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ICTV VIRUS TAXONOMY PROFILE

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ICTV Virus Taxonomy Profile: *Arenaviridae*

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Abstract

Members of the family *Arenaviridae* produce enveloped virions containing genomes consisting of two or three single-stranded RNA segments totalling about 10.5 kb. Arenaviruses can infect mammals, including humans and other primates, snakes, and fish. 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*

Typical member:	**lymphocytic choriomeningitis virus, Armstrong 53b (S segment: AY847350; L segment: AY847351), species *Lymphocytic choriomeningitis mammarenavirus*, genus *Mammarenavirus***
Virion	Enveloped, pleomorphic virions 40–200 nm in diameter with trimeric surface spikes
Genome	Two or three single-stranded, usually ambisense, RNA molecules called 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 derived by polymerase slippage or cap-snatching from cellular mRNAs
Host range	Fish (antennaviruses), mammals (mammarenaviruses) and reptiles (hartmaniviruses and reptarenaviruses), but possibly also bats and ticks
Taxonomy	Realm *Riboviria,* phylum *Negarnaviricota*, subphylum *Polyploviricotina*, class *Ellioviricetes*, order *Bunyavirales*. The family includes several genera and >40 species

VIRION

Virions are spherical or pleomorphic in shape, 40–200 nm in diameter, with dense lipid envelopes (Table 1 and Fig. 1). The virion surface layer is covered with club-shaped projections with 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 arenaviruses, a stable signal peptide (SSP). Isolated ribonucleoprotein (RNP) complexes appear as 'beads-on-a-string'-like structures [1–3].

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Abbreviations: GP, glycoprotein; GPC, glycoprotein precursor; IGR, intergenic region; NP, nucleoprotein; RNP, ribonucleoprotein; SSP, stable signal peptide.

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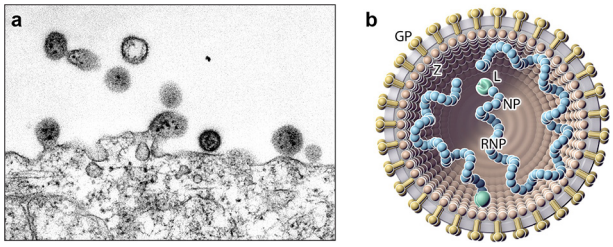

Fig. 1. (a) Electron micrograph of lymphocytic choriomeningitis virus particles, showing dark internal inclusion bodies, budding from an infected cell. (b) Schematic illustration of a (mammalian) arenavirus particle. Shown is the spherical and enveloped (grey) particle that is spiked with glycoproteins (GP, gold) around a layer of zinc finger matrix proteins (Z, brown; missing in hartmaniviruses). The small and large ribonucleoprotein (RNP) complexes inside the particle consist of nucleoprotein (NP, blue) and RNA-dependent RNA polymerase (L, green).

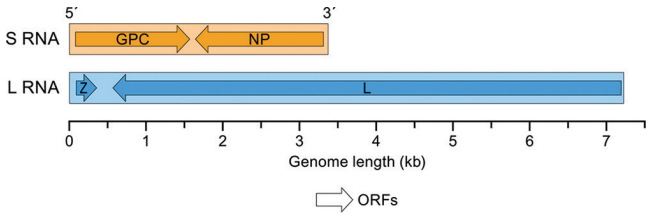

Fig. 2. Schematic representation of the bisegmented genome organization of the mammalian arenavirus lymphocytic choriomeningitis virus. The 5′- and 3′-ends of both segments (S and L) are complementary at their termini, probably promoting the formation of circular RNP complexes within the virion. GPC, glycoprotein precursor; L, RNA-dependent RNA polymerase; NP, nucleoprotein; Z, zinc finger matrix protein. ORFs are separated by non-coding IGRs with predicted hairpin structures (not shown).

GENOME

Arenavirus genomes consist of two or three single-stranded, typically ambisense RNA molecules, termed small (S), medium (M) and large (L). Some of these RNAs encode two proteins in non-overlapping ORFs of opposite polarities that are separated by non-coding intergenic regions (IGRs) (Fig. 2). The S RNA encodes nucleoprotein (NP) in the virus genome-complementary sequence, and, in many cases, the virus glycoprotein precursor (GPC) in the virus genome-sense sequence. The L RNA encodes the L protein in the virus genome-complementary sequence, and, in some cases, the zinc-finger matrix protein (Z) in the virus genome-sense sequence [1–4].

REPLICATION

Arenaviruses attach to cell-surface receptors and enter via the endosomal route. pH-dependent fusion with late endosomes releases the virion RNP complex into the cytoplasm. In some arenaviruses, this pH-dependent fusion event requires the previous participation of an intracellular receptor. The virus RNP directs both RNA genome replication and gene transcription. During replication, L reads through the IGR transcription-termination signal and generates uncapped antigenomic and genomic RNAs. In ambisense coding arrangements, transcription of mRNAs encoding GPC and Z occurs only after the first round of virus replication, during which S and L antigenomes are produced.

Arenavirus proteins are synthesized from subgenomic mRNAs that lack 3′-terminal poly(A) and in which the 5′-cap is followed by several non-templated bases, possibly the result of cap-snatching.

Virion budding occurs from the cellular plasma membrane, thereby providing the virion envelope [1–3].

TAXONOMY

Arenaviruses form a family in the order *Bunyavirales*. Within this order, arenaviruses are most closely related to members of the family *Mypoviridae*. Arenaviruses differ from most other bunyaviruses by having segmented genomes with an ambisense organization. The family includes several genera and >40 species. Some arenaviruses can cause severe and sometimes fatal diseases in humans (e.g. Lassa fever) [5]. Other arenaviruses cause disease in captive snakes [4, 6], and some arenaviruses can infect fish [4].

Resources

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

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Conflicts of interest
The authors declare that there are no conflicts of interest.

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