



HAL
open science

ICTV Virus Taxonomy Profile: Thaspiviridae 2021

Jong-Geol Kim, Khaled S Gazi, Mart Krupovic, Sung-Keun Rhee, Ictv Report Consortium

► **To cite this version:**

Jong-Geol Kim, Khaled S Gazi, Mart Krupovic, Sung-Keun Rhee, Ictv Report Consortium. ICTV Virus Taxonomy Profile: Thaspiviridae 2021. Journal of General Virology, 2021, 102 (7), pp.001631. 10.1099/jgv.0.001631 . pasteur-03318857

HAL Id: pasteur-03318857

<https://pasteur.hal.science/pasteur-03318857>

Submitted on 11 Aug 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



ICTV Virus Taxonomy Profile: *Thaspiviridae* 2021

Jong-Geol Kim¹, Khaled S. Gazi², Mart Krupovic³, Sung-Keun Rhee^{2,*} and ICTV Report Consortium

Abstract

Members of the family *Thaspiviridae* have linear dsDNA genomes of 27 to 29 kbp and are the first viruses known to infect mesophilic ammonia-oxidizing archaea of the phylum Thaumarchaeota. The spindle-shaped virions of Nitrosopumilus spindle-shaped virus 1 possess short tails at one pole and measure 64 ± 3 nm in diameter and 112 ± 6 nm in length. This morphology is similar to that of members of the families *Fuselloviridae* and *Halspiviridae*. Virus replication is not lytic but leads to growth inhibition of the host. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Thaspiviridae*, which is available at ictv.global/report/thaspiviridae.

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

Example:	Nitrosopumilus spindle-shaped virus 1 (MK570053), species <i>Nitmarvirus</i> NSV1, genus <i>Nitmarvirus</i>
Virion	Spindle-shaped, measuring 64 ± 3 nm in diameter and 112 ± 6 nm in length, with short fibres at one pole.
Genome	Linear dsDNA (27–29 kbp) with 176 bp terminal inverted repeats
Replication	Non-lytic, chronic infection. Protein-primed family B DNA polymerase is involved in viral DNA replication
Translation	Not characterized
Host range	Ammonia-oxidizing archaea of the genus <i>Nitrosopumilus</i>
Taxonomy	Single genus with one species

VIRION

The virion of Nitrosopumilus spindle-shaped virus 1 is 64 ± 3 nm in diameter and 112 ± 6 nm in length with a short tail at one pole (Table 1, Fig. 1). The predicted major capsid protein (81 amino acids) contains two highly hydrophobic α -helical regions. The spindle-shape morphology of the virion is very similar to those of members of the families *Fuselloviridae* [1] and *Halspiviridae* [2], which infect hyperthermophilic and hyperhalophilic archaea, respectively. When associated with the host cells, some virions are observed as elongated structures, with long thin tails connected to the cell surface [3, 4].

GENOME

The genome of Nitrosopumilus spindle-shaped virus 1 is linear dsDNA (27–29 kbp), terminating with 176 bp inverted repeats (Fig. 2). The virus genome is predicted to carry 48 genes. With

one exception, the proteins predicted to be encoded by Nitrosopumilus spindle-shaped virus 1 are unrelated to those of other archaeal and bacterial viruses. The exception, protein-primed B DNA polymerase, is also found in several groups of archaeal viruses and non-viral mobile genetic elements which, similar to Nitrosopumilus spindle-shaped virus 1, have linear genomes with terminal inverted repeats [4].

REPLICATION

The virus establishes a chronic infection and its replication is not lytic, with virions being continuously extruded into the environment [4]. The virus genome is likely to be replicated by the virus-encoded protein-primed family B DNA polymerase, as has been inferred for haloarchaeal halspiviruses [2] and crenarchaeal ampullaviruses [5]. In addition, the virus encodes

Received 15 June 2021; Accepted 15 June 2021; Published 30 July 2021

Author affiliations: ¹Department of Biological Sciences, Wonkwang University, Iksan, 54538, Republic of Korea; ²Department of Biological Sciences and Biotechnology, Chungbuk National University, Cheongju 28644, Republic of Korea; ³Archaeal Virology Unit, Institut Pasteur, Paris 75015, France.

*Correspondence: Sung-Keun Rhee, rhees@cbnu.ac.kr

Keywords: ICTV Report; taxonomy; *Thaspiviridae*.

001631 © 2021



This is an open-access article distributed under the terms of the Creative Commons Attribution License

