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ICTV Virus Taxonomy Profile: *Simuloviridae* 2023

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Abstract

The family *Simuloviridae* includes tailless icosahedral viruses with an internal lipid membrane. The capsid is constructed from two major capsid proteins, both with a single jelly-roll fold. The genome is a circular dsDNA molecule of 16–19 kb. All members infect halophilic archaea in the class Halobacteria (phylum Euryarchaeota) and are temperate viruses, their proviruses residing in host cells as extrachromosomal episomes. Once the lytic life cycle is triggered, production of virions causes cell lysis. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Simuloviridae*, which is available at [ictv.global/report/simuloviridae](https://www.ictv.global/report/simuloviridae).

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

| | |
|-------------|---|
| Example | Saline <i>Natrinema</i> sp. J7-1 virus 1 (AY048850), species <i>Yingchengvirus</i> SNJ1, genus <i>Yingchengvirus</i> |
| Virion | Tailless icosahedral virion with an internal lipid membrane, diameter about 70 nm; two major capsid proteins, both with a single jelly-roll fold |
| Genome | Circular dsDNA of 16–19 kb |
| Replication | Rolling circle replication |
| Translation | Prokaryotic translation using viral mRNA and host ribosomes |
| Host range | Halophilic archaea of the genera <i>Natrinema</i> and <i>Haloterrigena</i> , order Natrionalbales |
| Taxonomy | Realm <i>Varidnaviria</i> , kingdom <i>Helvetiavirae</i> , phylum <i>Dividoviricota</i> , class <i>Laserviricetes</i> , order <i>Halopanivirales</i> : one genus, three species |

VIRION

Virions of *Saline Natrinema* sp. J7-1 virus 1 are tailless icosahedra with a diameter of approximately 70 nm (Table 1, Fig. 1) constructed from two single jelly-roll major capsid proteins PB2 and PB6, and an internal membrane core enclosing the viral circular dsDNA genome [1, 2].

GENOME

The circular dsDNA genome of members of the family *Simuloviridae* is 16–19 kb with about 30 ORFs (Fig. 2). *Simuloviruses*

share 17–21 homologous ORFs including replication, regulation and virion structure-related genes; these gene modules are generally collinear among *simuloviruses* [3].

REPLICATION

Members of the family *Simuloviridae* have a temperate life cycle, their proviruses residing in host cells as extrachromosomal episomes [1, 3, 4]. The *Saline Natrinema* sp. J7-1 virus 1-encoded ORF4 is a transcriptional regulator belonging to the MazE superfamily and controls the lysis–lysogeny switch [3]. The virus is triggered to undergo the lytic life cycle upon

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Keywords: ICTV Report; taxonomy; *Simuloviridae*.

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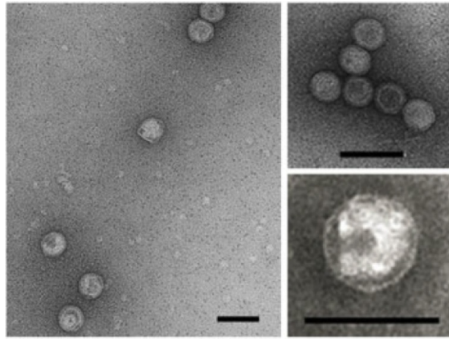


Fig. 1. Electron micrographs of Saline Natrinema sp. J7-1 virus 1 virions. Bars, 100 nm. Reproduced with permission from Liu *et al.* [2].

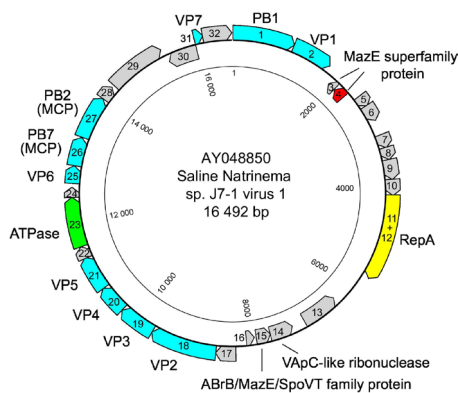


Fig. 2. Genome map of Saline Natrinema sp. J7-1 virus 1. Cyan, structural proteins; yellow, replication initiation protein RepA; green, putative genome packaging ATPase; red, transcriptional regulator controlling virus lysis-lysogeny switch.

References

- Zhang Z, Liu Y, Wang S, Yang D, Cheng Y, *et al.* Temperate membrane-containing halophilic archaeal virus SNJ1 has a circular dsDNA genome identical to that of plasmid pHH205. *Virology* 2012;434:233–241.
- Liu Y, Wang J, Liu Y, Wang Y, Zhang Z, *et al.* Identification and characterization of SNJ2, the first temperate pleolipovirus integrating into the genome of the SNJ1-lysogenic archaeal strain. *Mol Microbiol* 2015;98:1002–1020.
- Chen B, Chen Z, Wang Y, Gong H, Sima L, *et al.* ORF4 of the temperate archaeal virus SNJ1 governs the lysis-lysogeny switch and superinfection immunity. *J Virol* 2020;94:e00841–00820.

treatment with the DNA-damaging agent mitomycin C. Homologues of Saline Natrinema sp. J7-1 virus 1 ORF4 are encoded by Haloterrigena jeotgali icosahedral virus 1 and Natrinema versiforme icosahedral virus 1, implying that simuloviruses employ a common lysis-lysogeny regulatory mechanism [3]. Saline Natrinema sp. J7-1 virus 1 genome replication uses a rolling-circle mechanism, which depends on the virus-encoded replication initiation protein RepA belonging to the HUH endonuclease superfamily [5, 6]. A RepA homologue has been identified in Haloterrigena jeotgali icosahedral virus 1, but not in Natrinema versiforme icosahedral virus 1. Production of Saline Natrinema sp. J7-1 virus 1 virions causes cell lysis. Simuloviruses infect halophilic archaea of the genera *Natrinema* and *Haloterrigena*, order Natrionalbales.

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The family *Simuloviridae* includes a single genus, *Yingchengvirus*, with three species.

RESOURCES

Full ICTV Report on the family *Simuloviridae*: ictv.global/report/simuloviridae.

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Conflicts of interest

The authors declare that there are no conflicts of interest.