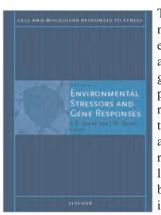
Stress... What stress?

Cell and Molecular Responses to Stress Volume (1): Environmental Stressors and Gene Responses

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This book addresses an urgent need to examine how environmental drives stress adaptation by combining phylogenetic with mitochondria-topopulation analysis of the relationship between stressors, their signalling to the genome and a suite of downstream survival responses tailored to supporting life in hostile environments. This bold approach inevitably exposes itself to the problem of meeting

the divergent ideas of what 'environment', 'stressors', 'gene responses' and 'adaptation' mean to the broad (ecologist to molecular biologist) audience that will read it. There is also the inevitable problem that the scope of the book precludes discussion of all the important stress gene families (cytokines are omitted, for example). Whatever your perspective, however, the knowledge explosion that will stem from the introduction of proteomics and genomics into comparative biology demands that we take stock of current understanding of environmental stress and its role in shaping species diversity. This volume is the first in the 'Cell and Molecular Responses to Stress' series, which has taken up this challenge as its broad goal. Although the general value of review compendia is inevitably limited by price, availability and time-span of relevance, the broad vocational appeal, high review quality and examination of concepts fundamental to stress detection and genomic signalling should guarantee this a lasting readership.

The volume is a multi-author compendium of twenty chapters broadly organised along the five themes of thermal, hypoxic/oxidative, osmotic stresses, pressure and transition metal toxicity. The first group of six chapters are probably the most crucial as they establish the conceptual framework for the book and provide the bulk of material relating to stress as a major mechanism in defining evolutionary traits and species distribution. The first two chapters by Hochachka and Suarez discuss the role of stress-sensing mechanisms and the design of respiratory pathways in adjusting metabolic output to meet acute (stressful) changes in aerobic metabolic demand. Travisano, Chow and Clarke, and Gilchrist, build on this introduction by skilfully examining the features of their defined environmental stress conditions (particularly thermal stress) that facilitate the selection and transmission of genotypic traits from one generation to another and which, ultimately, contribute towards the biogeographical range of species. Although 80~% of the volume is devoted to eukaryotic stress responses, it is within the prokaryotes that these themes are taken to their most extreme. Van de Vossenberg, Driessen and Konings complete this opening section by defining the characteristics of prokaryotic membrane ion transport and lipid mobility that enable them to thrive in almost any of the most extreme environments found on the planet.

The next series of chapters is devoted to the regulation of gene expression by oxygen and hypoxia/hyperoxia-evoked oxidative stress. Ma and Haddad begin with a review of oxygen signal transduction in the stabilisation of HIF-1 α transcription and translation, a transcription factor that is a key component in coordinating genomic responses aimed at the maintenance of aerobic oxygen supply and hypoxic defence. They present a novel approach to the study of hypoxia and cell survival using differential display and mutagenesis screening of the Drosophila genome to identify, map and clone genes involved in cell strategies to survive anoxic stress. The therapeutic potential of hypoxia/oxidative-stress-linked pathways in the treatment of ischaemia-reperfusion injury in the heart is explored in the two following chapters by Webster and Das and Maulik, which discuss second-messenger signalling pathways linking changes in the partial pressure of oxygen and other oxidative stresses characteristic of this condition with adaptive genomic responses. A most interesting, but unexpanded, theme within these chapters concerns current work aiming either to utilise the oxygen-sensing pathway itself to target beneficial 'survival' genes tailored to expressed in the environment of the region of injury itself or to utilise key environmental elements of ischaemia-reperfusion injury to evoke native expression of genes that defend tissue integrity as part of a preconditioning response.

Tailoring an appropriate response to a specific stressor is a key survival element, so it is particularly important to understand how different stress conditions yield specific responses through the expression of common stress gene families. The preceding themes examining thermotolerance and oxidative stress find molecular echoes in the next three chapters examining osmotic stress and prokaryotic anhydrobiosis by Stears and Gullans, Chen, Lu and Liu, and Kultz. Activation of heat shock transcription factor by members of the mitogenactivated protein kinase family plays a central role in signal transduction of hypo- and hyperosmotic stress, but is also wellknown to be of importance in regulating gene responses to thermal and oxidative stresses. Indeed, apart from an unidentified transcription factor, TonE binding protein, the heat-shock factor HSF may be the primary transcriptional regulator of gene responses to altered osmotic conditions. This is not, however, the only means of regulating genomic responses to changes in environmental tonicity. The biophysics of chromatin (de)condensation is crucially dependent on localised salt concentration and plays a role in the regulation

