



# ICTV Virus Taxonomy Profile: *Cruliviridae* 2023

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## Abstract

*Cruliviridae* is a family of negative-sense RNA viruses with genomes of 10.8–11.5 kb that have been found in crustaceans. The crulivirid genome consists of three RNA segments with ORFs that encode a nucleoprotein (NP), a glycoprotein (GP), a large (L) protein containing an RNA-directed RNA polymerase (RdRP) domain, and in some family members, a zinc-finger (Z) protein of unknown function. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Cruliviridae*, which is available at [ictv.global/report/cruliviridae](https://www.ictv.global/report/cruliviridae).

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

| Example     | Wēnlíng crustacean virus 9 (S: KX884858; M: KX884857; L: KX884856), species <i>Lincruvirus wenlingense</i> , genus <i>Lincruvirus</i>  |
|-------------|--|
| Virion      | Enveloped, spherical   |
| Genome      | 10.8–11.5 kb of trisegmented negative-sense RNA  |
| Replication | Largely undefined  |
| Translation | Unknown  |
| Host range  | Portunid crustaceans (crabs)   |
| Taxonomy    | Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Negarnaviricota</i> , class <i>Ellioviricetes</i> , order <i>Bunyavirales</i> ; the family includes the genus <i>Lincruvirus</i> and several species |

## VIRION

Crulivirids produce enveloped spherical particles [1, 2].

## GENOME

The crulivirid genome comprises three segments (small [S], medium [M] and large [L]) of linear negative-sense RNA with a total length of 10.8–11.5 kb (S segment: about 0.8–1.6 kb;

M segment: about 3.2–3.6 kb; and L segment: about 6.7 kb) (Table 1). Each segment contains one ORF that encodes an NP, a GP, and an L protein containing an RdRP domain; some members also encode a Z protein of unknown function on the S segment [1, 3, 4] (Fig. 1).

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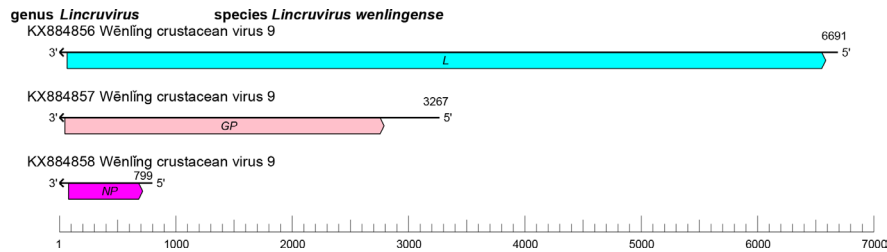
**Keywords:** ICTV Report; taxonomy; *Cruliviridae*; lincruvirus.

**Abbreviations:** GP, glycoprotein; L, large; NP, nucleoprotein; RdRP, RNA-directed RNA polymerase; S, small; Z, zinc-finger protein.

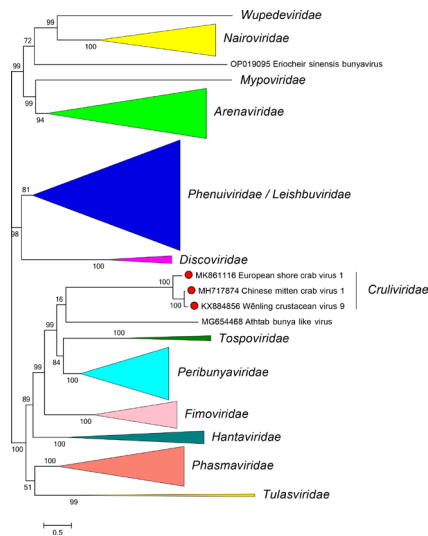
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**Fig. 1.** Genome organization of Wēnlíng crustacean virus 9. ORFs are coloured according to the predicted protein function (GP, glycoprotein gene; L, large protein gene; NP, nucleoprotein gene).



**Fig. 2.** Phylogenetic relationships of viruses in the family *Cruliviridae*. Branches for viruses in other families are collapsed. Numbers at nodes indicate bootstrap support where this was >70%. Details of the virus sequences and methods used are available in the full ICTV Report on the family *Cruliviridae*.

## REPLICATION

Enveloped virions enter host cells via endocytosis; morphogenesis occurs in small and large intracellular vesicles that release mature virions [1, 2].

## TAXONOMY

Current taxonomy: [ictv.global/taxonomy](https://www.ictv.global/taxonomy). Crulivirids are most closely related to fimovirids, hantavirids, peribunyavirids, phasmavirids, tospovirids and tulasvirids [4–6] (Fig. 2). The family

includes the genus *Lincruvirus* and several species for viruses that infect crustaceans. Crulivirids (i) have multisegmented, negative-sense single-stranded RNA genomes; (ii) encode proteins with high sequence identity to proteins of other bunyavirals; (iii) and have five conserved motifs (A–E) in their RdRP domain.

## RESOURCES

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

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### Conflicts of interest

The authors declare that there are no conflicts of interest.

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