

Archaea: Perspective in Industrial and Environmental Applications

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Perspective

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DESCRIPTION

The *archaea* domain comprises a group of prokaryotic microorganisms that are evolutionarily separated from bacteria and eukaryotes. Most of the archaea live in extreme environmental conditions, such as very high or freezing temperatures, highly alkaline or acidic pHs, extreme salinities, etc. Although most *archaea* are difficult to culture within the laboratory condition, nevertheless their omnipresence has been determined using culture-independent methods. *Archaea* exhibit diversity in their habitats and are taxonomically classified in different phyla based on modern molecular phylogenetic approaches. In the current classification, *archaea* have been classified into 27 phyla and these phyla have been grouped into three superphyla: Asgard, DPANN and TACK [1]. The current phylogenetic knowledge about *archaea* has revealed their importance in mediating many ecological processes, such as global carbon and nutrient cycling, and their key role in the origin and evolution of eukaryotes. *Archaea* are also potential sources of extremophilic enzymes, biogas production, and are predominant biodegraders in sewage treatment plants.

In the past few years, the continuous expansion of sequence information of archaeal genomes is opening door for the discovery of novel industrial enzymes which are expected to showcase better potential than those available from other organisms. Presently, more the 600 archaeal genomes have been sequenced; however, this number is still quite less than their actual number which might be present in nature. Comparative genomics of prokaryotes and eukaryotes may be used as a promising tool to explicate the genetic contents and their products in these exotic microorganisms. The information derived from these studies may be used to deduce the structure and gene sequence of extremophilic enzymes (thermophilic, acidophilic, alkalophilic, etc.) Further, genome mining and ancestral sequence reconstruction methods have been used as powerful tools to find novel extremophilic enzymes as per the need of the industrial processes [2]. A frequently used culture-independent method is based on the isolation, amplification and characterization of nucleic acid sequences (i.e., DNA and RNA) directly from an environment, using the metagenomics approach. Furthermore, the current progress in the chemical gene-synthesis approach has made it possible to directly synthesize a gene *in vitro* and express it in a host and to characterize the new gene product without the requirement of cultivating the source organism.

The uncultured microbes from the subdivision *Crenarchaeota* have been proposed as ammonia-oxidizers, most abundant in soil. They also make up a large proportion (around 20%) of the picoplanktonic microbes inhabiting the world's oceans. Unculturable *archaea* belonging to the subdivision *Euryarchaeota*, inhabiting deep-sea marine sediments are responsible for the anaerobic oxidation of methane, a potent greenhouse gas. On the contrary, the uncultivated methanogenic *Euryarchaea* inhabiting terrestrial anaerobic environments have been estimated to emit ~ 10%-25% globally [1].

Archaea are potential sources of many extremozymes such as amylases, glucoamylases, xylanases, cellulases, proteases, dehydrogenases, lipases, pullulanases, esterases, and DNA polymerases. These enzymes have been reported to have applications in biofuel production, food processing, bio-mining, starch processing, desulfurization of coal, detergents formulations, food and feed, beer and paper industry, peptide synthesis, biocatalysis in organic media, cellulose processing, textiles finishing, paper bleaching, molecular biology tools, oxidation-reduction reactions, fine chemicals synthesis and pharmaceuticals [3,4]. Archaeal extremozymes have been shown to have better catalytic efficiencies under harsh reaction conditions encountered in industrial processes [4]. Besides these, *archaea* are also extensively used in the commercial production of biogas and in sewage treatment plants and are expected to produce metabolites for sustainable development [5]. Lab culturing difficulties and lack of efficient genetic manipulation tools for *archaea* impede the large-scale production of enzymes and metabolites from them. These problems can be solved up to some extent by methods such as codon optimization of the synthetic gene for cloning and overexpression in a heterologous expression system. Though many proteins cannot fold correctly in the heterologous expression systems, which are a big issue for extremozyme, especially from *archaea*. Recently, a model expression system *Haloferax volcanii* was developed and successfully used for the production of some haloarchaeal proteins [6].

In the past few years, some databases have been created to store the genetic sequence information of *archaea* which will give a boost to research in this domain. Designing new and more efficient bioinformatics tools will also accelerate the bioprospecting for novel proteins and metabolites from *archaea*. Further, the decoding of *archaeal* genomic sequences will shed light on their yet undiscovered metabolic potential and shall give insights into their manipulation and optimal exploitation for the preservation, maintenance and sustainability of the congenial ecosystem and healthy environment on the earth.

REFERENCES

1. Baker BJ, et al. Diversity, ecology and evolution of archaea. *Nat Microbiol.* 2020;5:887-900.
2. Verma S, et al. Identification of new members of alkaliphilic lipases in archaea and metagenome database using reconstruction of ancestral sequences. *3 Biotech.* 2019;9:165.
3. Cabrera MA, et al. Biotechnological applications of archaeal enzymes from extreme environments. *Biol Res.* 2018;51:37.
4. Meghwanshi GK, et al. Archaeal lipolytic enzymes: Current developments and further prospects. *Biotechnol Adv.* 2022;61:108054.
5. Enzmann F, et al. Methanogens: Biochemical background and biotechnological applications. *AMB Expr.* 2018;8:1-22.
6. Martinez-Espinosa RM. Heterologous and homologous expression of proteins from haloarchaea: Denitrification as Case of Study. *Int J Mol Sci.* 2019;21:82.