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Unveiling the beauty of Archaea

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One of the greatest achievements in the life sciences in the 20th century was the recognition of three forms, or domains, of cellular life, i.e., Bacteria, Archaea, and Eukarya, in the three-domain theory put forward by Carl Woese and George Fox in 1977 [1]. According to their theory, Archaea, which were previously regarded as a peculiar group of bacteria, are no more closely related to Bacteria than to the Eucarya from a phylogenetic viewpoint and, thus, represent the third form of life. This theory was not widely accepted until 1996 when the genome sequence of *Methanocaldococcus jannaschii*, a methane-producing archaeon, was published [2]. The genetic blueprint of this organism offered strong support for the three-domain theory.

By some estimates, Archaea account for 20% of the total biomass on Earth [3]. The majority of known Archaea are extremophiles thriving in extremes of temperature, pH, salinity, etc. [4]. A number of hyperthermophilic Archaea have been isolated from hot springs and hydrothermal vents, halophilic Archaea from salt lakes, and acidophilic Archaea from acid mine drainage. Archaea also exist in "non-extreme" environments, including soils, wetlands, oceans, and the human colon [5]. Archaea are capable of a wide range of metabolic activities and are believed to serve important roles in driving the C, N, and S cycles on the planet [6]. Despite their resemblance in size and morphology, Archaea and Bacteria differ markedly in many important aspects, such as cell wall and membrane composition and DNA transactions [7–10]. Strikingly, Archaea employ genetic mechanisms similar to, but simpler than, those found in Eucarya [11]. Furthermore, a surprising variety of mobile genetic elements (e.g., viruses and plasmids) have been found in the domain Archaea [12]. Some archaeal viruses have unusual shapes that are never seen in bacteriophages or eucaryal viruses [13].

The landmark discovery of Archaea drew much attention to this new form of life. There was a further boost of interest in Archaea after the sequencing of the *M. jannaschii* genome. A number of laboratories have since become involved, at least partially, in studying Archaea for clues on the fundamentals and evolution of life or for enzymes or functions with potential applications. In the short period of less than 20 years since the end of the last century, our understanding of Archaea has significantly increased [13–21]. To date, nearly 200 archaeal genomes have been sequenced. Because of their unusual stability, proteins from thermophilic Archaea are favored for biochemical and structural biological studies. Some 5500 crystal structures of archaeal proteins, 60% of which are derived from thermophiles, are now available in PDB. Over 80% of them were obtained in the past decade.

In China, research on Archaea started in the late 1970s when the first extremophile laboratory was established at the Institute of Microbiology, Chinese Academy of Sciences (IMCAS). The laboratory isolated halophilic microorganisms from salt lakes in Qinghai province, China [22]. In the 1980s, scientists from IMCAS isolated the first thermoacidophilic archaeon, *Acidianus tengchongenses*, from hot springs in Tengchong, Yunnan Province [23,24]. From the late 1990s to the early 2000s, the pace of archaeal research accelerated and entered the molecular and genomic phase. Several archaeal laboratories devoted entirely to research on thermophilic, halophilic, or methanogenic Archaea were set

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up at IMCAS as well as at several universities. Their research covers chromosomal organization, genetic mechanisms, viruses and plasmids, synthesis of polyhydroxyalkanoates (PHAs), quorum sensing, enzyme stability, etc. [25–36]. Although moderate in size, the Chinese archaeal community has made important contributions to the understanding of Archaea and is now well respected in the field.

In this special archaeal issue, we have assembled five review articles on topics ranging from archaeal DNA replication, chromatin proteins, archaeal viruses, haloarchaeal cellular and organellar membrane-associated proteins, and psychrotolerant methanogenic archaea. Obviously, there are many more hot topics on Archaea than this issue can cover. However, we hope that these review articles will offer a glimpse into Archaea and convey our immense excitement derived from the study of these surprising organisms.