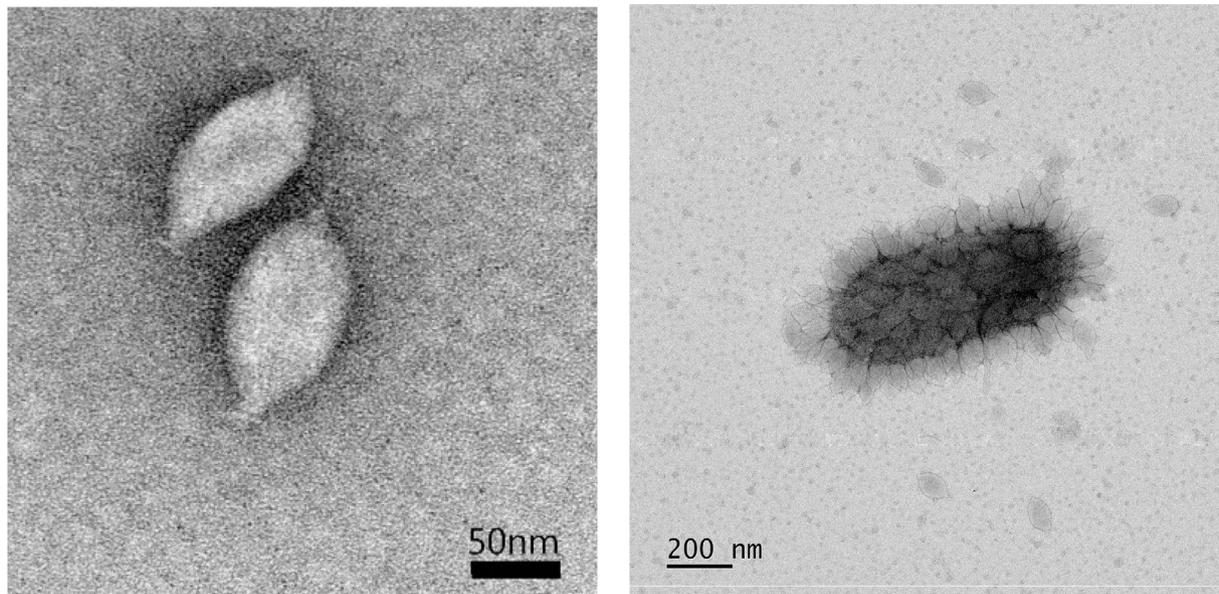


Fig. 1. (Left) Transmission electron micrograph of negatively-stained virions of Nitrosopumilus spindle-shaped virus 1. (Right) Virus particles attached to the surface of a host cell.

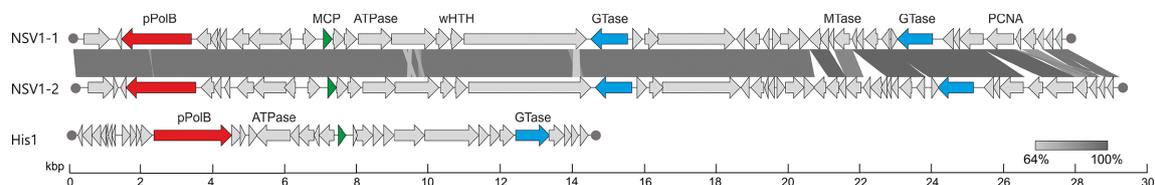


Fig. 2. Genome maps of Nitrosopumilus spindle-shaped virus 1 isolates NSV1-1 and NSV1-2, and of the haloarchaeal halospirirus His1. Shared ORFs are connected by shaded areas based on sequence identity. Functionally equivalent (but not necessarily homologous) genes are indicated with matching colours. Filled circles indicate terminal inverted repeats. pPolB, protein-primed family B DNA polymerase; MCP, major capsid protein (putative); wHTH, winged helix-turn-helix; GTase, glycosyltransferase; MTase, DNA methyltransferase; PCNA, proliferating cell nuclear antigen.

a proliferating cell nuclear antigen which is also likely to be involved in viral genome replication.

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The single genus *Nitmarvirus* includes one species *Nitmarvirus NSV1*.

RESOURCES

Full ICTV Report on the family *Thaspiviridae*: ictv.global/report/thaspiviridae.

Funding information

Production of this Profile, the ICTV Report, and associated resources was funded by a grant from the Wellcome Trust (WT108418AIA) and the National Research Foundation of Korea (NRF) grants funded by the Ministry of Science, ICT & Future Planning (2021R1A2C3004015).

Acknowledgements

Members of the ICTV Report Consortium are Stuart G. Siddell, Elliot J. Lefkowitz, Sead Sabanadzovic, Peter Simmonds, F. Murilo Zerbini, Donald B. Smith, Richard J. Orton and Mart Krupovic.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. Krupovic M, Quemin ER, Bamford DH, Forterre P, Prangishvili D. Unification of the globally distributed spindle-shaped viruses of the Archaea. *J Virol* 2014;88:2354–2358.
2. Bath C, Cukalac T, Porter K, Dyal-Smith ML. His1 and His2 are distantly related, spindle-shaped haloviruses belonging to the novel virus group, Salterprovirus. *Virology* 2006;350:228–239.
3. Häring M, Vestergaard G, Rachel R, Chen L, Garrett RA, et al. Virology: independent virus development outside a host. *Nature* 2005;436:1101–1102.
4. Kim JG, Kim SJ, Cvirkaite-Krupovic V, WJ Y, Gwak JH, et al. Spindle-shaped viruses infect marine ammonia-oxidizing thaumarchaea. *Proc Natl Acad Sci U S A* 2019;116:15645–15650.
5. Prangishvili D, Krupovic M, ICTV Report Consortium. ICTV Virus Taxonomy Profile: *Ampullaviridae*. *J Gen Virol* 2018;99:288–289.