
This is the first time a book has been devoted to the effects of heat stress on development and to a discussion of the roles of heat-shock proteins in development. Its chapters collect together a large number of experimental observations, many of them buried, up until now, in the developmental biology, molecular and cell biology journals. The first chapters emphasize the pronounced effects of stress on developmental events. Heat and chemical stressors are well-known teratogens, their action on certain key proteins of development being the probable reason that stress often exerts dramatic effects on embryonic morphology. A conditioning pretreatment with mild heat shock can often protect against these teratogenic effects, as discussed in detail for the snail, Lymnaea stagnalis, for the fruit fly, Drosophila melanogaster, and for mammalian embryogenesis. In metazoans this protective acquisition of tolerance is usually attributed to the synthesis of stress (heat-shock) proteins. However, there is a general tendency of the text to ascribe total attribution of acquired thermotolerance to these proteins and to ignore the possibility that physiological changes caused by a mild preconditioning stress treatment may also play a role in the acquisition of stress tolerance.

A single chapter describes the use of heat-shock promoters for investigating untimely or ectopic expression of developmental proteins, a useful experimental approach that has helped unravel many of the factors controlling Drosophila development. Later chapters are devoted to the cell-specific and developmental control of stress protein synthesis. They lead us through heat-shock protein synthesis in plant tissues, seed development and germination, pollen development and germination; in the development of Drosophila and Xenopus; and finally in mammalian gametogenesis and embryogenesis. Stress proteins are often induced quite independently of stress, in response to control of the cell cycle, viral infections or exposure to cytokines. Also the heat-shock inducibility of these proteins is strangely altered in certain specialized cell types or even completely absent in certain early embryonic states. The detailed consideration given to how stress proteins and stress protein genes participate in these phenomena makes this text fascinating reading and a valuable supplement to the several books and review articles now published on the heat-shock response.


This is a massive volume recording the contributions by participants at a recent conference which was evidently well attended and successful. In the foreword, the editors give some interesting statistical information showing that there were 595 delegates from 32 countries contributing 76 talks and 415 posters. This volume contains the contributions by invited speakers as well as numerous free communications selected on the basis of not more than one per person submitting an abstract.

The contents of the book are grouped in 24 subject areas, as follows, with the number of contributions given in parentheses. 1. Gene regulation and vitamin D (15); 2. Receptors for 1,25(OH)2D3 (23); 3. Structure–function studies of vitamin D steroids (9); 4. Chemistry of vitamin D (13); 5. Vitamin D metabolism and catabolism (5); 6. Vitamin D hydroxylases: biochemistry and regulation (19); 7. Hormone secretion and vitamin D (7); 9. Intestinal and renal transport of calcium and phosphorus (4); 10. Non-genomic actions of vitamin D steroids (9); 11. Cell differentiation and vitamin D (12); 12. Skin and vitamin D (13); 13. Cancer and vitamin D (9); 14. Immunology and vitamin D (21); 15. Bone and vitamin D (17); 16. Calbindins: structure–function and regulation (23); 17. Assays for vitamin D steroids (12); 18. Other basic science topics (15); 19. Nutrition and vitamin D (15); 20. Neonatology, pregnancy, and vitamin D (5); 21. Gerontology and vitamin D (7); 22. Osteoporosis and vitamin D (14); 23. Renal osteodystrophy and vitamin D (12); 24. Other clinical topics (30).

The book has been compiled from camera-ready papers and the quality of production is satisfactory. Research workers in the field will find it a valuable reference work but non-specialist will have difficulty in seeing the wood for the trees. In any case, the price of the book, though not unreasonable in relation to its size, will allow purchase only by well-endowed research libraries.

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Genetic variability of quantitative traits in Drosophila melanogaster (fruit fly) natural populations: analysis of wild-living flies and of several laboratory generations. Heredity, 80(3):326-335; 26 ref. Godey-Herrera R, Bustamante M, Campos P, Cancino JL, 1997. The development of larval behaviours in sympatric Chilean populations of Drosophila melanogaster and Drosophila simulans. Behaviour, 134(1/2):105-125; 33 ref. Gromko MH, 1987. Transmission of Mucor piriformis to fruit of Prunus persica by Carpophilus spp. and Drosophila melanogaster. Plant Disease, 74(4):287-291. Mizuguchi Y, de Almeida JR, Cerqueira R, de Xerez R, 1985. The fruit fly, Drosophila melanogaster, is used as a model organism to study disciplines ranging from fundamental genetics to the development of tissues and organs. Drosophila genome is 60% homologous to that of humans, less redundant, and about 75% of the genes responsible for human diseases have homologs in flies (Ugur et al., 2016). Moreover, Drosophila is equipped with a complex branched system of interconnected tubules that is responsible for the oxygen transport, the tracheal system, an organ that is comparable in structure and function to the circulatory system of mammals (Affolter et al., 2009). The freshwater snail Lymnaea stagnalis (L. stagnalis) has served as a successful model for studies in the field of Neuroscience. However, a serious drawback in the molecular analysis of the nervous system of L. stagnalis has been the lack of large-scale genomic or neuronal transcriptome information, thereby limiting the use of this unique model. In this study, we report 7,712 distinct EST sequences (median length: 847 nucleotides) of a normalized L. stagnalis central nervous system (CNS) cDNA library, resulting in the largest collection of L. stagnalis neuronal transcriptome data currently ava