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1 Woese C, Fox G. Phylogenetic structure of the prokaryotic domain: the primary kingdoms. Proc Natl Acad Sci USA, 1977, 74: 5088–5090
2 Bult C, White O, Olsen G, *et al*. Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. Science, 1996, 273: 1058–1073
3 DeLong E, Pace N. Environmental diversity of bacteria and archaea. Syst Biol, 2001, 50: 470–478
4 Pikuta E, Hoover R, Tang J. Microbial extremophiles at the limits of life. Crit Rev Microbiol, 2007, 33: 183–209
5 DeLong E. Everything in moderation: archaea as 'non-extremophiles'. Curr Opin Genet Dev, 1998, 8: 649–654
6 Schäfer G, Engelhard M, Müller V. Bioenergetics of the Archaea. Microbiol Mol Biol Rev, 1999, 63: 570–620
7 Krieg N. Bergey's Manual of Systematic Bacteriology. New York: Springer, 2005. 21
8 Golyshina O, Pivovarova T, Karavaiko G, *et al*. *Ferroplasma acidiphilum* gen. nov., sp. nov., an acidophilic, autotrophic, ferrous-iron-oxidizing, cell-wall-lacking, mesophilic member of the Ferroplasmaceae fam. nov., comprising a distinct lineage of the Archaea. Int J Syst Evol Microbiol, 2000, 50: 997–1006
9 De Rosa M, Gambacorta A, Gliozzi A. Structure, biosynthesis, and physicochemical properties of archaebacterial lipids. Microbiol Rev, 1986, 50: 70–80
10 Gaasterland T. Archaeal genomics. Curr Opin Microbiol, 1999, 2: 542–547
11 Kelman L, Kelman Z. Multiple origins of replication in archaea. Trends Microbiol, 2004, 12: 399–401
12 Lipps G. Plasmids: Current Research and Future Trends. Norfolk: Caister Academic Press, 2008. 27
13 Prangishvili D, Forterre P, Garrett R. Viruses of the Archaea: a unifying view. Nat Rev Microbiol, 2006, 4: 837–848
14 Cavicchioli R. Archaea—timeline of the third domain. Nat Rev Microbiol, 2011, 9: 51–61
15 White M. Homologous recombination in the archaea: the means justify the ends. Biochem Soc Trans, 2011, 39: 15–19
16 Horvath P, Barrangou R. CRISPR/Cas, the immune system of bacteria and archaea. Science, 2010, 327: 167–170
17 Luijsterburg M, White M, van Driel R, *et al.* The major architects of chromatin: architectural proteins in bacteria, archaea and eukaryotes. Crit Rev Biochem Mol Biol, 2008, 43: 393–418
18 Barry E, Bell S. DNA replication in the archaea. Microbiol Mol Biol Rev, 2006, 70: 876–887
19 Egorova K, Antranikian G. Industrial relevance of thermophilic Archaea. Curr Opin Microbiol, 2005, 8: 649–655
20 Jarrell K, Walters A, Bochiwal C, *et al*. Major players on the microbial stage: why archaea are important. Microbiology, 2011, 157: 919–936
21 Sato T, Atomi H. Novel metabolic pathways in Archaea. Curr Opin Microbiol, 2011, 14: 307–314
22 Wang D, Zhou P, Tain X, *et al.* Identification of new species of extreme halophilic bacteria. Acta Microbiol Sin, 1984, 24: 304–309
23 Zhong H, Chen X, Li Y, *et al.* A new genus of thermo- and acido-philic bacteria–*Sulfosphaerellus*. Acta Microbiol Sin, 1982, 22: 1–7
24 He Z, Li Y, Zhou P. Study on reclassification of extremely thermoacidophilic archaea strain S5. Acta Microbiol Sin, 2001, 41: 259–264
25 Guo L, Feng Y, Zhang Z, *et al*. Biochemical and structural characterization of Cren7, a novel chromatin protein conserved among Crenarchaea. Nucleic Acids Res, 2008, 36: 1129–1137
26 Zhang Z, Gong Y, Guo L, *et al.* Structural insights into the interaction of the crenarchaeal chromatin protein Cren7 with DNA. Mol Microbiol, 2010, 76: 749–759
27 Wu K, Lai X, Guo X, *et al*. Interplay between primase and replication factor C in the hyperthermophilic archaeon Sulfolobus solfataricus. Mol Microbiol, 2007, 63: 826–837
28 Hu J, Guo L, Wu K, *et al*. Template-dependent polymerization across discontinuous templates by the heterodimeric primase from the hyperthermophilic archaeon Sulfolobus solfataricus. Nucleic Acids Res, 2012, 40: 3470–3483
29 Zhou L, Zhou M, Sun C, *et al*. Precise determination, cross-recognition and functional analysis of the double-strand origins of the rolling circle replication plasmids in haloarchaea. J Bacteriol, 2008, 190: 5710–5719
30 Li Z, Lu S, Hou G, *et al*. Hjm/Hel308A DNA helicase from Sulfolobus tokodaii promotes replication fork regression and interacts with Hjc endonuclease *in vitro*. J Bacteriol, 2008, 190: 3006–3017
31 Zhang L, Zhang L, Liu Y, *et al*. Archaeal eukaryote-like Orc1/Cdc6 initiators physically interact with DNA polymerase B1 and regulate its functions. Proc Natl Acad Sci USA, 2009, 106: 7792–7797
32 Xiang X, Chen N, Huang X, *et al*. Spindle-shaped virus STSV1: virus-host interactions and genomic features. J Virol, 2005, 79: 8677–8686
33 Zhou L, Zhou M, Sun C, *et al.* Genetic analysis of a novel plasmid pZMX101 from *Halorubrum saccharovorum*: determination of the minimal replicon and comparison with the related haloarchaeal plasmid pSCM201. FEMS Microbiol Lett, 2007, 270: 104–108
34 Zhang G, Zhang F, Ding G, *et al*. Acyl homoserine lactone-based quorum sensing in a methanogenic archaeon. ISM J, 2012, doi: 10.1038/ismej.2011.203
35 Zhang Y, Ju J, Peng H, *et al*. Biochemical and structural characterization of the intracellular mannanase AaManA of *Alicyclobacillus acidocaldarius* reveals a novel glycoside hydrolase family belonging to clan GH-A. J Biol Chem, 2008, 283: 31551–31558
36 Huo Y, Hu Z, Zhang K, *et al*. Crystal structure of group II chaperonin in the open state. Structure, 2010, 18: 1270–1279