



HAL
open science

ICTV Virus Taxonomy Profile: Sedoreoviridae 2022

Jelle Matthijnssens, Houssam Attoui, Krisztián Bányai, Corina P D Brussaard, Pranav Danthi, Mariana del Vas, Terence S Dermody, Roy Duncan, Qin Fang, Reimar Johne, et al.

► **To cite this version:**

Jelle Matthijnssens, Houssam Attoui, Krisztián Bányai, Corina P D Brussaard, Pranav Danthi, et al.. ICTV Virus Taxonomy Profile: Sedoreoviridae 2022. *Journal of General Virology*, 2022, 103 (10), 10.1099/jgv.0.001782 . hal-04356197

HAL Id: hal-04356197

<https://hal.inrae.fr/hal-04356197>

Submitted on 20 Dec 2023

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: *Sedoreoviridae* 2022

Jelle Matthijnssens^{1,*}, Houssam Attoui², Krisztián Bányai³, Corina P. D. Brussaard⁴, Pranav Danthi⁵, Mariana del Vas⁶, Terence S. Dermody⁷, Roy Duncan⁸, Qín Fāng (方勤)⁹, Reimar Johne¹⁰, Peter P. C. Mertens¹¹, Fauziah Mohd Jaafar¹², John T. Patton⁵, Takahide Sasaya (笹谷孝英)¹³, Nobuhiro Suzuki (鈴木信弘)¹⁴, Taiyun Wei (魏太云)¹⁵ and ICTV Report Consortium

Abstract

Sedoreoviridae is a large family of icosahedral viruses that are usually regarded as non-enveloped with segmented (10–12 linear segments) dsRNA genomes of 18–26 kbp. Sedoreovirids have a broad host range, infecting mammals, birds, crustaceans, arthropods, algae and plants. Some of them have important pathogenic potential for humans (e.g. rotavirus A), livestock (e.g. bluetongue virus) and plants (e.g. rice dwarf virus). This is a summary of the ICTV Report on the family *Sedoreoviridae*, which is available at ictp.global/report/sedoreoviridae.

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

Example:	rotavirus A RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2] (Seg1: DQ838640; Seg2: DQ838635; Seg3: DQ838645; Seg4: DQ841262; Seg5: DQ838599; Seg6: DQ838650; Seg7: DQ838610; Seg8: DQ838615; Seg9: DQ838620; Seg10: DQ838625; Seg11: DQ838630), species <i>Rotavirus A</i> , genus <i>Rotavirus</i>
Virion	Non-enveloped, icosahedral, 60–100 nm virions composed of 1–3 concentric capsid proteins layers
Genome	18–26 kbp of segmented linear dsRNA, with each of the 10–12 segments ranging from 0.6 to 5.8 kbp
Replication	Replication occurs in the cytoplasm in electron-dense structures called viroplasm or virus inclusion bodies
Translation	From full-length transcribed mRNAs, which possess a 5'-terminal cap but no poly(A)-tail
Host range	Mammals, birds, crustaceans, arthropods, algae and plants
Taxonomy	Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Duplornaviricota</i> , class <i>Resentoviricetes</i> , order <i>Reovirales</i> : >5 genera and >35 species

VIRION

Sedoreovirid particles are icosahedral (Table 1). The protein capsid is organized as 1–3 concentric layers of capsid proteins, with an overall diameter of 60–100 nm [1]. Members of the family *Sedoreoviridae* lack large surface projections on the subviral particle, giving them an almost spherical or 'smooth'

appearance (Fig. 1), in contrast to members of the family *Spinareoviridae*, which have spikes or turrets at the 12 icosahedral vertices.

GENOME

Sedoreovirids contain 10–12 segments of linear dsRNA comprising 18–26 kbp in total, with individual segments

Received 15 June 2022; Accepted 20 June 2022; Published 10 October 2022

Author affiliations: ¹University of Leuven, Leuven, Belgium; ²National Institute for Agricultural Research (INRA), Maisons Alfort, France; ³Veterinary Medical Research Institute, Budapest, Hungary; ⁴NIOZ Royal Netherlands Institute for Sea Research & University of Utrecht, Texel, The Netherlands; ⁵Indiana University, Bloomington, USA; ⁶Instituto de Agrobiotecnología y Biología Molecular (IABIMO), Buenos Aires, Argentina; ⁷University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania, USA; ⁸Dalhousie University, Halifax, Nova Scotia, Canada; ⁹Wuhan Institute of Virology, Wuhan, PR China; ¹⁰German Federal Institute for Risk Assessment, Berlin, Germany; ¹¹University of Nottingham, Nottingham, UK; ¹²Ecole Nationale Vétérinaire d'Alfort, Maisons Alfort, France; ¹³National Agriculture and Food Research Organization, Fukuyama, Japan; ¹⁴Okayama University, Kurashiki, Japan; ¹⁵Fujian Agriculture and Forestry University, Fuzhou, PR China.

*Correspondence: Jelle Matthijnssens, jelle.matthijnssens@kuleuven.be

Keywords: ICTV Report; taxonomy; *Sedoreoviridae*; *Reovirales*.

