

UC Irvine

UC Irvine Previously Published Works

Title

ICTV Virus Taxonomy Profile: Arenaviridae 2023.

Permalink

<https://escholarship.org/uc/item/993982f4>

Journal

Journal of General Virology, 104(9)

Authors

Charrel, Rémi
Gonzalez, Jean-Paul
Günther, Stephan
et al.

Publication Date

2023-09-01

DOI

10.1099/jgv.0.001891

Copyright Information

This work is made available under the terms of a Creative Commons Attribution License, available at <https://creativecommons.org/licenses/by/4.0/>

Peer reviewed



ICTV Virus Taxonomy Profile: *Arenaviridae* 2023

Sheli R. Radoshitzky^{#1}, Michael J. Buchmeier², Rémi N. Charrel³, Jean-Paul J. Gonzalez⁴, Stephan Günther⁵, Jussi Hepojoki^{6,7}, Jens H. Kuhn⁸, Igor S. Lukashevich⁹, Víctor Romanowski¹⁰, Maria S. Salvato¹¹, Manuela Sironi¹², Mark D. Stenglein¹³ and Juan Carlos de la Torre^{14,*}

Abstract

Arenaviridae is a family for ambisense RNA viruses with genomes of about 10.5 kb that infect mammals, snakes, and fish. The arenavirid genome consists of two or three single-stranded RNA segments and encodes a nucleoprotein (NP), a glycoprotein (GP) and a large (L) protein containing RNA-directed RNA polymerase (RdRP) domains; some arenavirids encode a zinc-binding protein (Z). This is a summary of the International Committee on Taxonomy of Viruses (ICTV) report on the family *Arenaviridae*, which is available at www.ictv.global/report/arenaviridae.

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

Example	lymphocytic choriomeningitis virus (S: AY847350; L: AY847351), species <i>Mammarenavirus choriomeningitidis</i> , genus <i>Mammarenavirus</i>
Genome	Two or three single-stranded, usually ambisense, RNA molecules (segments): small (S), medium (M), and large (L)
Replication	Ribonucleoprotein complexes containing anti-genomic RNA serve as templates for synthesis of genomic RNA
Translation	From capped and non-polyadenylated mRNAs. The 5' cap structure is obtained via cap-snatching from cellular mRNAs
Host range	Fish (antennaviruses), mammals (mammarenaviruses), reptiles (hartmanviruses and reptarenaviruses), and potentially also ticks
Taxonomy	Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Negarnaviricota</i> , class <i>Ellioviricetes</i> , order <i>Bunyavirales</i> ; >4 genera and >59 species

VIRION

Arenavirids produce virions that are spherical or pleomorphic in shape and 40–200 nm in diameter, with dense lipid envelopes (Table 1 and Fig. 1). The virion surface layer is covered with club-shaped projections that have distinctive stalk and head regions. These projections consist of trimeric spike structures of two virus-encoded membrane glycoprotein (GP) subunits (GP1 and GP2) and, in the case of some arenavirids, a stable signal peptide (SSP). Isolated ribonucleoprotein

(RNP) complexes are organized into ‘beads-on-a-string’-like structures [1, 2].

GENOME

Arenavirid genomes consist of two or three single-stranded, typically ambisense, RNA segments (small [S], medium [M], and large [L]). Some of these RNAs encode two proteins in non-overlapping open reading frames of opposite polarities that are separated by

Received 14 August 2023; Accepted 17 August 2023; Published 13 September 2023

Author affiliations: ¹Center for Drug Evaluation and Research, Food and Drug Administration, Silver Spring, MD 20903, USA; ²University of California, Irvine, CA 92697, USA; ³Unité des Virus Emergents, Marseille CEDEX 05, France; ⁴Georgetown University, Washington, DC, USA; ⁵Bernhard Nocht Institute for Tropical Medicine, 20359 Hamburg, Germany; ⁶University of Helsinki, 00014 Helsinki, Finland; ⁷University of Zurich, Zurich, Switzerland; ⁸Integrated Research Facility at Fort Detrick, Fort Detrick, Frederick, MD 21702, USA; ⁹University of Louisville, Louisville, KY 40202, USA; ¹⁰Universidad Nacional de La Plata—Consejo Nacional de Investigaciones Científicas y Técnicas, 49 y 115 s/n La Plata, Argentina; ¹¹University of Maryland, College Park, MD 20742, USA; ¹²Scientific Institute IRCCS “E. Medea”, 23842 Bosisio Parini, Italy; ¹³Colorado State University, Fort Collins, CO 80523, USA; ¹⁴The Scripps Research Institute, La Jolla, CA 92037, USA.

*Correspondence: Juan Carlos de la Torre, juanct@scripps.edu

Keywords: *Arenaviridae*; arenavirus; ICTV Report; mammarenavirus; reptarenavirus; taxonomy.

Abbreviations: GP, glycoprotein; GPC, glycoprotein precursor; IGRs, intergenic regions; L, large; M, medium; NP, nucleoprotein; RNP, ribonucleoprotein; S, small; SSP, stable signal peptide; Z, zinc-binding protein.

#The content of this publication should not be interpreted as necessarily representing the official policies, either expressed or implied, of the U.S. Department of Health and Human Services.

