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International conference on extremophiles 2014

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More than 300 participants representing research organizations from 40 countries will meet September 7–11, 2014 at the 10th International Congress on Extremophiles in Saint Petersburg, Russia. This conference will include topics on genetics, genomics, ecology and diversity, physiology, and applications of extremophilic microorganisms. We are pleased to introduce our Special Issue that includes a selection of articles from the speakers in the plenary sessions and workshops of the forthcoming Extremophiles conference representing the broad and versatile range of work going on in our very active community. Invited speakers have contributed research papers and reviews covering their respective topics to be discussed at the meeting. The topics of these articles illustrate recent and remarkable progress and feature the best of the latest in research on extremophiles.

Sorokin, Muyzer, and co-workers review the progress of current techniques and methods to identify key processes and genes in carbon, nitrogen, and sulfur biogeochemical cycles mediated by cultured and uncultured bacterial and archaeal microorganisms from soda lakes (Sorokin et al. 2014), while Ventosa and his team illustrate different methodologies that have been used to investigate the microbial diversity and ecology of the hypersaline environments of the multi-pond saltern at Santa Pola in Spain (Ventosa et al. 2014). Halophilic microorganisms in hypersaline environments are also the topic of a comprehensive review by Oren. This article focuses on the taxonomy and classification of the archaeal family Halobacteriaceae (Oren 2014). Another review by Santos and her team sheds light on the adaptation of marine microorganisms to thrive in hot environments by

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accumulating unusual compatible solutes. The article focuses on mannosylglycerate, a solute associated with osmoadaptation in thermophilic prokaryotes, but unrelated with stress protection in red algae. Therefore, this compound is a very interesting example to investigate the evolutionary history and physiological roles of such production pathways in diverse lineages of the Tree of Life (Borges et al. 2014).

Deep-sea bacteria and their enzyme systems isolated from a sediment core were investigated in a research project developed in the groups of Antranikian and Horikoshi. Metagenome sequencing enabled the identification of more than 200 genes encoding carbohydrate-active enzymes from psychrophiles. Ten different glycoside hydrolases were produced in recombinant form and investigated toward their potential for industrial applications (Klippel et al. 2014).

Hedlund and partners review the synergistic impact of combined metagenomic- and single-cell genomic approaches to identify, classify, and understand uncultivatable extremophilic microorganisms (Hedlund et al. 2014). The outstanding cooperative original work by the groups of Koonin and Prangishvili deals with the genome-wide identification of poorly characterized, fast evolving, and clustered genomic regions in archaeal genomes that are composed of viruses, mobile elements, defense and membrane-associated systems. Such gene clusters were denoted as “dark matter islands” and their existences were compared in thermophiles and mesophiles (Makarova et al. 2014). Ciaramella and co-workers review recent exciting scientific advances to understand repair and defense mechanisms in hyperthermophilic Bacteria and Archaea. These extremophiles thrive in an environment that favors genome instability and the authors report on the coordinated action of highly specific repair enzymes focussing on reverse gyrase and DNA alkyltransferase (Vettone et al. 2014).

Two original papers from Albers’ and Ishino’s team shed light on archaeal physiology and development. *Sulfolobus acidocaldarius* is the model organism used by Albers and co-workers to investigate the cleavage activity of a series of class III signal peptidase PibD mutants (Henche et al. 2014). Ishino’s laboratory demonstrates interaction of proteins within the archaeal ternary complex TaMCM-TaGINS-TaCdc6-2 supporting evolutionary differences in DNA replication complexes of Archaea and Eukaryotes (Ogino et al. 2014). Moreover, Thomm and co-workers contributed a review, which deals with new findings concerning transcriptional regulation in the Archaea. They focus on the TrmB family of bacterial-like transcription regulators capable of modulating the eukaryotic-like transcription apparatus in Archaea (Gindner et al. 2014).

We thank our authors for their outstanding contributions and hope that you enjoy reading this Special Issue.

Yours sincerely,
Garabed Antranikian—Editor-in-Chief
Elizaveta Bonch-Osmolovskaya—Chair of Extremophiles 2014 and Guest Editor
Haruyuki Atomi—Managing Editor
Aharon Oren—Managing Editor
Michael W. Adams—Guest Editor
Helena Santos—Guest Editor

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