Trends in Microbiology | **Microbe of the Month**

Haloferax volcanii

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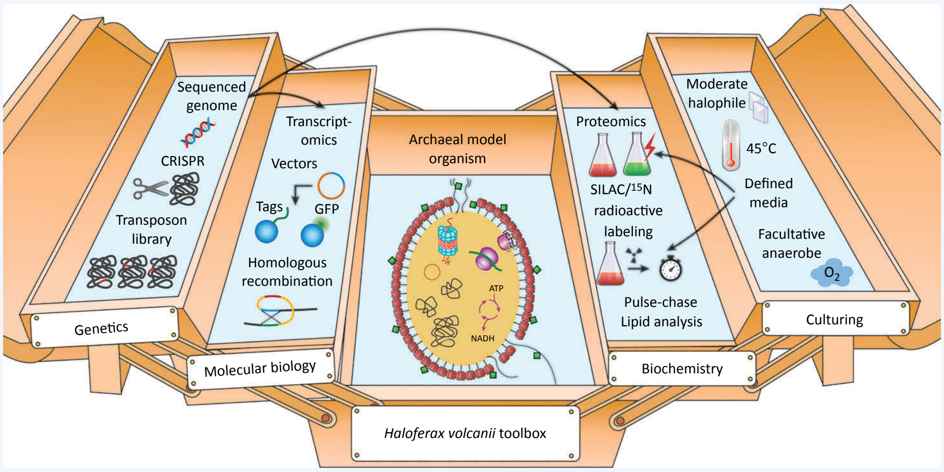
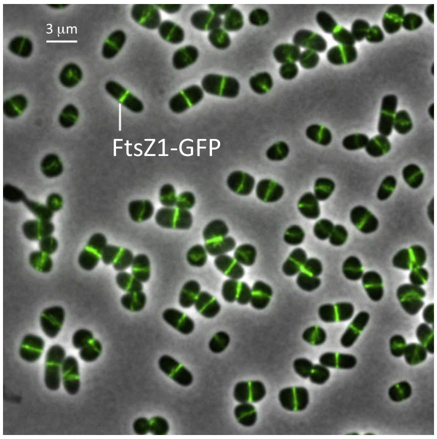


Trends in Microbiology

Isolated from the Dead Sea in 1975, *Haloferax volcanii* thrives in high salt environments and has emerged as an important archaeal model system. An extensive repertoire of genetic, molecular biological, and biochemical tools has been developed for this fast-growing, easily cultivated haloarchaeon, including expression vectors and gene-deletion strategies, including CRISPR. Its low mutation rate and ability to grow on defined media allow straightforward application of methods such as metabolic labeling, and the sequenced genome laid the foundation for transcriptomics and proteomics studies. These tools have allowed examination of key pathways such as transcription, noncoding RNAs, protein synthesis and degradation, protein glycosylation, motility, and biofilm formation. With the collaborative spirit of the *H. volcanii* community, this model system has become invaluable not only for enhancing our understanding of archaea but also for improving the development of biotech applications.



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TAXONOMY AND CLASSIFICATION:
DOMAIN: Archaea
PHYLUM: Euryarchaeota
CLASS: Halobacteria
ORDER: Halobacteriales
FAMILY: Halobacteriaceae
GENUS: *Haloferax*
SELECTED SPECIES: *Haloferax volcanii*
DS2 – first sequenced strain

KEY FACTS:

First isolated by Benjamin Elazari Volcani.

Chemoorganotroph, uses polysaccharides, sugars, and amino acids as carbon sources.

Pleomorphic disk-shaped, or, when motile, rod-shaped cells.

First archaeon shown to transfer genes by a natural mating system.

Cells have one main chromosome (2.9 Mb), three secondary ones, (85–690 kb) and a plasmid (6.4 kb). They contain six origins of replication and 3996 genes encoding proteins.

Polyploid cells can contain up to 30 chromosome copies.

Archaea-specific features include, among others, archaella that drive motility, ether-linked isoprenoid membrane and cell wall composed of S-layer glycoprotein, the best-studied archaeal glycoprotein (*N*- and *O*-glycosylation), which is C-terminally lipid-anchored.

Bacteria-like CRISPR, transcription regulators, chemotaxis machinery, and extracytoplasmic proteases.

Eukaryote-like basal transcription factors, proteasome substrate targeting and degradation.

Several pathways, for example, thiamine biosynthesis, performed by chimera of eukaryote- and bacteria-like pathways.

About 50% of exported proteins are transported across the membrane via the Tat pathway; mostly predicted lipoproteins.

Survival in high salt depends on salt-in strategy maintaining homeostasis and low protein pI preventing misfolding.

Nonpathogen with simple growth conditions and low risk of contamination due to high salt media; great tool for K-16 experiments demonstrating principles of microbiology, genetics, and evolution.

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Resources

www.haloarchaea.com/resources/halohandbook/

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