of cell cycle events and the targeting of cells into the apoptosis cascade. A reminder that eukaryotic cells are comparative newcomers to the art of osmosensing is the final chapter in this section by Billi and Potts, which discusses the biology of anhydrobiosis in prokaryotes, with special attention to the expression of pathways involved in the synthesis of vitrifying agents (trehalose and sucrose are two examples given), which may be a key to stabilising protein structure in the absence of water. The chapter ends on a tantalising, but again unexplored, note, which points towards the possibility of conferred anhydrobiosis, at least in bacteria, by expression of transgenes involved in sucrose polymerisation.

The concluding six chapters of the book deal with such a wide range of topics that it is hard to classify them on any one sub-theme, and the reader is left wondering if they could not have been better arranged among the preceding chapters. Muller and coauthors provide insight into the use of stressresponse genes as biomarkers of marine pollutants. Their focus on heat-shock chaperones induced by stressors as diverse as xenobiotics, heavy metals, heat, osmotic and pH stress serves to highlight both the diverse expression characteristics and conserved phylogenetic importance of this gene family as an immediate response to varied environmental stressors. A later chapter by Norris and Hightower complements this theme by exploring the role of heat-shock proteins in conferring thermotolerance to tropical and desert fish in the genus Poeciliopsis and includes a cladistic analysis of the sHSP/αcrystallin superfamily and a review of the diversity of functionally important HSPs in this genus. Nestled between this recurrent HSP theme is a thorough overview of redox and bioenergetic stress as regulators of mitochondrial function by Learey and Moyes. As it deals closely with reactive oxygen intermediates and redox regulation of gene transcription from the mitochondrial and nuclear genome, its integration with other themes within the book would have been better served if it had been situated among earlier chapters.

Despite the Editors' intention to maintain a phylogenetic perspective on the overall theme of the book, it is a pity that only a single chapter is given over to stress gene expression in plants. This, to my mind, is an important oversight, as the identification of environmentally regulated beneficial stress genes in plants has fuelled their practical application in commercial crop production to a level of success unrealised in animal biology. Warren, Thorlby and Knight offset this by providing an excellent and exhaustive review of the regulation, experimental mutation and transgenic potential of cold-induced genes in this species have animal homologues, the relevance of this area clearly extends beyond the plant world.

The examination of insect diapause and prokaryotic gene expression in the deep sea provides an excellent opportunity to examine alternative environmental cues, such as day length and pressure, as regulators of gene expression and cell function. In the case of diapause, Delinger discusses the possibility that circadian 'clock genes' regulate forms of developmental diapause in insects that modulate tissue differentiation by peptide hormones. Kato and co-authors take the example of prokaryotic piezophiles to examine how pressure-regulated operon transcriptional complexes are activated by pressures as high as 50~MPa. The function of the respiratory chain is also examined in this environment, where the expression of specialised cytochromes is necessary to overcome diffusion limitation resulting from the combination of low temperature and high pressure. The final chapter of the volume (Zhu, McKendry and Chavez) examines copper ion homeostasis in yeast and deals with the peculiar requirements of genes involved in metal sensing and transport to offset metal ion toxicity against their physiological role in supporting respiratory chain, antioxidant and redox reactions. As this potentially vast topic area is confined to a single chapter, crucial roles for transition metal sensing and transport in the feedback regulation of a wealth of stress gene families are under-explored in the book.

In the preface to the volume, the Editors state that their goal was to explore metabolic and genetic responses to environmental stresses with an added emphasis on the role that these may play in defining ecological and evolutionary species traits. This goal carries with it the need to integrate the varied perspectives presented within the book and, so, the volume would have benefited from clearer organisation and a summarising chapter contrasting the unifying versus exceptional themes among stress-evoked gene responses. Whether or not the volume ultimately succeeds in achieving the task of defining exactly what constitutes 'environmental stress' and 'adaptive gene responses', depends on the perspective of the individual reader; however, my impression is that it comes a good deal closer than any other book published in this area. Its broad phylogenetic, evolutionary, ecological and molecular treatment of the topic makes it a highly recommended read for anyone interested in understanding how cells, tissues, organisms and populations sense and respond to change in the outside world.

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