001891 © 2023 The Authors



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

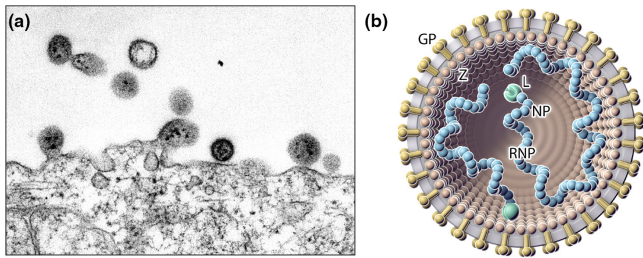


Fig. 1. (a) Electron micrograph of lymphocytic choriomeningitis virus budding from an infected cell. (b) Illustration of a particle in (a) showing the spherical and enveloped particle (grey) that is spiked with glycoproteins (GP, gold) around a layer of zinc-binding proteins (Z, brown). The small (S) and large (L) ribonucleoprotein (RNP) complexes inside the particle consist of nucleoprotein (NP; blue) and large (L; green) protein.

non-coding intergenic regions (IGRs) (Fig. 2). The S RNA encodes a nucleoprotein (NP) in the virus genome-complementary strand and, in many cases, a virus glycoprotein precursor (GPC) in the virus genome-sense strand. The L RNA segment encodes a large (L) protein in the virus genome-complementary strand and, in some cases, a zinc-binding protein (Z) in the virus genome-sense sequence [1–3].

REPLICATION

Arenavirions attach to cell-surface receptors or attachment factors and enter via the endosomal route. Some viruses engage intracellular receptors in endosomes. pH-dependent fusion with late endosomes releases the virion RNP complex into the cytoplasm. The virus RNP directs both RNA genome replication and gene

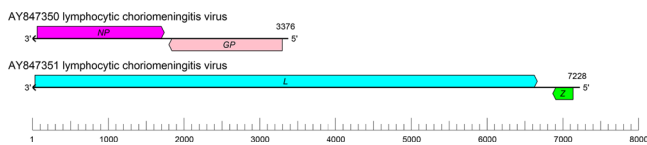


Fig. 2. Mammarenavirus genome. The ends of both segments are complementary at their termini, likely promoting the formation of panhandle RNP complexes within the virion. GP, glycoprotein gene; L, large protein gene; NP, nucleoprotein gene; Z, zinc-binding protein gene.

References

1. Radoshitzky SR, Bào Y, Buchmeier MJ, Charrel RN, Clawson AN, et al. Past, present, and future of arenavirus taxonomy. *Arch Virol* 2015;160:1851–1874.
2. Radoshitzky SR, Buchmeier M, de la Torre JC. *Arenaviridae: the viruses and their replication*. In: Howley PM, Knipe DM and Whelan SPJ (eds). *Fields Virology*. Volume 1 (Emerging Viruses), 7th ed. Philadelphia, Pennsylvania, USA: Wolters Kluwer/Lippincott Williams & Wilkins; 2020. pp. 784–809.
3. Shi M, Lin X-D, Chen X, Tian J-H, Chen L-J, et al. The evolutionary history of vertebrate RNA viruses. *Nature* 2018;561:197–202.

transcription. During replication, L protein reads through the IGR transcription–termination signal and generates uncapped antigenomic and genomic RNAs. Transcription of mRNAs encoding GPC and Z occurs only after the first round of virus replication, during which S and L antigenomes are produced. Arenavirid mRNAs lack 3'-terminal poly(A) tracts but have several non-templated 5' bases, consistent with the use of a cap-snatching mechanism to initiate transcription. Virion budding occurs from the cellular plasma membrane, thereby providing the virion envelope [1, 2].

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The family *Arenaviridae* is included in the negarnaviricot order *Bunyavirales*. Arenavirids are most closely related to myxovirids, nairovirids, phenuivirids and wupedevirids. Arenavirids differ from most other bunyavirals by having segmented genomes with ambisense organization. The family includes several genera and >59 species. Some arenavirids can cause severe diseases in humans (e.g. Lassa fever) [4]. Other arenavirids cause disease in captive snakes [3, 5].

RESOURCES

Full ICTV Report on the family *Arenaviridae*: www.ictv.global/report/arenaviridae.

Funding information

Production of this summary, the online chapter, and associated resources was supported by the Microbiology Society. This work was supported in part through the Laulima Government Solutions, LLC, prime contract with the U.S. National Institute of Allergy and Infectious Diseases (NIAID) under Contract No. HHSN272201800013C. J.H.K. performed this work as an employee of Tunnell Government Services (TGS), a subcontractor of Laulima Government Solutions, LLC, under Contract No. HHSN272201800013C. The content of this publication should not be interpreted as necessarily representing the official policies, either expressed or implied, of the U.S. Department of Health and Human Services or of the institutions and companies affiliated with the authors.

Acknowledgements

We thank Stuart G. Siddell, Elliot J. Lefkowitz, Sead Sabanadzovic, Peter Simmonds, F. Murilo Zerbini, Evelien Adriaenssens, Mart Krupovic, Jens H. Kuhn, Luisa Rubino, Arvind Varsani (ICTV Report Editors) and Donald B. Smith (Managing Editor, ICTV Report). We also thank Anya Crane and Jiro Wada (Integrated Research Facility at Fort Detrick), for critically editing the text and preparing figures.

Conflicts of interest

The authors declare that there are no conflicts of interest.

4. Radoshitzky SR, Kuhn JH, Jahrling PB, Bavari S. Hemorrhagic fever-causing mammarenaviruses. In: Bozue J, Cote CK and Glass PJ (eds). *Medical Aspects of Biological Warfare*. Fort Sam Houston, USA: Borden Institute, US Army Medical Department Center and School, Health Readiness Center of Excellence; 2018. pp. 517–545.
5. Pontremoli C, Forni D, Cagliani R, Sironi M. Analysis of reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. *Infect Genet Evol* 2018;64:212–218.