

Special Issue on  
**Genetic Manipulation in the Archaea: Current Progress  
 and Future Perspectives**

# CALL FOR PAPERS

In 1977, Carl Woese (University of Illinois at Urbana-Champaign) and his colleagues discovered the third domain of life-Archaea, which was considered to overturn one of the major dogmas of biology. The first genome sequence obtained from the archaeon *Methanococcus jannaschii* in 1996 revealed that archaea are more closely related to eukarya than to bacteria. Thereafter, archaea have been used as simple and robust models to study the essential cellular processes. Additionally, archaea, especially hyperthermophilic archaea, are of deep interest because of their thermostable enzymes for industrial/biotechnological applications.

Genetic techniques are fundamental and powerful to elucidate specific gene functions. Unlike eukarya and bacteria with genetics well-established, genetic manipulation in archaea is still challenging due to several major reasons: i) these organisms usually inhabit harsh environments (extreme conditions of temperature, pH, salinity, or pressure) and are therefore assumed to be difficult to isolate and culture in laboratory conditions (i.e., the ammonia-oxidizing archaea); ii) very few bacterial antibiotic markers are effective in archaea; 3) DNA delivery generally has a very low efficiency. Over the past decade, a suit of genetic approaches has been made in archaea including multiple selectable/counterselectable markers, shuttle vectors, high efficiency transformation procedures, *in vivo/vitro* transposon mutagenesis, reporter gene technologies, and versatile gene knock-in and knock-out methods. More recently, it has been reported that the endogenous CRISPR-Cas system can be utilized to enable precise genome editing (deletion, insertion, and site-specific mutagenesis) and efficient posttranscriptional gene silencing in *Sulfolobus* but are yet to be broadly applied in other archaea. For a more-depth understanding of the archaeal biology, additional sophisticated genetic tools are still required to be further developed.

In this special issue, we invite authors to submit original research and review articles addressing topics related to this issue.

Potential topics include but are not limited to the following:

- ▶ Augmentation of genetic tools in the archaeal model systems including Sulfolobales, Thermococcales, halophiles, and methanogens
- ▶ Development of genetic systems in the ammonia-oxidizing archaea (AOA) that are discovered in almost every aquatic and terrestrial habitat
- ▶ Novel genetic approaches such as transposon mutagenesis, CRISPR-Cas-based genome editing, RNA interference, and reporter systems in archaea
- ▶ Genetic analysis of genes responsible for essential cellular processes of archaea
- ▶ Application of archaea as metabolic engineering platforms for bioproduct and biofuel formation

Authors can submit their manuscripts through the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/archaea/cpfc/>.

#### Lead Guest Editor

Changyi Zhang, University of Illinois at Urbana-Champaign, Champaign, USA  
*cyz@illinois.edu*

#### Guest Editors

Norio Kurosawa, Soka University, Tokyo, Japan  
*kurosawa@soka.ac.jp*

Ling Deng, University of Copenhagen, Copenhagen, Denmark  
*lingdeng@food.ku.dk*

Xiangdong Chen, Wuhan University, Wuhan, China  
*xdchen@whu.edu.cn*

Nan Peng, Huazhong Agricultural University, Wuhan, China  
*nanp@mail.hzau.edu.cn*

#### Manuscript Due

Friday, 26 May 2017

#### First Round of Reviews

Friday, 18 August 2017

#### Publication Date

Friday, 13 October 2017