Stress genes: Role in physiological ecology

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Even cells well adapted to their ecosystems maintain the capacity to respond to sudden environmental changes, namely stressors, and mount defensive action at the molecular and genetic levels. This action is the stress (heat-shock) response whose central players are the stress (heat-shock) genes and proteins. Most ecosystems in nature are often upset by stressors which means that the stress genes and proteins are frequently called into action throughout the life of every organism. It follows that these genes and proteins are protagonists in physiological ecology. This is the common theme of the ensuing chapters that deal with different aspects of the stress response and its players.

The chapter on regulation of the heat-shock response in bacteria shows that regulatory signals and factors vary with the phylogenetic branch and the genes.These are organized into units of regulation, such as the g*roEl/S* and *hsp70(dnaK)* operons. They are regulated differently in the γ proteobacteria (*e.g., Escherichia coli*) in which the key element is the σ^{32} factor, as compared with the low GC gram positives (*e,g., Bacillus subtilis*) in which the critical factor is a repressor that binds the CIRCE element. The latter would be the first regulatory system to have appeared in bacterial evolution, but it was lost and replaced by others in some of the extant lineages.

The chapter on transcription initiation of stress genes in archaea introduces a new field only recently opened for investigation. Archaea are amazing organisms for all those familiar with bacteria and eukaryotes because of their many distinctive features, some of which are puzzling. For example, while the product of the *hsp70(dnaK)* gene, the molecular chaperone Hsp70(DnaK), is very similar in sequence and other structural details with functional implications to the homologs from bacteria, the transcription signals and factors do not resemble the bacterial but the eukaryotic counterparts. This chapter summarizes what is known on transcription and regulatory factors for archaeal stress genes and suggests promising research directions.

Likewise, the chapter on the heat-shock response in hyperthermophiles also discusses fascinating aspects of archaea, and other organisms, that live in extreme environments with very high temperatures (above 90 °C) and hydrostatic pressures. The key question is: How do the molecules —enzymes, DNA— maintain their conformation and function under extreme conditions? The means evolved for these purposes are briefly described in this chapter: stress genes and proteins, molecular chaperones, chaperonins, thermoprotectants, formation of multicellular structures, and others.

The chapter on metal stress in environmental flora is extremely interesting and stimulating. It narrates an adventure of discovery of novel stress genes in *E. coli* with methods applicable to other organisms, too. These new genes are pertinent to the stress response caused by stressors that are common pollutants of relevance to public health, such

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as arsenic, aluminum and selenium. In this regard, the chapter also offers the perspective on how stress genes might be useful tools for detecting and monitoring environmental pollution.