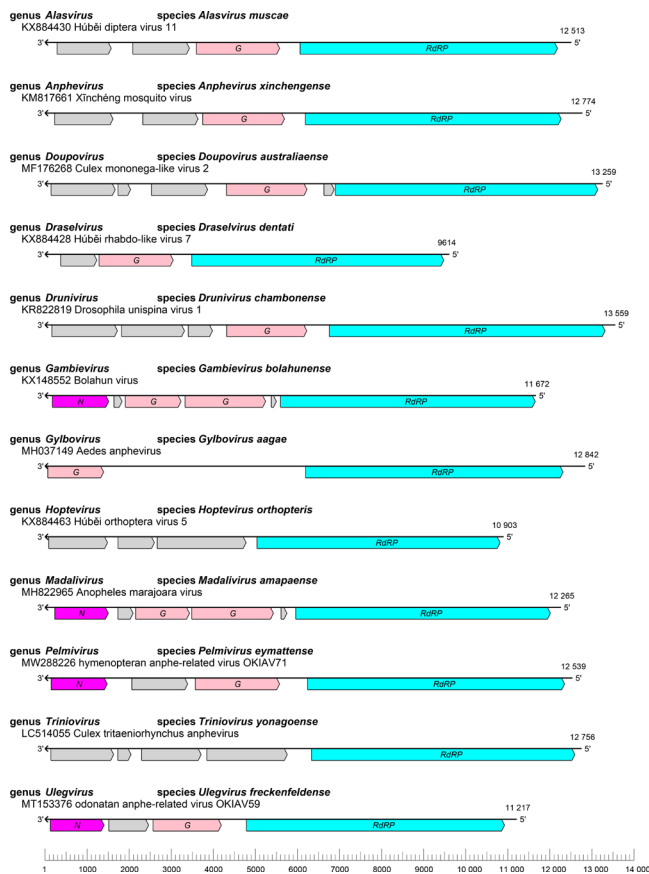


Fig. 1. Genome organization of a representative virus from each genus in the family *Ximoviridae*. ORFs are coloured according to their predicted protein function: N, nucleoprotein gene (magenta); G, glycoprotein gene (pink); RdRP, RNA-directed RNA polymerase gene (cyan).

References

1. Parry R, Asgari S. *Aedes anphevirus*: an insect-specific virus distributed worldwide in *Aedes aegypti* mosquitoes that has complex interplays with *Wolbachia* and Dengue virus infection in cells. *J Virol* 2018;92:e00224-18.
2. Scarpassa VM, Debat HJ, Alencar RB, Saraiva JF, Calvo E, *et al.* An insight into the sialotranscriptome and virome of Amazonian anophelines. *BMC Genomics* 2019;20:166.
3. Batson J, Dudas G, Haas-Stapleton E, Kistler AL, Li LM, *et al.* Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. *eLife* 2021;10:e68353.
4. Manni M, Zdobnov EM. A novel anphevirus in *Aedes albopictus* mosquitoes is distributed worldwide and interacts with the host RNA interference pathway. *Viruses* 2020;12:1264.

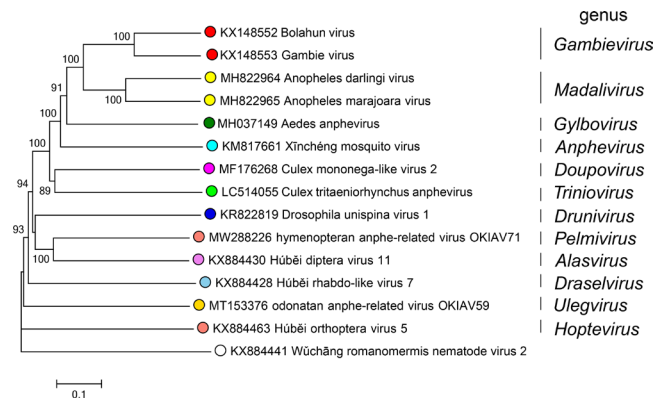


Fig. 2. Phylogenetic tree of ximovirid RdRP amino acid sequences. The virus Wüchāng romanomermis nematode virus 2 (family *Lisoviridae*) was used as an outgroup. Circles at tips are coloured by genus.

RESOURCES

Full ICTV Report on the family *Ximoviridae*: [ictv.global/report/ximoviridae](https://www.ictv.global/report/ximoviridae).

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Conflicts of interest

The authors declare that there are no conflicts of interest.

5. Shi M, Neville P, Nicholson J, Eden J-S, Imrie A, *et al.* High-resolution metatranscriptomics reveals the ecological dynamics of mosquito-associated RNA viruses in Western Australia. *J Virol* 2017;91:e00680-17.
6. Stanojević M, Li K, Stamenković G, Ilić B, Paunović M, *et al.* Depicting the RNA virome of hematophagous arthropods from Belgrade, Serbia. *Viruses* 2020;12:975.
7. Sharpe SR, Morrow JL, Brettell LE, Shearman DC, Gilchrist AS, *et al.* Tephritid fruit flies have a large diversity of co-occurring RNA viruses. *J Invertebr Pathol* 2021;186:107569.
8. Zhang W, Gu Q, Niu J, Wang J-J. The RNA virome and its dynamics in an invasive fruit fly, *Bactrocera dorsalis*, imply interactions between host and viruses. *Microb Ecol* 2020;80:423-434.