001782 © 2022 The Authors



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

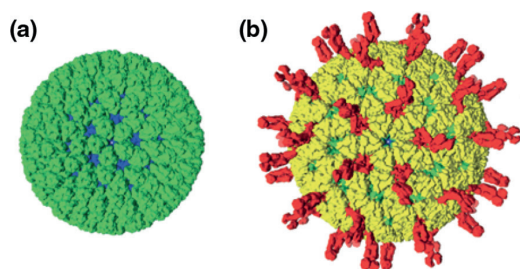


Fig. 1. Sedoreovirid particle structure (e.g. rotavirus A). Particles are coloured based on functional similarity (blue – core shell, green – middle layer, yellow – outer capsid, red – membrane penetration and receptor binding). (a) Subviral particle. (b) Virion. The diameter of the mature virion is roughly 80 nm (excluding spikes). Adapted from [7].

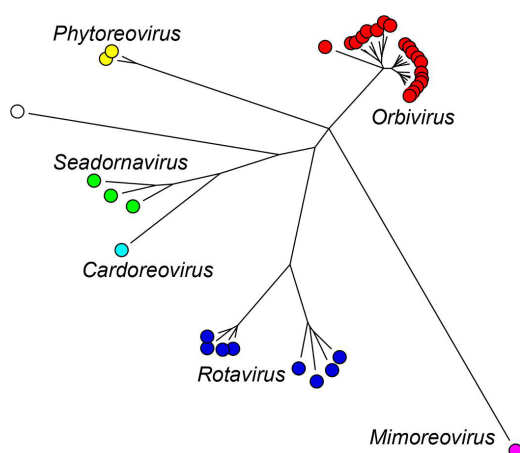


Fig. 2. Sedoreovirus phylogeny based on RNA-directed RNA polymerase amino acid sequences. For details see full ICTV Report.

ranging from 0.6 to 5.8 kbp. The positive-sense strands of each duplex are modified with a 5'-terminal type 1 cap structure but no 3'-poly(A) tail. The viral RNAs are mostly monogenic with relatively short 5'- and 3'-non-coding regions, although some segments have a second or third functional ORF [2].

REPLICATION

Virus cell entry varies between genera but usually results in loss of outer-capsid components. The resulting transcriptionally

active particles are released into the cytoplasm. The 5'-capped mRNAs are synthesized by structural enzymatic components of the particle and are released through pores at the icosahedral apices of the virion into the cytoplasm. Viroplasm, also known as virus inclusion bodies, are distributed throughout the cytoplasm. These neo-organelles are sites of viral mRNA synthesis, genome replication and particle assembly [3]. Sets of a single copy of each capped mRNA are incorporated into progeny virus particles [4]. These mRNAs serve as templates for negative-sense strand synthesis, thereby reconstituting genomic encapsidated dsRNAs. Progeny virions are released without compromising cell viability (e.g. budding) or following cell lysis, depending on the cell type [1, 5].

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The family *Sedoreoviridae* includes several genera (Fig. 2) and >35 species [6] of viruses infecting mammals, birds, crustaceans, arthropods, algae and plants. The number of genome segments (10–12) is characteristic of viruses within a single genus. Other factors distinguishing different genera are host (and vector) range, disease signs and capsid structure. The amino acid sequence of the relatively conserved RNA-directed RNA polymerase can be used for comparison across taxonomic boundaries. Among the members of a species, protein and RNA sequences are relatively conserved, being serologically cross-reactive and including specific RNA packaging signals. This high degree of functional and structural compatibility allows viable progeny virus strains to be generated by reassortment between viruses of the same species.

RESOURCES

Full ICTV Report on the family *Sedoreoviridae*: ictv.global/report/sedoreoviridae

Funding information

Production of this Profile, the ICTV Report and associated resources was supported by the Microbiology Society.

Acknowledgements

Members of the ICTV (10th) Report Consortium are Stuart G. Siddell, Elliot J. Lefkowitz, Sead Sabanadzovic, Peter Simmonds, F. Murilo Zerbini, Donald B. Smith and Jens H. Kuhn.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. Jaafar FM, Attoui H, Mertens PPC, de Micco P, de Lamballerie X. Structural organization of an encephalitic human isolate of Banna virus (genus *Seadornavirus*, family *Reoviridae*). *J Gen Virol* 2005;86:1147–1157.
2. Belhouchet M, Mohd Jaafar F, Firth AE, Grimes JM, Mertens PPC, et al. Detection of a fourth orbivirus non-structural protein. *PLoS One* 2011;6:e25697.
3. Papa G, Borodavka A, Desselberger U. Viroplasm: assembly and functions of rotavirus replication factories. *Viruses* 2021;13:1349.
4. Boyce M, McCrae MA, Boyce P, Kim JT. Inter-segment complementarity in orbiviruses: a driver for co-ordinated genome packaging in the *Reoviridae*? *J Gen Virol* 2016;97:1145–1157.
5. Fu H. Mechanisms controlling the infection of *Culicoides* biting midges with bluetongue virus. University of Hertfordshire; 1995. <https://uhra.herts.ac.uk/handle/2299/14153>
6. Attoui H, Jaafar FM, Belhouchet M, de Micco P, de Lamballerie X, et al. *Micromonas pusilla* reovirus: a new member of the family *Reoviridae* assigned to a novel proposed genus (*Mimoreovirus*). *J Gen Virol* 2006;87:1375–1383.
7. Trask SD, McDonald SM, Patton JT. Structural insights into the coupling of virion assembly and rotavirus replication. *Nat Rev Microbiol* 2012;10:165–177.